## STIC-Biotech/ChemLib

From: Sent:

Ibrahim, Medina A.

Thursday, June 05, 2003 5:39 PM STIC-Biotech/ChemLib

T : Subject:

10/090, 035

(ST.C)

Please search the following:

DNA encoding SEQ ID NO:2 or 4.
 SEQ ID NO:1-4.
 oligo of SEQ ID NO:1 and 3

Please search both commercial and patent databases, including pending. Thanks

Medina A. Ibrahim Patent Examiner GAU:1638 CM1-9E03 mailbox-9E12 (703)306-5822

> **Edward Hart** Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher:
Phone:
Location:
Date Picked Up: 6 6/03
Date Completed: 6/10/03 Searcher Prep/Review:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:/	
NA Sequences:	,
AA Sequences:	F
Structures:	
Bibliographic:	_
Litigation:	
Full text:	
Patent Family:	
Other:	

, N	VENDOR/COST (where applic.) STN:
^	· · · · · · · · · · · · · · · · · · ·
#	DIALOG:
, ,	Questel/Orbit:
	DRLink:
	Lexis/Nexis:
	Sequence Sys.: (D) (O)

WWW/Internet: Other (specify):

THIS PAGE BLANK (USPTO)

•

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

THIS PAGE BLANK (USPTO)



## STIC SEARCH RESULTS

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Results Feedback Form	
> I am an examiner in Workgroup: Example: 1610	
> Relevant prior art found, search results used as follows:	
102 rejection	
103 rejection	
Cited as being of interest.	
Helped examiner better understand the invention.	
Helped examiner better understand the state of the art in their technology.	
Types of relevant prior art found:	
☐ Foreign Patent(s)	
<ul> <li>Non-Patent Literature         <ul> <li>(journal articles, conference proceedings, new product announcements etc.)</li> </ul> </li> </ul>	
> Relevant prior art <b>not found:</b>	
Results verified the lack of relevant prior art (helped determine patentability).	
Results were not useful in determining patentability or understanding the invention.	
Comments:	

Drop/off or send completed/forms to STIC/Biotech-Chemillibrary, CM1;= Circ Desk



THIS PAGE BLANK (USPTO)

```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                   em_htgo_other:*
                                       em_htg_other:*
                                                                                                                           em_htgo_hum:*
em_htgo_mus:*
                                                              em_htg_pln:*
em_htg_rod:*
                                                  htg_mus:*
                                                                                        em_htg_mam: *
                                                                                                  em_htg_vrt:*
                                                                                                               em_sy:*
                                                                                                                                                                                                                                                     Query
Match 1
Score
                                                                                                                                                                                                                                                     Result
                                                                                                                                                                                                                                                                                           O
                                                                                                                                                                                                                                                                                                                                                                                      June 16, 2003, 08:47:15; Search time 1860 Seconds (without alignments) 1455.140 Million cell updates/sec
                                                                                                                                              1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
                                                                                                                                                                                                                                                                                    4109280
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                              nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                      lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                  2054640 seqs, 14551402878 residues
                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                  Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                         US-10-090-035-2
                                                                                                                                                                          BLOSUM62
                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                        Scoring table:
                                            OM protein -
                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jatabase
                                                                     Run on:
```

```
M74590 MOUSE delta
M73963 Mus musculu
L13969 Mouse delta
AP005381 Oryza sat
AP005381 Oryza sat
AP005381 Oryza sat
AP005381 Oryza sat
AP005385 Pattus no
AL646071 Ralstonia
AL646091 Mus muscu
AL646098 Mus muscu
AL646081 Ralstonia
AL1646081 Ralstonia
AL1646081 Ralstonia
AL1646081 Ralstonia
AC100745 Mus muscu
Continuation (3 of
AC119146 Rattus no
AP003483 Homo sapi
AC016583 Homo sapi
AC016581 Homo sapi
AF016544 Mus muscu
L36435 Mus muscu
R56436 Mus muscu
                                                                          AP003416 Oryza sat
AP003436 Oryza sat
AP003436 Oryza sat
AP009108 Oryza sat
AJ242802 Sporobolu
AF291784 Sinorhizo
AF003103 Arabidops
AF002598 Arabidops
AF003563 Arabidops
AF004561 Pseudomon
ALIGLS90 Arabidops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL591665 Mouse DNA
AB023233 Homo sapi
AL33821 Neurospor
AC067762 Homo sapi
AL138704 Human DNA
AC091884 Homo sapi
SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMFLCHR16_02
                                                                                                                                                                                                                              ATCHRIV86
ATAP21
                                                                                                                                                                                                                                                                                                                                                        AC127187
AL646071
NCB24H17
BC027007
AC005960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL646081
AC100745
                                                                     57.8 173699
57.8 174218
57.8 185095
57.8 185481
44.2 562
18.3 300000
18.1 815
                                                                                                                                                                                                                            18.1 198780
18.1 206420
18.0 1898
18.0 2330
18.0 3041
                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                  158414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.5
87.8
87.8
87.8
87.8
87.8
87.8
87.8
```

ALIGNMENTS

RESULT 1

9b\_sts: \*
9b\_sts: \*
9b\_sy: \*
9b\_un: \*
9b\_vi: \*
em\_ba: \*
em\_fun: \*

gb\_pl:\*

gb\_htg: gb\_in:\* gb\_om:\*

em\_ov:\* em\_pat:\* em\_ph:\*

em\_or:\*

em\_in:\* em\_mu:\* em\_om:\*

em\_pl:# em\_ro:# em\_sts:# em\_un:#

```
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Direct Submission

AL Direct Submission

AL Submitted (14-Mar-2001) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(B-mail:tsasaki@nias.afferc.go.jp, URL:http://rgp.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 7002 this sequence version replaced gi:18181981.

On May 15, 7004 this sequence version replaced gi:18181981.

On May 15, 7002 this sequence version replaced gi:18181981.

On May 15, 7002 this sequence version replaced gi:18181981.

On May 15, 7004 this sequence version as searched against (ctp://ncbi.nlm.dh.gov/blast/db) and the cDNA sequence database at (ftp://ncbi.nlm.dh.gov/blast/db) and the cDNA sequence database at Kgp. Protein homologies of the coding regions were searched against Kgp. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTN 2.0 with the corresponding DBJA accession no. and RGP clone ID.

A gene with identity or significant homology to aprotein is classified based on the protein name to indicate the homology (covering such as same name, 'putative' and 'like protein'. A gene preddicted with a gene preddiction of the sequence is from try the sequence of Pd456E05 clone has an overlap with P0470Al2 (DDBJ: This sequence of Pd456E05 clone has an overlap with postiled annotation of this entry is available at his minotation of this entry is available at hitp://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"WCCLMFISTCACVCVERQOTQNADWLATPPAPAFAAAAFALYYY
YWLASCSDQNQCVAHARWRAVWASIIIN"
YWLASCSDQNCCVAHARWRAVWASIIIN"
YWLASCSDQNGCVAHARWRAVWASIIIN"
12007, 12076,12765, 12881,
13131, 13310, 13459, 13587,13600, 13758,14527, 14631,
15002, 15131,15421, 15487,17632, 17717,17924, 17952))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(11701. .11960,11998. .12076,12765. .12881, 13131. .13310,13459. .13587,13660. .13758,14527. .14631, 156002. .15131,15421. .15487,17632. .17717,17924. .17952))
          PLN 17-MAY-2002
                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                          Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0456E05.
AP003416
                                                                                                                                                                                     Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA.
clone:P0456E05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                   Sasakl, T., Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="p0456E05"
join(9483 .9641,10723. .10785)
/gene="p0456E05.1"
join(9483 .9641,10723. .10785)
/gene="p0456E05.1"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB92602.1"
/db_xref="G1:20804923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Only in Database (2001)
2 (bases 1 to 173699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"taxon:39947
                                                                                                                                                AP003416.4 GI:20804922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
AP003416/c
                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                    VERSION
KEYWORDS
SOURCE
```

COMMENT

```
join(36977. _37082,37255. _37479,37607. _37701,37823. _38015,
38424. _38764.39169. _39399,39493. _39645)
/gene="P0456E05.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .38015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22377. 22536)
/gene="p0456E05.3"
join18574. 21678,18821. .18984,20752. .21058,21870. .22177,
22377. .22536)
/gene="p0456E05.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                            RFLAATRPISVQGDLNLFPSLPYSCSLAAAGLVL"
join(18574. .18678,18821. .18984,20752. .21058,21870. .22177,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="WRPSAAAGGGGGGGRRKAAAAAAAASREWLVVPASGQARVEEA /translation="WRPSAAAGGGGGGGGRRKAAAAAAAAASREWLVVPASGQARVEEA GRHAVWARTGLPARDLRVLDPLLSYPSTILGRERATVWNERSYKAVITAABTLLDNSK BPAGEFCOLDGARVALASSDQAAEFTDMEGESSAVTSPFPALTSTPNELEDTNRNN NVGGWTHSNSMPTITAAKDGORTKULPFEFRALEVCLESAGKSLEEFTSTLEOGAYNN LDELTSKISHPITTAAKDGORTKULPFEFRALEVCLESAGKSLEEFTSTLEOGAYN NN DGEISFESKREVDPSQUEAVDNEDDFRESAGNORTIGTKPHIEELEMALTAFKLTR DGEISFESKREVPDPSQUEAVDNEDTRISKSPONDOFFDSTRESADVSNGTFIGTKPHIEELEMALTAFVFVD DGTLMRLSHLAREYNDOFEDYINHULDDEMONANGSTRAVVGLFGM NIGISLYADFTHETHOTHAGGGREGOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/protein_id="pabg2605.1"
/db_xref="G1:20804926"
/translation="MYKVATYFAMTFGAFLEWQSMDRVHVWIALHQDEKKERWEREQE
/translation="MYKVATYFAMTFGAFLEWGSMDRVHVWIALHQDEKKERWEREQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(26102. .26407,26766. .26901,27028. .27170, 27656. .27784. .28402,28988. .29359))
/gene="P0456E05.5" /note="hypothetical protein" magnesium transporter-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MCEGYRRAGDAAAAADVDVITSSGRRRIPAHSTVIASASPVLES
ILORRIKKERDAAAGGGKVRRAVVLIRGVTDDAAAAVRLIYAGSSGBEEIDEKSAA
OMLVLAHARYTVPWLKRRCGAAGSRITTABSVVDJMQLAALCDAPQLHLRCTRLIAKEF
RAVEKTEAMRFLQENDPWLELDILQRHHDADLRRKKRRRRREGOGVYVELSEBADCLS
HICTEGGTEVGFVGRAPAAAPCPAYATACRGLQLLIRHFSRCHRTSCPRCORWWOLLR
ILHAALCDLPDOHUCNTPLCMQFRRKEEERVAAARAKARAGDDDDKWGLLVKKVRVBRAMS
                                                                                                                                                                                                                                                                                                                                       EADSFFCFMELLSGFRDNFCQKLDNSAVG10GTLSKLSQLVAKYDGELQRYLEITTEI
NPOEYAFRWITLLLYQEFNFADTIHIWDTLLSDPDGPQGRSIYRDGTGESMYTNIETS
VAHAYQSSRNSAVPVVEKLHRCRKATGAARLQFAAAPFLSPFRSPETTENAEAPFPC
                                                                                                                                                                                                                                      GGRENETVKWALLKHENFDGSLWVGELAQLSKKVIDLDELRMLAAQGVPDGAAVRPTV
WKLLLGYLPSDRALMEQELAKKRSOYAAFKEEFLSNPYSEIIEQIDRDYKRTHPDMHF
                                                                                                                                                                                                                                                                                                          FCGDSSFAKSNQESLKNILIIFAKLNAGIRYVQGMNEILAPLFFVFRNDPDDKNANFA
                                                                                                                                                                                                     /translation="MHEPLYRVHKKQQPVTAQHRPRLRGEATTLGSIRGRRRGSPHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains EST AU070785(R10238)
/note="contains EST AU070785(R10238)
similar to Arabidopsis thaliana chromosome 3, At3948360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .37701,37823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains ESTs D46801(S11706), AU095929(S11706)"
/note="contains ESTs AU101913(S0657),AU101912(S0657) similar to rabGAP domains protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(26102. .26407,26766. .26901,27028.
27656. .27784.28154. .28402,28988. .29359))
/gene="P0456E05.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Join (36977, 37082,37255, 37479,37607, 3
38424, 38764,39169, 39399,39493, 39645)
/gene="P0456E05.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="proline transport protein-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(23558. .23638,24837./gene="P0456E05.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(23558. .23638,24837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains EST AU162265(E30874)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/protein_id="BAB92606.1"
/db_xref="GI:20804927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAB92604.1"
/db_xref="G1:20804925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0456E05.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLGKRRQMSCSQC
```

ᠬ

```
Lee,J.-S., Hahn,J.-H., Yoon,U.-H., Lee,M.-C., Yun,D.-W., Kim,H.-I.
and Eun,M.Y.
Oryza sativa PAC P0456E05 genomic sequence
L Unpublished
Lo 174218)
Lee,J.-S., Hahn,J.-H., Foon,U.-H., Lee,M.-C., Yun,D.-W., Kim,H.-I.
Cryza sativa PAC P0456E05 genomic sequence
L Unpublished
L 174218
L 2 (bases 1 to 174218)
L 2 (bases 1 to 174218)
L 3 Hahn,J.-H., Eun,M.Y. and Kim,H.-I.
Direct Submission
L Submitted (27-MAR-2001) Rice Genome Sequencing Project, National Institute of Agricultural Science and Technology(NIAST), RDA, 249
Seodun-dong, Suwon 441-707, Korea (E-mail:]hhahn@rda.go.kr,
Tel:82-31-290-0309, Fax:82-31-290-0308)
The National Program
                                                                                                                      60 GlyhisglyPheValValargGluThrargValGluGluAspIleAsnThrGysThrGly 79
157400 AACGACTACCTGATGGTGCGCGAGACCAAGGTGGAGGAGGACTTCAACACCCTGCACGGC 157341
                                              AC091071

Oryza sativa (japonica cultivar-group) chromosome 1 clone P0456E05,
*** SEQUENCING IN PROGRESS ***, 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza satīva (japonica cultivar-group).
Oryza satīva (japonica cultivar-group).
Oryza satīva (japonica cultivar-group)
Eukaryota, viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza
                            23
         40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisHisHisHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 53113: contig of 53113 bp in length 53114 53213: gap of unknown length 17404: contig of 119191 bp in length 17404: contig of inknown length 172504: gap of unknown length 172505 174218: contig of 1714 bp in length.
                                                                                                                                                                                                                                                                            157340 GAGTTCCGCGAGCGCAAGCAGAGCTTCCTGCTCAAGTCCGAC 157299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174218
57
14
19
4
                                                                                                                                                                                                                                          80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="P0456E05"
38377 c 37185 g 49417 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-2 (1-93) x AC091071 (1-174218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /variety-"Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC091071.1 GI:13450004
HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.09e-17
295.00
75.53%
60.64%
57.84%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC09107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                              RESULT 2
AC091071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                              셤
                                                                                                                         ö
                                                                                                                                                                               셤
                                                                                                                                                                                                                                          ò
/ULTAINSTACT O. L. T. LULOUNG SECOND CONTROL OF CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_de="BAB92609.1"

/db_xref="G1:080430"
/translation="WAASRRLARKLPSLISKHQRLISPEIDVEQAAESPASSSSIPLD
PSLPILPLAVSHLEPPSPLALESVHASTPAALLRILRARHHPRLAALDHLLLLAAA
SDSPAFRPDHRLTSLLASRLAESRRLPSLRRLLELVLFRPCPCTDDSIFACPELLPF
RKAILAFAASGGIPAASDALASLRRAADSPLPAEFVIILHALARRRHFDTVRFYGE
WYSTHRWHPDVYTFVIILISSCRAGVDAAMWHFOEMRRSCSPTGVSFNILMRGFFR
EGRCKEGIKVARRUKGAVEVUELILERNWVSCLGVPAGVTVLECLMKGFFR
FOLLDLVEELCFRYNVERAVEVUELLERNWVSCLGVPAGVTVLECLMKGKLDKACO
MMGRAWAABIVPDTISCNYIFEALCEAGRFVDARRLEAGAEKFORDKACO
FGRGIRRGEAAVLDEMLDAGYVPUNIATYNRILDGLHMGRSMQLQQKCSHHRNAAN"
/gene="P0456E05.9"
/gene="P0456E05.9"
/gene="P0456E05.9"
/gene="P0456E05.9"
/gene="P0456E05.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157511 GCCGGCTTCCTCGGCCGCGCGCGCGCGCGCACGTCGTCGTCGTCGTCAAGAAGAGACGTTCCAG 157452
                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene""P0456E05.7"
/note="contains ESTs AU101665(R2414), D24709(R2594)
slmilar to Arabidopsis thaliana chromosome 5, At5g14420
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetAlaTyrTyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaPro--- 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="hypothetical protein
similar to salt-inducible protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB92608.1"
/db_xref="G1:20804929"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-090-035-2 (1-93) x AP003416 (1-173699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51367. .52887
/gene="P0456E05.8"
51367. .52887
/gene="P0456E05.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.08e-17
295.00
75.53%
60.64%
57.84%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity
Best Local Similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
```

à g

셤 ŏ 셤 ò

a δy

ò

g ò

```
join(10813. 10841,11094. .11205,11289. .11432,11817. .11921,
12046. .12129,12315. .12430,12535. .12636,12715. .12828,
12916. .12972,13222. .13288,13356. .13409,13798. .13872,
13956. .13999,14389. .14490)
                                                                                                                                                                                                                                                                                                  join(10813. .10841,11094. .11205,11289. .11432,11817. .11921,
12046. .12129,12315. .12430,12535. .12636,12715. .12828,
12916. .12972,13222. .13288,13356. .13409,13798. .13872,
13956. .13991,14389. .14490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MARRENGGGTSEVGGGNGEARGERREQRSGRREARGARRELPRRG
SPASPRSGRREAGGEGSGGGRAPYINVTRRSRKPWRDSSGGRRDHAASRHDSIHT
SERTINNNGATIKLRPTENGTRERCCKPSLVTPINAGILGCHLCVLARLLCLRQGRW
RHAARHAVRNEALGYVVVLRIPSPVAATWRRKQQCATGALLPRYEAHTIENTIGE
GEEEHUVRQPPQGGLRTLRLHQQPRRYESTSCARIGGGSRAGEKHPTLNCQHQRHDRT
TDDATVRWTTLKRKTTCASVCHGRVOVWVQAPYQG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAQYYSEVDHCAEEMNRPPHAGGEHYAVRRESYEEVDEMARAGR
GHHHGNGGGGGHLGYSGSRHGDAHLGGHREEHLVHGDEHRHGHGGGRQYDSCTGQYYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="bbb90277.1"
/db_xref="G1:20161353"
/db_xref="G1:2016135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVKKQYSYREEEEYDAGGYAHHGGGŸQKOYSSYRRDEEECDAAAGGGYGRHHCAGGG
AVKOHATYKOHQAIEGYNGCGAGGYNYNRHQAVAVAGGQHHYGGATAAAYGNASNKO
HFTAAAAGHHSSGGHTQYHHQSYECEBEDSDEDDDEEDDDDESDDDDGHCPPSROG
SVHSYHQAAYQHEEKQHAGGRNHYHAYERHEEHGGGAQRYQKYESSTQVGYAGGGGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGAEGLAPGIVVPETDLYLRRLWGEPSEDLTSQPRYLITFTYGYSQRANIDAAVKKFS
ENTIMEHYDGRYNDWDEFFWSKRAIHVSVRRQTKWWYAKRFLHPDIVAPYDYIFIW
DEDLSVQHFNAEAYIKLVRKHGLEISQPGLEPDKGLTWQWTKRLGDQEVHKYTEERPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(19564. 19724,21382. 21688,22059. .22217,
22387. .22505,22923. .23035,23239. .23318))
/gene="P0470A12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="maktaligrssglprsnegmrllfsavigvmlgylfgisfptvn
vtklhfpssiisyiedkdsgittotllnhamtsanskknnsesnsdeipkiyvptnp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WCTDPHLPPCAAFVELMATVESRDAWROVWHMIQNDLVHGWGLDFALRRCVEPAHEKI
GVVDSOWVIHQVIPSLGNQGTAENGRTPWEGVRARCRKEWGMFQKRLADAEKAYYLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(19564. .19724,21382. .21688,22059. .22217,
22387. .22505,2923. .23035,23239. .23318))
/gene="P0470A12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(27239. .27499,30542. .30622,30720.
30998. .31165))
/gene="P0470A12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5, P0574H01.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(15118. .16344)
/gene="P0470A12.2"
/note="contains_EST_AU069076(C51993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to Oryza sativa chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(23929, .24237)
/gene="P0470A12.4"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="p04/0A12.4"
complement(23929. .24237)
/gene="p04/0A12.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB90279.1"
/db_xref="G1:20161355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(15118. .16344)
/gene="P0470A12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB90278.1"
/db_xref="G1:20161354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB90276.1"
/db_xref="G1:20161352"
/db xref="taxon:39947"
                                                                                                                                                                                                                                                                                 'gene="P0470A12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="P0470A12.1
                                                                            'clone="P0470A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

AL Shamitted (21-Mah-2001) Takuji Sasaki, National Institute of
Direct Submission

Direct Submission

Al Submitted (21-Mah-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(F-mali tsaaskifelias affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7460)

On Oct 17, 2001 this sequence version replaced gi:13430001.

Genes were predicted from the integrated results of the following:
Genes were predicted from the integrated results of the following:
GRNSCANI.0, BLASTNI.0, BLASTNI.0, BLASTNI.0, BLASTNI.0, BLASTNI.0, BLASTNI.0, BLASTNI.0, DIAGEDIA GATABASE, II

(ACT.)/Arcbi.nlm.in.gov/blastydb) and the cDNA sequence database at KRSP. Protein homologies of the coding regions were searched against KRSP. Protein homologies of the coding regions were searched against KRSP. Protein homologies of the coding regions were searched against the identified cDNA sequences using BLASTNI.0, With the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology (covering such as same name, 'putative-' and 'like protein.' A gene without significant homology to any protein with the protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to 77 of the PAC clone. The orientation of the sequence is from SP6 to 77 of the PAC clone. The corientation of the sequence is from SP6 to 77 of the PAC clone. The orientation of the sequence is from SP6 to 77 of the PAC clone. The corientation of the sequence is from SP6 to 77 of the PAC clone. The corientation of the sequence as a static of packal and assembly quality together with humology to specificate and sequence is from SP6 to 77 of the PAC clone. The protein and saffic 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0470A12.
                                                   Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                     39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0470A12.
                                                                                                                                                                                                                                                                                                                                                                                   40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHisGly
                                                                                                                                                                                                                     20 AlaGlyPheGlyArgHisGlyGlyValGlnGlnHisValValValLysGluLysPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0470A12
Published Only in Database (2001)
2 (bases 1 to 185095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 li. .185095)
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16292 GAGTTCCGCGAGCGCAAGCAGAGCTTCCTGCTCAAGTCCGAC 16333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP003436.2 GI:16197551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
AP003436/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
```

SGS

SOS

```
ACO91088

ACO91088

ACO91088

*** SEQUENCING IN PROGRESS ***, 4 ordered pleces.

ACO91088.

ACO9108.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All Det, J. D. J. Hamin, J. H., IOOH, D. Th., Lee, M. C., IUH, D. T., ALH, D. T., ALH, D. T., IOOH, D. T., Lee, M. C., IUH, D. T., IUH, M. Y. and Kim, H. -I.

Cr 2 (bases 1 to 185481)

B. Jaces 1 to 185481)

B. Hahn, J. H., Eun, M. Y. and Kim, H. -I.

B. Hahn, J. H., Eun, M. Y. and Kim, H. -I.

Charlette of Agricultural Science and Technology (NIAST), RDA, 249

Secdun-dong, Suwon 441-707, Korea (E-mail: jhhahn@rda.go.kr,
Tel:82-31-290-0309, Fax:82-31-290-0308)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* are represented as runs of N. The order of the pieces

* are represented as runs of N. The order of the pieces

* are represented as runs of N. The order of the pieces

* are represented as runs of N. The order of the pieces

* the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

11216 11315: contig of 11215 bp in length

* 11316 93352: contig of luknown length

* 11316 11315: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrCly 79
27343 AACGACTACCTGATGGTGCGGGAGGACCAGGAGGAGCATCAACACCTGCACCGGC 27284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetalaTyrTyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaPro--- 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                      complement(join(47978. .48051,48179. .48239,48314. .48339,48314. .49298. .49298. .49552. .49552. .49553. .49598. .50378. .50213,50317. .50378. 50507. .50561,50738. .50841,50926. .51048,51175. .51219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 AlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 GluvalAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-2 (1-93) x AP003436 (1-185095)
                                                                                                                                                                                                                                                         3.29e-17
295.00
75.53%
60.64%
57.84%
                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC091088
                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACADATATALIVANDLUGANVILLARITRU-
JOINT(40309, 40472,40627, 40802,40913, 41002,41120, 41176,
41290, 41359,41646, 41710,42307, 42361,42603, 42730,
42818, 42906,43104, 43173,43622, 43723,43820, 43909,
43983, 444311,44519, 44630,44713, 44799,46231, 46311,
/gene="Pod/70A12.7" 46836,46920, 47036)
19417(40309, 40472,40627, 40822,40913, 41002,41120, 41176,
42818, 42906,43104, 4313,43622, 43723,43820, 43909,
43983, 44131,44519, 44630,44713, 44799,46231, 46311,
/gene="Pod/70A12.7" 46836,46920, 47036)
/gene="Pod/70A12.7" 5836,46920, 47036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /procein_16="RAB90282.1"
/brocein_16="RAB90282.1"
/db_xref="G1:20161358"
/translation="MAAGGLEPSRALLLLVIAAVAVAPLASAVRPVSDAHRSAAAEL
FAASPGGSGGDLETTYEAVATROLLGVEKOKGLIGKACKFAAEKLASSSSSPARDLEH
FAASPGGSGGDLETTYEAVBREKATIKOTROLLELYSVGGLISIREGHUVVLPD
ANTISGVLKCSVDSGVYDDVATRLKATIKOTROLLELYSVGGLISIREGHUVVLPD
ANTISGVLKCSVDSGVYBDVATRLKATIKOTROLLELYSVGGLISIREGHUVVLPD
ANTISGVLKCSVDSGVYDDVATRLKATIKOTROLLELYSVGGLISIREGHUVVLPD
KNDIVKLEPDIKSVDGTFYFDEKVVDARSTFAAGIALEALSAVVSTSPAAVASGKLNI
FGSAAPPLANVLAGGSAKDCFNQIEVPPLVLSLPSKYPSLTSKDOLKVEVTTV
ISLAGGCHETIVATGGTNTEAIFFTKELQFDLDNNVYTLDIAPLKIDVGKTSVETTV
ISLAGGCHETIVATGGTNTEAIFFTKELQFDLDNNVYTLDIAPLKIDVGKTSVET
ISLAGGREYEYTGGTTREPREPGRYFREHQVFLKKHDESKVEHLFVVGGSRQFKTS
VSLSANHLQKLRLSFGLSTPELGKTFRFPHQYFLKKHDESKVEHLFVVGGSRQFKTS
PESKFGKKEISHFRSPEKRPPKELSFAFFGLTLLPIVGFLIGLMRLGVNLKNFPSL
PRAKQEKRYLSGRYDLELAVGDAAMENSFLRALGHIELDDFAPREPREPRAPQPAQUD
PRABAFASLFHAGIGAVLLYVLFWIKLDLFTLKYLSFLGVFLVFVGHRALSYLSST
SAKQKTA"
                                                                                                                                                                                                                                                                                        /translation-*MDSGGTASPAGVAGDGAGGRGSVFRGDDAPKLLAALKEMKEGLD
LUTGKVKALTRKVKKNQLPTADGIGYLEAKHHLLLSYCQDIVYYLLRKAKGLSVBGHP
VVSRLVEIRELEKIRPIDKKMEYOIQKLTNAADSGAAQEKEVDYCSEEVRSVTPIGG
FLGRGGYQDHVVKETFQEIDRSGSGRHHHNNHGNDYLMYRETKVEEDFNTCTGEFR
ERKQSFLLKGD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join) 34770. 34734,34836. 34921,35025. 35117, 35201. 35364,35440. 35601,35682. 35861,35978. 36414, 36513. 36568) 
//gene="P0470A12.6" //gene="contains ESTs AU058030(C61369),AU088621(C61369)"
ement(join(27239. .27499,30542. .30622,30720. .30899,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(34470. ,34734,34836. ,34921,35025. ,35117,
35201. ,35364,35440. ,35601,35682. ,35861,35978. ,36414,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(47978. .48061,48179. .48239,48314. .48378,48478. .48759,48837. .48911,49020. .49094,49242. .49288,49552. .49625,49763. .49964,50111. .50213,50317. .50376,50307. .50561,50738. .50841,50926. .51048,51175. .51219,
                                          30998. .31165),
/gene="pod70A12.5"
/note="contulns EST AU070442(S15668)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51967. .52059,52148. .52561))
                                                                                                                                                                                                                   /protein_id="BAB90280.1"
/db_xref="G1:20161356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36513. .36568))
/gene="P0470A12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
```

CDS

gene

```
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11481430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gouzy, J.
                                                           143
                                                                                                          Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
SMES91784/c
                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
PUBMED
                                                              BASE COUNT
ORIGIN
                                                                                                                       ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                        Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                   156781 GGGGGCTTCCTCGGCCGCGGCGTGCAGCACGTCGTCAAGAAGAGAGCTTCCAG 156840
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Autorial actions at a stapfianus.
Sporobolus stapfianus.
Sporobolus stapfianus.
Sporobolus stapfianus.
Sporobolus stapfianus
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Viridiplantae; Streptophyta; Diliopsida; Poales; Poaceae; PACC. Clade; Chloridoideae; Eragrostideae; Sporobolus.

I (bases 1 to 562)
Neale,A.D., Blomstedt,C.K., Bronson,P., Le,T.N., Guthridge,K., Frans,J., Gaff,D.F. and Hamill.J.D.
Frans,J., Gaff,D.F. and Hamill.J.D.
Gessication of the resurrection grass Sporobolus stapfianus Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SST242802 562 bp mRNA linear PLN 27-NOV-1999 Sporobolus stapfianus mRNA for putative glycine-rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                                                                                                                                                                                                                                                             39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (27-Max-1999) Neale A.D., Biological Sciences, Monash
University, Wellington Rd Clayton, Victoria, 3168, AUSTRALIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             20 AlaclyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLySGluLySPheGlu
                                                        1. 185481
/organism="Oryza sativa (japonica cultivar-group)"
/organism="Oryza sativa"
/db_xref="taxon:39947"
/chromosome="1"
/clncmes="10470A12"
a 41522 c 41493 g 50653 t 374 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138783: contig of 45331 bp in length 13883: gap of unknown length 14 185481: contig of 46598 bp in length. Location/Qualifiers
                                                                                                                                                                                              185481
57
14
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .562
Coganisma-"Sporobolus stapfianus"
/db_xref-"taxon:56623"
/clone-"SDG137c"
                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                              US-10-090-035-2 (1-93) x AC091088 (1-185481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ242802.1 GI:6478143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 562)
                                                                                                                                                                                               3.3e-17
295.00
75.53%
60.64%
57.84%
  93453
138784
138884
                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neale, A.D
                                                                                                                                              ิส
                                                                                                                                              51439
                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                        Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
SST242802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                 FEATURES
                                                                                                                                                                                                                       Score:
                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
Direct Submission
Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO
EU Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MELILO EU Consortium:
Laboratoire de Biologie Moleculaire des Relations
Laboratoire de Biologie MOR215-CNRS-INRA, BP27, F-31326 Castanet,
Plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
France, Laboratoire de Genetique et Developpement UMR6061-CNRS,
France, ARTG GmbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany,
Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25,
D-33615 Bielefeld, Germany, Unite de Biochimie physiologique,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SME591784 300000 bp DNA linear BCT 05-JUL-2002 Sinorbizoblum meliloti 1021 complete chromosome; segment 3/12. AL591784 AL591688 AL591784.1 GI:15073438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sinorhizobium melliloti.
Sinorhizobium melliloti
Bacteria; proteobacteria; alpha subdivision; Rhizobiaceae group;
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.

Rhizobiaceae; Sinorhizobium.

1 (bases 1 to 30000)
Boistard,P., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J.,
Gapela,D., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J.,
Godite,P., Becker,A., Butry,M., Cadleu,E., Dreano,S., Gloux,S.,
Godite,T., Goffeau,A., Kahn,D., Kiss,F., Lelaure,V., Masuy,D.,
Portetelle,D., Puehler,A., Purnelle,B., Ramsperger,U.,
Renard,C., Thebault,P., Vandenbol,M., Weidner,S. and Galibert,F.
Analysis of the chromosome sequence of the legume symbiont
                                                                       /translation="MAHFEEVDY EBVTSMAKPGFGRHGGGGVQOFVVKETFEEVEQV TPRGRSGHHGGHRGNGGGGGHFQARETKFERHQHAHRRVPRAGGERPCGG" 153 c 154 g 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHis 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 Gly-----GlyHisGly-----PheValValArgGluThrArgValGluGluAsp 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetalaTyrTyrGlnGlu---ValAspTyrCysSerGluGluValArgSerValAlaPro 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sinorhizobium meliloti strain 1021
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
21396507
/product="putative glycine-rich protein"
/protein_id="CAB61838.1"
/db_xref="G1:6478144"
                                                                                                                                                                                                                                  562
59
11
20
11
                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                              (1-562)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 300000)
                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-090-035-2 (1-93) x SST242802
                                                                                                                                                                                                                                       3.68e-13
225.50
70.00%
59.00%
44.22%
```

gene

CDS

FEATURES

```
WDPRFAAAGSGGASGQFGLLPLLAGTLYIAFVAMLFAVPIGLFAAIYWAEYASPRLRS
TAKPLLEVLAGIPTIVYGFFALVTVGPFLRDISTQLNGLVTGNYQNFIQAQSVTTAGI
VWGIMLIPFYSSLSDDIITQVPRALRDGSLGLGATRSETVKKVILPAALPGIVGALLL
TASRAVGETMIVVLAAGVAARWQLNPLEPMTTVTVKIVNQLTGDLEFTSPQTLVAFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="PROBBLE PHOSPHATE TRANSPORT ATP-BINDING ABC
TRANSPORTER PROTEIN"

/protein_di="Cac4c805:1"

/db_xref="Cac4c805:1"

/db_xref="SPTEMBL:0928a1"

/db_xref="SPTEMBL:0928a1"

/db_xref="SPTEMBL:0928a1"

/dranslation="MNIMSEAAVERALDQKMNTVPYKMIGNDVSVYYGEKRALFDVNL

NIRENTVYTALIGPSGCORSTELATIONNNDTTENTOFTIDTEDITORSIDVVEL

RARVGWYFORPNFPKSIYDNVSYGFRIHGLARTKAELDEVYTSLGKAGLMNEVKDR

LQEPGTGLSGGQOORLCIARAVAVSPEVILMDEPCSALDPLATAKVEELIHELRAFT

10TYTHSMQAARVSQRYTAMFHLGNLVEENDTDKMFTNPDDQRTGDYIMGREG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="PROBABLE PHOSPHATE TRANSPORT SYSTEM
TRANSCRIPTIONAL REGULATOR PROTEIN"
/protein_id="Cac45086.1"
/db_xref="G1:1507344"
/db_xref="SWISS-PROT:052989"
/translation="MSHAHIMSAFDEELKYLTRRISEMGGLAEQMVADSVRALVNSDL
                                                                                                                                                                                            GITLEVITIGATION CONTRINGUE TO THE TOTAL OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4959. 5672
/gene="phoU OR SMC02141"
4959. 5672
/gene="phoU OR SMC02141"
/function="cell processes; transport of small molecules"
/function="cell processes; transport of small molecules"
/note="Product confidence: probable
gene name confidence: probable
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       small molecules"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="cell processes; transport
/note="Product confidence : probable
Gene name confidence : probable
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/evidence=not_experimental
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start-1
/evidence-not_experimental
/transl_table-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="pstB OR SMc02142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/transl_table=11
/product="PUTATIVE PHOSPHATE-BINDING PERIPLASMIC PROTEIN"
/product="PUTATIVE PHOSPHATE-BINDING PERIPLASMIC PROTEIN"
/protein_id="CAC45081.1"
/db_xref="STREMBL:0928A4"
/db_xref="STREMBL:0928A4"
/franslation="MKSLEKTVAALVASAAFAGVAARDQIQVAGSSTVLPYAKIVAE
NFGETFPDERTPYVESGGSSAGLKEFCKGVGEDTIDIANSSKRIKDSEVEACKAAGVT
EIOEVKIGYGDIVFATDAGNADALAKPEHLYKALABEIVVDGKLUNNPYKKNSEVDAS
LDDABIAAYIPGEKHGTRENFEREILAAGCKDSGADVIKAAVSDERQGFSKCVAVRK
DGMAVDIDGDYTETLARIASNKNGIGVFGLSFYENNADKLKVATVNGIVPSTETIASG
EFVVSRRAHIGVIPGLKEYVEFFVDDQMIGPDSFLAEVGLVAAPDAEREEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="Ca045082.1"
/db_xref="C1:15073440"
/db_xref="C1:15073440"
/db_xref="C1:15073440"
/translation="MSTSLLLIAIIGFIAFLAGRARSFARSGGKLASLHSLPGYHG
SYVAIWAMLPALLLIAWLIAAPIYIDYTYRSSLPEPVQNGGAATVQLALGOVKSVAA
GFERLSADELAAIENGSTNMREVLASKGVALAGEGEPYMVOSAAQFNAMRQYSKWLMS
AVVLLVSVAGGLYAIRNIDVRFRAAIGWSASCSARSSSPRP"
Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20, B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6, B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr http://sequence.toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAC45083.1"
/db_xref="G1:15073441"
/db_xref="SPTREMBL:Q92SA3"
/translation="MLGSLIVASSALILTTVGIVASMLSEAGREFTMVSPFEFFFGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"PROBABLE PHOSPHATE TRANSPORT SYSTEM PERMEASE ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1241. 1846
//gene="SMc02145"
1241. 1846
//gene="SMc02145"
//function="miscellaneous; hypothetical/partial homology"
//note="product confidence: hypothetical
Gene name confidence: hypothetical
predicted by Codon_usage
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 small molecules"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1813. 2724
/gene="pstC OR SMC02144"
1813. 2724
/gene="pstC OR SMC02144"
/gene="pstC OR SMC02144"
/function="cell processes; transport of small molecules"
/note="product confidence: probable
Gene name confidence: putative
predicted by Codon_usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/evidence=not_experimental
/transl_table=11
/product="HYPOTHETICAL SIGNAL PEPTIDE PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115...1149
//gene="skc02146"
//gene="skc02146"
//function="cell processes; transport of sme
//note="product confidence : putative
Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                            /organism-"Sinorhizobium meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                        /strain="1021"
/db_xref="taxon:382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSPORTER PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SMc02146"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                     .1149
```

gene

SOS

gene

CDS

```
218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
ATAJ2598
REFERENCE
AUTHORS
                                          TITLE
JOURNAL
                                                                                                                                                                                             CDS
                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                       BASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19931 CGTCATGCCTTCGATGGCATTGGTCTGGCCGTCATTGAGGTTGATGGCGGCGGCGATGAG 19872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19811 ATAAAGGGCAATCGCCTCCATGACGGGTACGGTCAGGATCACGGT------CGAAAG 19761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear PLN 27-JUL-1997 protein RAP2.10 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

[ (bases 1 to 814)  
Okamuro J.K., Caster, B., Villarroel, R., Van Montagu, M. and
alaokvisddtilddaeroigekalvtiakropmasdlreimgsirlaadlervgdlg
kntakrviavagsgiprklarglehlaelalvolkevldvyasrspekansirerdbe
idaiytslerelliymmedprnitpcthllecaknierigdhatniaetiyymatgao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GlyHisGlyPheValValArgGlu 67
                                                                5783. .6466
/gene="phoB OR SMC02140"
5783. .6466
/gene="phoB OR SMC02140"
/gene="phoB OR SMC02140"
/function="small molecule metabolism; global functions;
                                                                                                                                                                                                                                     /product="PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGluLysPheGlu-----GluValAspThrValSerArgAlaGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AlaAsnHisHisHisHisGlyHisHisGly-----AlaAsnHisHisHisGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19760 CGAAGGGCGAGGGGATGTTCACCACTGCCTGCATGCGGTTGGCGAGCGC 19710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jofuku, K.D.
The AP2 domain of APETALA2 defines a large new family of binding proteins in Arabidopsis
Proc. Natl. Acad. Sci. U.S.A. 94 (13), 7076-7081 (1997) 9738147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 ThrArgValGluGluAspileAsnThrCysThrGlyGluValHisGluArg 84
                                                                                                                                                                                                                                                                                                                                                   300000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF003103
Arabidopsis thaliana AP2 domain containing partial cds.
                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                       global regulatory functions" // note="predicted by Codon_usage
                                                                                                                                                                                                                                                                       /protein_id="CAC45087.1"
/db_xref="GI:15073445"
/db_xref="SWISS-PROT:052990"
                                                                                                                                                                                                   /codon_start=1
/evidence=not_experimental
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-090-035-2 (1-93) x SME591784 (1-300000)
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                    predicted by Homology
predicted by FrameD"
                                                  PQGERPKDDMTSTLGSVTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĀF003103
AF003103.1 GI:2281644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                   1,01e+03
93.50
39.18%
28.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....... 09
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity
                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF003103
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                           ..
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
/Lranslation="refersblikervpllsswptcssispsacnreavnitsfeffif
Kisldrefcgflkspekttmetatevatvvstpavtaavatrrdkpykgirmekwg
kwyaeirepnkrsriwlgsysfpeaaaraydpavtrikgesarlnepellagvtvtgg
Ggggvugggdwsayiirraaevgaqvdaleaaggskrihhhhqqqqnkhybvdnhs
Dyrikddlmecsskegfrkcngslervdlnkledpeftsddd"
278. .445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLN 23-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TINY-like protein.

Arabidopsis thaliana.

Arabidopsis thaliana.

Arabidopsis thaliana.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Prassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                                                          Santa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1. .781
/note="putative DNA binding protein; similar to A.
thaliana APETALA2 encoded by GenBank Accession Number
                                                                                                                                                                                                              'note="similar to EST with GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 815)

Energyn, N., Heijnen, L., De Keyser, A., Van Asseldonck, M., De Clercy, R., Verbakel, H., Gielen, J., Zabeau, M., Villarroel, R. Jesse, T., Neyt, P., Hogers, R., Van Den Daele, H., Ardiles, W.,
                                       Jofuku.K.D.
Direct Submission
Submitted (08-MAY-1997) Biology, University of California,
Cruz, CA 95064, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              /codon_start=2
/product="AP2 domain containing protein RAP2.10"
/protein_id="AAC49776.1"
/db_xref="G1:2281645"
2 (bases 1 to 814)
Okamuro,J.K., Caster,B., Villarroel,R., Van Montagu,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  815 bp mRNA linea Arabidopsis thaliana mRNA for TINY-like protein. AJ002598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814
124
117
511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                              /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
1. .814*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.000 . 445
/note="encodes AP2 domain"
/note="encodes AP2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-090-035-2 (1-93) x AF003103 (1-814)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ002598.1 GI:2632062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.82
92.50
50.70%
33.80%
18.14%
                                                                                                                                                                                                                                         T76017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
DB:
```

```
Spermatophyta; Magnollophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae; eurosida II; Brassicales; Brassicacee; Arabidopsis.

1 (bases 1 to 1009)

Scheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carnhocl, P., Dale, J.M., Goldsnith, A.D., Hayashizaki, Y., Ishida, J., Jang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Onodera, C.S., Palm, C.J., Pham, P. K., Quach, H.L., Sakurai, T., Satou, M., Seli, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Arabidopsis cona clones
                                                                                                                                                                                                                                                                                                                                         To Charles I to 1009)

1S Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bubyer, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Laminch, P., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lih, J., Liu, S.X., Miranda, M., Narusaka, M., Mayven, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, T., Yamanura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, K.W., Theologis, A. and Ecker, J.R.

Submitted (24-SEP-2001) Salk Institute Genomic Analysis Laboratory (SignAL), Plant Biology Laboratory, The Salk Institute for Hallogy Laboratory, The Salk Institute for Hallogical Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Cheuk R., Chan. H., Kim.C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin Neumann, G., Lean, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu,G., Yu,S., Davis, R.W., Theologis, A., and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="AT4936900/C7A10_460"
/protein_id="AA115314.1"
/brotein_id="AA115314.1"
/brotein_id="C1:16323159"
/translation="ATETATEVATUSTPAVTYAAVATRKRDKPYKGIRMRKWGKWVAE
IREPNKRSRIWLGSYSTPEAAARAYDTAVFYLRSPSARLNFPELLAGYTYTGGGGGV
NGGGDMSAAITRRKAAREVGAQVDALEAAAGAGGNRHHHHHQHGRGNHDYVDNHSDYRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAS (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ಭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIS. Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDLMECSSKEGFKRCNGSLERVDLNKLPDPETSDDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RAFL09-50-B19(R14720)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="compared to genome'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202. .792
/note-"TINY-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1009
183 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /replace-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                          REFERENCE
                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                               Terryn, N. S. E.

S Terryn, N. S. E.

Direct Submission

L Submitted (14-NOV-1997) Terryn N. S. E., Genetics, Flanders
Interuniversity institute for biotechnology, K. L. Ledeganckstraat
35, 9000 Gent. BEGINM

this CDNA is corresponding to EST 140D13 (T76017).

I. Cortion/Qualifiers

1. 915

/organism="Arabidopsis theliana"
/db_xref="Exacn:3702"
/map="93.cw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="Spremel.024643"
/tlanslation="Ffetssllrfruplisswptcssispsacnrfavnitsfffif
Kisldrffcgflkspekttmetatfravyorapavyaaavangreffif
Kwaelfredhrrbritigsystpeaaaraydtavfilgspremerpfilgstrupgyrggggvngggdwsaayirrraevgaovabartydragavarggggvngggdwsaayirrkaaevgaovabalbaagaggnrhhhhqqrgnhdyvungs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY057683 1009 bp mRNA linear PLN 22-OCT-2001
Arabidopsis thaliana AT4g36900/C7Al0_460 mRNA, complete cds.
AY057683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg 69
Schueller,C., Mayer,K., Dehais,P., Rombauts,S., Van Montagu,M., Rouze,P. and Vos,P.
Evidence for an ancient chromosomal duplication in Arabidopsis thaliana by sequencing and analyzing a 400-kb contig at the APETALA2 locus on chromosome 4
FEBS Lett. 445 (2-3), 237-245 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   815
24
12
24
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        665 ATTAATGATCTTATGGAGTGTAGTAGTAAA 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"TINY-like protein"
/protein_id-"CAA05630.1"
/db_xref-"GI:2632063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"TINY-like protein"
/product-"TINY-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-090-035-2 (1-93) x ATAJ2598 (1-815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY057683
AY057683.1 GI:16323158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana.
thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.83
92.50
50.70%
33.80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLI_CDNA.
Arabidopsis t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                 10094464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                      Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                JOURNAL
                                                                                                                                      MEDLINE
                                                                                                                                                              PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                        COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
AY057683
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

õ

ö g

```
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stover. C. V. Phan, X.O., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowaik, D.J., Lagrou, M., Garber, R.L., Golter, P.L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brinkman, E., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R., Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Hackey, M.J., Brinkman, E., Hugrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, R.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wogg, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E. W., Lory, S. and Olson, W.V.
Direct Submission Lory, S. and Olson, W.V.
Direct Submission Genome Center, University of Washington, University of Washington Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10757 bp DNA linear BCT 30-AUG-2000 PA01, section 122 of 529 of the complete
                                                                                                                                                                      196 GGAGGAGGAGTGAACGGTGGTGGAGATATGTCGGCGGCGTATATAAGGAGAAAAGCGGCG 555
                                                                                                                                                                                                                                              615
                                                                                                                                                                                                                                                                                                       69
                                                                                                                                    GlyPheGlyArgHisGlyGlyGlyGlyGlyGlnGlnHisValValVsGluLySPheGlu 39
                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                            53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
                                                                                                                                                                                                            AsnHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="probable MFS transporter"
/protein_id="AAG04705.1"
/db_xref="G1:9947254"
                                                                                                                                                                                                              24
11
11
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pseudomonas aeruginosa'
               Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                 70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
Matches:
                                                     Indels:
                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:287"
110. .1651
                                                                                                        US-10-090-035-2 (1-93) x AY057683 (1-1009)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PA1316"
/110. .1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110. .1651
/gene="PA1316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:9947253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 10757)
92.50
50.70%
33.80%
18.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE004561 AE004091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE004561.1
                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE004561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome.
                  Percent Similarity:
                                                                                                                                              21
                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sonrce
                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
AE004561/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                  Op
                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                 g
                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                            õ
                                                                                                                                               ò
```

7.

```
/translation="MSTAVLNKHLADAHEVGHDHDHAHDSGGNTVFGFWLYLMTDCVLFASSYFATYAVLVHHTAGGPSGKDIFELPYVLVETAILLVSSCTYGLAMLSAHKGAKGG AIAWLGVTFLLGAAFIGMEINEFHHLIAEGFGPSRSAFLSSFFTLVOMHGLHVSAGLL WMLVLMAQIWTRGLTAQNNTRWMCLSLFWHFLDIVWICVFTVYYLMGAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="GI:9947258"
/translation="MSSAAHDNHGAGHGSLGSYAIGFVLSVILTAIPFYMVMDGGFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFTMGSGGDVNGFFGVATMLISIPTGVKLFNNLFTIYKGRLRFSTPILWTLGFNVTFT
IGGNTGVLLAIPGADFLLHNSLFLIAHFHNTIIGANVGTLAGFAFKFRFAFUDE
KWGKRSFWGUNGFYNAFBHPITILGFRGMTRLNHYDNPLMKPYLVVAFFGRAVLIFCG
KAGCALGFVSVRNRKGLADVNGDPRGKTLEWATSSPPFYNRAELPKVODVDAFHD
MKKAGTAYRKLPAYOPIHMFKNTAAGFSIAVFAFVFGFAAINHIWMLMAVGFVGMIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AGG04706.1"
/db_xref="G1:9947255"
/db_xref="G1:994725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLGEFARTGWVAYPPLSELAYSPGVGYDYTWALQISSMGTLLTGINFLYTVFKKRTP
GWKLMOMPIFFWTCTFANILIVASFPILTAALGLLSLDRYLDMHFFTNELGGNAMMYI
NLFWAWGHPEVYILILPAFGIFSEVTATFAGKRWFGYKSMVWASAAITFLGFTVWLHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="G1:9947256"
/translation="MFCKITLSANPYHEPIVMVTLAVVALLGLGVVGAITYYRKWTYL
/translation="MFCKITLSANPYHEPIVMVTGFADAIMMRGGLALABGANHGYLPPEHYDQI
FTEMLISVDHKKIGVYXIVVALVYKGFADAIMMRGGLALABGANHGYLPPEHYDGI
FTEMLYYMXIIFDNAMPFWIGLMNLAVPLGIGARDVAFPFLNSLSEWLLVVSSAMLVNVSL
                                               GWOSTFLINLPIGLIALALGEWGIEETAHPEHAAFDDIGGLISVVWIGALTYALIAAG
EGGWLSPTAWPALLIAGVGLIGFLFVERRTARPLIPHGLFROGFAVCNLASFVIGFS
GYASLFFLSLFFOOVOGASAQOAGFTATAPDFLAMGALSMLFGRLQRHVPLRRLLVLGY
LVIGLAMLAGAGGGTAXPRVGLLIVALGIGMGLAVPGTGLAVMASYARERSGMASA
TMNTLROAGMAVGTALGALLGALLSGRAIVVLGDRLBGLGIADAQRLATQAVTAHRLPGSL
AGLDAELPAALAEGFRLAMLVAGASALLAAALLWRLRVSAGFAADTVGASGRFRGVQL
RAVQGIAGALLIPGALSILTQAFHDPGQRAQVIGGWTSFSALSLILGPLLGGLLVEHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
/product="cytochrome o ubiquinol oxidase subunit III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="cytochrome o ubiquinol oxidase subunit IV"
/protein_id="AAG04709.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="cytochrome o ubiquinol oxidase subunit II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="cytochrome o ubiquinol oxidase subunit I" /protein_id="AAG04707.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIVRSYNQDVDYYVQPEEIEKIESARFQQLAKQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAG04708.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PA1319"
5260. 5889
/gene="cyoc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PA1318"
3280. .5256
/gene="cyob"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="PA1320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="PA1317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5889. .6224
/gene="cyoD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5260. .5889
/gene="cyoC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5889. .6224
/gene="cyob"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2278. .3273
/gene="cyoA"
                                                                                                                                                                                                                                                                                                                                                                                                                                 2278. .3273
/gene="cyoA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3280. .5256
/gene="cyoB'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trans!
                                                                                                                                                                                                                                                                                                                                                                                       OADRH"
```

Mon Jun. 16 14:55:54 2003

```
Arabidopsis thaliana.

ISM Arabidopsis thaliana.

Enkaryota: Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

E of Asses I to 189780)

E of Arabidopsis sequencing, project.

Direct Submission

AL Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Blochemic, Am Klopferspitz 18a, D-82152 Martinsried, E-mail: lemcke@mips.blochem.mpg.de.mayer@mips.blochem.mpg.de.project Coordinator: Mike Bewan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/this fragment has an overlap with ArCHRIV85 at the 5' end and an Overlap with ArCHRIV87 at the 3' end.

Location/Qualifiers

I. 199780

I. 199780

I. 199780

I. 199780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana DNA chromosome 4, contig fragment No. 86.
ALI61590.2 GI:7270623
                                                                                                                                                                                                         6032 GATGGTCGCGTGGCGCGCGAGAAGCCGCCGTCGATGAACGGGATCGCGGTGAG 5973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGKGGGCVPSKKKKPATTGDGPGIDDDNDATNAPIQIDDDQTTI
DGDRTTATNGGTTPAITTAAKISSPLKIFVVFYSMYGHVESLAKRMKKGVDSVEG
VEATLYRVPETLSGEVVEDMRAPVKDLEIPEITAAEITAAGSELRGEPFYKGGMAQM
RAFPDSTGSLMKEDSLAGKPAGFFVSTGTQGGGGETTAMTAITOLVHHGMLFVPIGYT
FGAGMFKMDSIRGGSPYGAGVFAGGGSREATFELALAEHQGNYMAAIVKRLAQP"
                                                                                                                                                                 4 TyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaProAlaGlyPheGly 23
                                                                                                                                                                                                                                                                                                 43
                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                  24 ArgHisGlyGlyGlyValGlnGlnH18ValValLysGluLysPheGluGluValAspThr
                                                                                                                                                                                                                                                                                                                                                                                             44 ValSerArgAlaGlyAlaAsnHisHisHisHisHis-----GlyHisHisGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="strong similarity to minor allergen, Alternaria alternata, PIR2:S43111 contains EST gb:R64949, AA651052"
                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AT4936750"
join(12203. 12795,13548. 13776)
/gene="AT4936750"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
                                 Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="minor allergen"
/protein_id="CABB0341.1"
/db_xref="G1:7270624"
                                                                                                             US-10-090-035-2 (1-93) x AE004561 (1-10757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /variety="Columbia"
//db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5972 GATCACCGAGAGCACGAAGCC 5952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ValHisGluArgArgGluSer 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                           18.14%
                        Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
ATCHRIV86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                    å
                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=1.
/product="probable TonB-dependent receptor"
/protein_1d=*Aa604711.1"
/protein_1d=*Aa604711.1"
/db_xref="c1:9947261"
/db_xref="c1:9947261"
/db_xref="c1:9947261"
/translation="MDRRNEPSPLPTRRPLAPLMLLMAACSSPALAEDAARKDDPLEL
GADTYTGEQASSRYERSASAKTAPLLOFTUTVPORVTOGONALSLRQVLSNVSG
ITFNAGEGGGGGSGDSINIRGFSRANANMQVDGLRBSAGTRSDLFRLAATUSTVRGFNSV
ITFNAGEGGGGSGDSINIRGFSRANANMQVDGLRBSAGTRSDLFRLAATUSTVRGFNSV
ITFNAGEGGGGSGDSINIRGFSTHGGAGGGTDPTRLTLSYFHQRDDNLPDYGVALNGR
KLDGYSRHDYFGMRLDEERIDDWYATKLEHDFSDFGCANLIYSTSHARDYTSAS
YDRTTYSTNGGFRLSAGTRSAGTRSAGTRSAGTRSAGTRSTAGTRYFSST
YDRTTYSTNGGFRLSAGTRSAGTRSAGTRSAGTRSAGTRSAGTRSTAGTRST
TSFNPSAGHLYTTGSGVTFATAGTRGTRSAGTRAGTRSTAGTRAGTRST
TSFNPSAGHLYTTGSGVTFATAGTRGTRSAGTRAGTRSTAGTRSTAGTRST
TSFNPSAGHLYTTGSGVTFATAGTGGTRSTAGTRAGTRSTAGTRST
TSFNPSAGHLYTTGSGVTFATAGTGGTRSTAGTRSTAGTRSTAGTRSTAGTRST
TSFNPSAGHLYTTGSGVTFATAGTGGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRSTAGTRST
                                                                                                                                                                                                                              /trans__table=11
/product="gruchrome o ubiquinol oxidase protein CyoE"
/product="gruchrome"
/protein_id="AaG0470.1"
/db_xref="G1:9947259"
/translation="WKLKRYLLIVAREGIIFGNLIAVAGGYFLAARGSVEPMLLLATVI
GLGLVVASGCYLNWCIDDRHMERTRGRYVTVGGISLKAALAHEGULGGAGFGLLW
WRTNPLITALAGFGYFVYVGLYSLWFKRRSOYGTLVGSISGAMPPVVGYCAVSGFFLAA
GAASLIAFCLMGWHSYAATAIFRLKDYSAAGIPVLPVARGIRAYTKIHIVLXILAFWA
ATLALCIGGYAGYGYLLVAVAVSLWWLAIALTGYWTADDRVWARKLFAFSIVAITALS
/364. 9552
/gene="PA132"
HATILTMVVLGLVQVVVHLICFLHMNMSSEGRWNVMAFIFTVIVILLVVGLSLWIIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MarknavkDNLEQIQHQSYSELQELLSEANSMLADSAAFAGDKA
DSANARIGALLEKANDALGKGGSAVAERSRHAVDATESYIGANPWQTVAITTAVGLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MISIKKNIGLLAWTAALAACASNPNDLPDFPEHEYAATQQVGEG
VINGDLYLTSASGAIQKGTNTKVALEPATSYMKAYYAKFGNLDAAKRDPDVQPPVLDP
RRATYVREATTDQNGRFDFDHIPNGTYXISSELTWSAQSDGKTITEGGTVTKLVTVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDLKLQLNLDNLFDKAYVERVRQVYGNQSRSSAIEYGDGRTAILSAIYAF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10757
29
7
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"hypothetical protein"
/protein_id-"AAG04712.1"
/db_xref-"G1:9947261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"hypothetical protein"
/protein_id-"AAG04713.1"
/db_xref-"GI:9947262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3283 g 1981 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10083. .10595
/gene="PA1324"
10083. .10595
/gene="PA1324"
/codon_start=-1
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7364. .9562
/gene="PA1322"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9691. .10023
/gene="PA1323"
9691. .10023
/gene="PA1323"
                                                                                                                'note-"PA1321"
                                                                                                                                                                                                      /codon_start=1
                                                                                        'gene-"cyoE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQPQKVLLTR"
                                 ADMLAMPMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3675 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.5
92.50
41.38%
33.33%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFLLGRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
```

/number=7 15954. 16061 /gene="AI4936760"	/number=7 1606216128 /gene="Ar4g36760"	/number=8 1612916204 /gene="AT4936760"	/number=8 1620516339 /gene="AT4936760"	/number=9 16340, .16439 /gene="AT4936760" /number=9	1644016520 /gene="AT4g36760" /number=10	1652116617 /gene="Artq36760" /numbr=10 1672	/gene="A14936760" /number=11 16673.:16767 /gene="A14936760"	/number=11 1676816872 /gene="AT4936760"	/number=12 16873.17001 /gene="AT4936760" /number=12	1700217073 /gene="AI4936760"	/number=13 17074 .17161 //////////////////////////////////	/gumber=13 /number=13 17162 17286	/gene="A14936760" /number="17373 17287. 17373	/gene="A14g36760" /numbe="A14g36760" /137417541	/gene="114g36/b0" /number=15 1777919152	/gene="Ar4g36770" complement(1779, .19152)	/gone="114g36//U" complement(1779. 19152) /gone="1114g3670"	/note="strong similarity to UDP-glucose Glucosyltransferase, Manihot esculenta, PIR2:S41951 Contains UDP-glycosyltransferases signature AA343-386	contains Est guistagravor /codo_start=1 /product="glucosyltransferase-like protein" /protein.id="CAB0143.1"	/db_xref="G1:7270626" /translation="MELHGALVASPGMGHAVPILELGKHLLNHHGFDRYTVFLVTDDV SRSKSLIGKTLMEEDPKFVIRFIPLDVSGQDLSGSLLTKLARAMRKALPEIKSSVMEL	EPRRYTYPOLIGTEALEVAKELGINKHVHVTTSANELAH I TRAJALAGALARAGA SIGALLIPGCSPYKFERAQOPRYT IRELAESQRIGDEVITADGYEVNYHHBLEQVYTG SFLDPENLGRYMRGYPTPVQELVRPAEPGIKHGVLDMLDLQPKESYVYYTLGYVGAL	TFEQTNELAYGLELTGHRYWWYRPPAEDDPSASMIDATANELEFULFEFULFER DE DOLL DE	IPSAYFT" complement(1777919152)
intron	exon	intron	exon	intron	exon	intron	intron	exon	intron	exon	intron	exon	intron	exou	9090	eueb	CDS						exou
1220312795 /gene=*Ar4936750"	/ number=1 1279613547 /gen=AT4g36750"	// Nambor 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	/Mumber_a 1428317541 /gene="AT4G36760" /gene="AT4G36760"	join(14283. 14342.14482. 14545).4445. 14575, 14575, 14575, 15120, 15120, 15237. 15632, 15717. 15803,15809. 15953,16062. 16872, 16872, 16802. 17073,17162. 17286,17374. 17541)	/gene="AT4G36760" /note="similarity to cytoplasmic aminopeptidase P, Rattus norwegicus, PATX:G2760920 norwegicus, brancono a monoson 1"	<pre>concains EST 9D:NSOUGO, A1330300.1 /codon_statt=1 /product="aminopeptidase-like protein" /protein_id="CAB80342.1"</pre>	/db_xref-"G1:7270655" /translation-"MASHSPELDALVVPSEDYHQSEYVSARDKRREFVSGFSGSAGLA /translation-"MASHSPELDALVVPSEDYHQSEYVSARDKRREFVSGFSGSAGLA LITRKREARLWTDGRYFLOALQOLSDEWTLMRWGEDPLVEVWMSDNLPEEBANIGVDSWC VSVDTAARROGKSFAKKNQKLITTTDLVDEVWKSRPPSEMSPVVVHPLEFSGSSYSHK	FEDLRAKLKQEGARGIVIAALDEVAWLYNTRGTDVAYCPVVHAFALLTIDSAFLYVOR KRVSDEANGYFRGLGVEVRRYTDVISDVALLASDRLISSFASKTVQHEAAKDMEIDSD QPDRIWUDPASCCYALYSKLDAEKVLLQPSPISLSKALKNPVELEGIKNAHVRDGAAV WOOT VETT NOONGEN VOA SCRYET, REPASKIKTREVENKELSIANSKEHFRG	VOLTHY LONGY THE SEPERATOR TO THE STATE OF T	GDKGYLQFEHITWAPYQVKLIDLDELITKEELDWLNITHSACALLLAFFRANKI EREMAN. KATEPYSVSA	1428314342 /gene="AT4936760" /number=1	1434314481 /gene="AT4936760"	/number=1 1448214545 /gene="AI4936760"	/number=2 14546. 11464 /gene="AT4936760"	/ 14645 14784 /gene="AT4936760"	/number=3 14785. 14873 //occmara26760"	/gume=_ A14930.00 /numbe=_ A14930.00 14874 .15158	/gene="AT4g36760" /number=4 1515915236 /rene="AT4g15760"	/ Journber 4 15632 / Jene="Artq36760"	/number=5 15633. 15716 /gene="AT4936760"	/number_0 15717. 15803 /gene="A14936760"	/number=6 15804 . 15888 /gene="Ar4g36760"	///www.er-0 1588915953 /gene-"AT4g36760"
exon	intron	exou	gene	CDS							exon	intron	exon	intron	exou	intron	exon	intron	exon	intron	exon	intron	uoxe s

```
/translation="Silinnpevlinkardeidrmigydrileesdipnipylonivset
Irlypaapmilphyaskdckyggydmprgtmiltinamaihrdpilmddppsekreere
Kegerkkimprgigrracpgsglagrivtlsigsliocfewerigeeevdmtegpglt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="cytochrome P450-like protein"
/product="cytochrome P450-like protein"
/protein_id="CAB16769.1"
/db_xref="c1:4006851"
/db_xref="SPTREMEL:02114"
/tb_xref="SPTREMEL:02154"
/translation="MEGQTLIFFEFFISLSLTFIIGRIKRRPNLPPSPSWALPVIGHL
RLLKPPLHRVFLSVSESLGDAPIISLRLGNRLVFVVSSHSLAEECFTKNDVVLANRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="similarity to cytochrome P450 Glycyrrhiza echinata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <3. .560
/gene="C7A10.10"
/note="similarity to cytochrome P450, Nicotiana tabacum,
PATX:E1188611</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contains Cytochrome P450 cysteine heme-iron ligand signature [FGLGRRACPG]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contains Cytochrome P450 cysteine heme-iron ligand signatures [FGLGRRACPG] and 474:[FGLGRRACPG]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(978. .1475,1630. .2016,2114. .2731)
/gene="C7A10.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product=cytcohrome like protein"
/protein_id="CAB16768.1"
/db_xref="GI:4006850"
                                                                                                                                           thallana"
                                                                                                                                                                                                                                 103943. .129912
/organism="Arabidopsis thaliana"
                                                                                            /organism="Arabidopsis thallana'
                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="cosmid CIC7A10.4F04"
166717. .183138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism*"Arabidopsis thallana" /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thallana"
/db_xref="taxon:3702"
/clone="cosmid CIC7A10.3A06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="cosmid CIC7A10.3A06"
189687. .192093
/organism="Arabidopsis thallana"
/db_xref="taxon:3702"
/clone="cosmid CIC7A10.4B06"
192023. .206420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="cosmid CIC7A10.4E12"
                                                                                                                                      /clone="cosmid CIC7A10.5E03"
87372. .105097
                                                                                                                                                                                           /db_xref="taxon:3702"
/clone="cosmid CIC7A10.4G12"
                                                                                                                                                                                                                                                                       /db_xref="taxon:3702"
/clone="cosmid cic7Al0.6B05"
126229. .145429
                                                                                                                                                                                                                                                                                                                                                                          /clone="cosmid CIC7A10.3F11"
144619. .166550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="cosmid CIC7A10.2C07"
171021. .189737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPKARPLEAMCRARDFVGKILPDSS"
3. .560
/gene="C7A10.10"
              /organism="Arabidopsis
/db_xref="taxon:3702"
/clone="BAC TAMU8H13"
68418. .87492
                                                                                                                 /db_xref="taxon:370;
                                                                                                                                                                                                                                                                                                                                                     /db_xref-"taxon:37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="C7A10.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  978. .2731
/gene="C7A10.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=
                                                                         source
                                                                                                                                                                                                                                   source
                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission

**Landamental Companies and Conditionator: Mike Bevan, Molecular Genetics Department, Cambridge Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, Con Mar 7, 1999 this sequence version replaced gi:4006849.

Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/S.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           PLN 30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 206420)
Bovan, M., Terryn, N., Vos, P., Heijnen, L., Mewes, H.W., Mayer, K.F.X.
                                                                                                                                                                                                                                                                                                                                                                      21 GlyPheGlyArgHisGlyGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAP21
Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment
                                 20838. .21773
/gene="AT4g36780"
comptement(f01n(20838. .21101,21528. :21773))
/gene="AT4g36780"
comptement(f01n(20838. .21101,21528. .21773))
/gene="AT4g36780"
                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: :::|||:::
77042 ATTAATGATCTTATGGAGTGTAGTAGAA. 77074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/varlety="Columbia"
/db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                                                                                                                                                                                                                                            US-10-090-035-2 (1-93) x ATCHRIV86 (1-198780)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 206420)
EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                                                                                                Gaps:
gene="AT4g36770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 1.
299707
299707.1 GI:4376087
                                                                                                                                                                                                                92.50
50.70%
33.80%
18.14%
                     number-1
                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                         Pred. No.:
                                 gene
                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAP21/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
```

exon

exon

exon

gene

CDS

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="Wildingleden"/
LHLIKPPLHRTFLSLSKSIGNAPVFHLRLGARLEVYISSRSTAESCFTKNDVLANRP
LHLIKPPLHRTFLSLSKSIGNAPVFHLRLGARLEVYISSRSTAESCFTKNDVLANRP
LHLIKPPLHRTFLSLSKSIGNAPVFHLRLGARLEVYISSRSTAESCFTKNDVLANRP
LSTISKHLGYNATYLLLGASYGOHWRNIRRIAAVEIFSTHRLNSFLYIRKLISH
LSTROSLHGFVEVENRTTLIALASNTTITMLAGKRYFGEDNDDAKLYKNLLYSBAYTSAG
AGNPIDYLSILRWYSSYEKRIKNLGARFDFLQKTVDERREKKGFTMIDHLLALQD
RLOPDYYDVINGILIKTIIAGTDTSSYTLEWAMSNILNHPBILKRARMEIDHLALQD
RLYDBSDIVMLSYLGGSTVLETLRMYPAVPLLLPHLSSEDCKYGGTDIPSGTWVILNAM
AMHRDPEVWEDPEIRKPREKEGEREKISSREKKGGTNURINNAM
AMHRDPEVWEDPEIRKPREKEGEREKISSREKKISSGAGAHRLINQALGSLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arote—"similarity to cytochrome P450 monooxygenase, Arote—"similarity to cytochrome P450 monooxygenase, Contains ATP/GTP-binding site motif A (P-loop) [ARAIVGKT], Cytochrome P450 cysteine heme-iron ligand signature
SLASKHISYGCTTVVTASYÖDHWRNLRRIGAVEIFSAHRLNSFSSIRRDEIHRLIACU
SRNSSLEFTKVEMKSHENLTFNNIRMLAGKCYYGOGAEDDPEAKKVRELIAEGMGC
FGAGNTADYLEILTWITGSEKRIKKIASRLDEFLQGLVDERREGKEKRONTWVDHLLC
LQETQPEYYTDNIIKGIMLSLILAGTDTSAVTLEWTLSALLNHPQILSKARDEIDNKY
GLNRLYRESDLSHLPYLQNIYSESLRLYPASPLLVPHVASEDCKYGGYMPRGTMLLT
NAMAIHRDPKIWDDPTSKRPRFEKEGEAQKLLGFGLGGGGTAQRHASITIGS
LIQCFEWERIGEEEVDWTEGGGGVIMPKAIPLVAMCKARPVVGKILNESA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jilo. 5137
/gene="7Al0.30"
/gene="7Al0.30"
/gene="7Al0.30"
/gene="7Al0.30"
/gene="7Al0.30"
/note="strong similarity to cytochrome P450, Glycyrrhiza cechnata, PATX:D1023287
Contains Cytochrome P450 cysteine heme-iron ligand signature 431:[FGMGRRACPG]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contains EST gb:T43640, Aa395149, T42716, T41670" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFEWERVGEDFVDMTEDKGATLPKAIPLRAMCKARSIVDKLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5994. .7942
/gene="C7504. .6494,6880. .7263,7340. .7942)
join(5994. .6494,6880. .7263,7340. .7942)
/gene="C7A10.40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"cytochrome P450-like protein"
/protein_id="CAB16770.1"
/db_xref="G1:4376088"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"cytochrome P450-like protein"
/protein_id="cAB16753.1"
/db_xref="G1:2464850"
/db_xref="SPTRRMBL:023155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=2
4465. .4534
/gene="C7A10.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4535. .5137
/gene="C7A10.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3115. .3615
/gene="C7A10.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3616. .4089
/gene="C7A10.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1090. .4464
/gene="C7A10.30"
                                                                                                                                                                                                                                                                                                                                     1630. .2016
/gene="C7A10.20"
                                                                                                                                                                                                                                                                                                                                                                                                             9017. .2113
gene="C7A10.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1114. .2731
/gene="C7A10.20"
                                                                                                                                                                                           978. .1475
/gene="C7A10.20"
                                                                                                                                                                                                                                                             1476. .1629
/gene="C7A10.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=3
                                                                                                                                                                                                                                                                                                                                                                                           number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'number=1
                                                                                                                                                                                                                                                                                                                 number-
                                                                                                                                                                                                                                           'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                                                                     intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
```

CDS

```
||| ||| :::||||||||| :::
178372 GGAGGAGGAGTGAACGGTGGAGATATGTCGCCGGCGTATATAAGGAGAAAAGCGGCG 178313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hariharan, M., Kelley, D.E. and Perry, R.P.
Bariharan, M., Kelley, D.E. and Perry, R.P.
Delta, a transcription factor that binds to downstream elements in several polymerase II promoters, is a functionally versatile zinc finger protein
Froc. Natl. Acad. Sci. U.S.A. 88 (21), 9799-9803 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROD 27-APR-1993
/translation="MDLTQILLLSFLELTISIKLLLTKSNRKPNLPPSPAYPLPVIGH
LHLLKQPVHRRFHSISKSLGNAPIFHLRLGNRLVYVISSHSIAEECFTKNDVVLANRP
DIIMAKHVGYNFTNMIAASYGDHWRNLRRIAAVEIFSSHRISTFSSIRKDEIRRLITH
LSRDSLHGFVEVELKSLLTNNAFNNIIMWVAGKRYYGTGTEDNDEAKLYRELIAEIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyPheGlyArgHisGlyGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M74590.1 GI:192940
delta-transcription factor.
Mus musculus (strain CS7BL/6J, sub_species domesticus) cDNA to
mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 Glu------AsnHisPThrValSerArgAlaGlyAla------AsnHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUSDELTA 1898 bp mRNA linear F
Mouse delta transcription factor mRNA, complete cds.
M74590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178192 ATTAATGATGATGTAGTAGTAGTAGTAAAA 178160
                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_species="domesticus"
/db_xref="taxon:10090"
43. .1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. 1898
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name="delta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-090-035-2 (1-93) x ATAP21 (1-206420)
                                                                                                                                                                                                            /number=1
6495. .6879
/gene="C7A10.40"
                                                                                                                                                                                                                                                               /number=1
6880. .7263
/gene="C7A10.40"
                                                                                                                                                                                                                                                                                                                                                     855
92.50
50.70%
33.80%
18.14%
                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1946404
                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUSDELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
```

```
/evidence-experimental
/product="tornortif DNA binding protein"
/protein_id="AAA40521"
/protein_id="AAA40521"
/db_xref="G1:20221"
/db_xref="G1:202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse delta/YY1/NF-E1/UCRBP transcription factor, exon 1. L13969 L13969.1 GI:293843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 CCGCCCATGATCGCGCTGCAGCCGCTGGTGACGGACGAC------CCGACCCAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGluGlu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HisGlyPheValvalArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3041)
Safrany, G. and Perry, R.P.
Characterization of the mouse gene that encodes the delta/YXI/MF-EI/UCRBP transcription factor
Proc. Natl. Acad. Sci. U.S.A. 90 (12), 5559-5563 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ValAspThrValSerArgAlaGlyAlaAsnH1sH1sH1sH1sH1sGlyH1sH1sGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (library: 129SV Stratagene) 4-6 weeks liver DNA.
Mus musculus
      'function="MuLV UCR-motif DNA-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2330
22
7
26
16
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription factor; zinc-finger protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="1iver"
/dev_stage="4-6 weeks"
/tissue_lib="1295V Stratagene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 ValHisGluArgArgGluSerPheLeuAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-090-035-2 (1-93) x MUSUCRBP (1-2330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601
                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                   1348. .2330
/gene-"UCRBP"
2301. .2306
/gene-"UCRBP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.34
92.00
40.85%
30.99%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8516301
                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 of 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
MUSTRANS01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
ROD 27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 H1sGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2330)
Flanagan, J.R., Becker, K.G., Ennist, D.L., Gleason, S.L., Clagers, P.H., Levi, B.Z., Appella, E. and Ozato, K.
Cloning of a negative transcription factor that binds to the upstream conserved region of Moloney murine leukemia virus 92107191
1309593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSUCRBP
Mus musculus UCR-mot1f DNA-binding protein (UCRBP) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                           1898
22
7
26
16
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M73963.1 GI:202270
DNA-binding protein; zinc-finger protein.
Mus musculus cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111111 ::: 111 ::: 337 GIGCACCACCAGGAGGIGATGATCCTGGIGCAG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 ValHisGluArgArgGluSerPheLeuAlaArg 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .2330 / Corporation of the control of the corporation of the corpor
                                                                                                                                                                                                                                                                                                                           411 t
                                                                                                                                                                                                                                                                                          KFAQSTNLKSHILTHAKAKNNO"
453 c 525 g 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-2 (1-93) x MUSDELTA (1-1898)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103. .1347
/gene="UCRBP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="UCRBP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .102
/gene="UCRBP"
                                                                                                                                                                                                                                                                                                                                                                                                                               7.56
92.00
40.858
30.998
18.048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                  509
                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
MUSUCRBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGS
                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
```

9

```
61 HisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                        Length: ...
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                   499 t
                                                                                                                                  US-10-090-035-2 (1-93) x MUSTRANS01 (1-3041)
                                                                                                                                                                                                                                                                                              Search completed: June 16, 2003, 11:37:14
Job time: 2119.5 secs
                /bound_molety="SP1"
1776. 2885
/number=1
a 886 c 980 g
1076. .1808
1728. .1737
                                                                          12.3
92.00
40.85%
30.99%
18.04%
                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                           919
 promoter
protein_bind
                                                                    Alignment Scores:
Pred. No.:
                                         BASE COUNT
ORIGIN
                           exon
                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                      셤
                                                                                                                                                                    g
                                                                                                                                                                                     à
                                                                                                                                                                                                                      ò
```

```
Job time : 1458.61 secs
                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
Ulfferentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:11 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade: Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 GACACACCAAGGGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 GGTGAGGTCGGTCGCCCGGCCTTCGGCCGCCACGGCGGCGGCGTCCAGCAGCACGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATCAACACCTGCACCGGCGAGGTCCACGAGGCGAGGGAGAGCTTCCTCGCCAGGGTA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 496
/organism="zea mays"
/outtivar="W23"
/db_xref="texon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
/fissue_type="tessel, kernal, silk, husk, root, leaf"
/lab_host="bH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                         Malze EST's from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 67.5%; Score 456.4; DB 10; Length 496; Best Local Similarity 98.5%; Pred. No. 7.5e-41; Matches 471; Conservative 0; Mismatches 6; Indels 1;
                                                                                                                       Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 227
Fax: 650 725 8227
Fax: 650 725 8221
Email: walbotestanford.edu
Plate: 945002 row: E column: 06.
                                                                                               University
Unpublished (1999)
                                                              Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486
                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                      JOURNAL
COMMENT
                                                                                                                                                                                                                                                   FEATURES
```

ð

õ g ò g ò g

g õ

õ q ò

ð

Search completed: June 16, 2003, 03:55:49 . .

```
locac....

1. .539
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="603 - stressed root cDNA library from
/clone_lib="603 - stressed root cDNA library from
/dissue_type="seedling"
/tissue_type="seedling"
/do_bost="E. coli XL Gold"
/lab_host="E. coli XL Gold"
/note="Organ: root; Vector: pBluescriptII SK(+) XR;
/note="Organ: root; Vector: pBluescriptII SK(+) XR;
/note="Organ: root; Organ: root; Organ: root; Vector: pBluescriptII SK(+) XR;
/note="Organ: root; Organ: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW787314 496 bp mRNA linear EST 16-MAY-2000 45002E06.X1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483
                                                                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACACCAACCAACGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 CCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGGGGGGCCCAGGGGTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                     USA
Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USP Tel: 650 723 2227
Fax: 650 725 8221
Email: walbockstanford.edu
Plate: 603016 row: F column: 02.
                                                                                                                                                                                                                                                                                                                                                                          Score 460; DB 9; L
Pred. No. 2.9e-41;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 ACTAATACCTACATCAAAAA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTAATACCTAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:7844111
                                                                                                                                                                                                                                                                                                                                                                              y Match 68.0%;
Local Similarity 97.6%;
les 488; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW787314.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mays.
mays
                                                                                                                                                                                                                                                                                                                                  91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
AW787314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ğ
            A1855425 539 bp mRNA linear EST 15-JUL-1999 603016F02.x1 603 - stressed root cDNA library from Wang/Bohnert lab A1855425 A1855425 GI:5499558 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
1; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACCTTGGCTATCGTACGTGCACGCA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAAT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412
                                                                                                                                                                                                                                                                                                                                                                      GGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292
                                                                                                                                                                                                                                                                                                       GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 126
                                                                                                                                                                                                                                                                                                                           CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCCGGCGCCA---ACCACCA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 CCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGGGGAGACCAGGGTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAACTGAGCCGCCCGGCGGCGATCCACGCCCGTTCGTGCTTGCCTGCGTGCTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanford
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                     tch 68.5%; Score 462.8; DB 12; Length 550; Bl Similarity 96.8%; Pred. No. 1.4e-41; 482; Conservative 0; Mismatches 13; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poclade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 539)
Walbot,V.

Maize ESTs from various cDNA libraries sequenced at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTAAAAAAAAAAAA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 ACTAATACCTACATCAAA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University
Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays.
                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484
                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 482
                                                                                                                                                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                                                                                                                                                                    113
                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                                      187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
AI855425/C
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

g ŏ g ŏ

g ŏ g δ

g ò

a ò g ò

ŏ

ä

```
S EST.

S EST.

S EST.

Zea mays.

IISM Zea mays.

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida: Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

NCE I (bases 1 to 550)

ONS Qiu,F., Gui,F., Gui,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks (ANL Unpublished (2001)

NT On May 25, 2001 this sequence version replaced g1:14206705.

Contact: Patrick S. Schnable

Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA Tel: 515-294-0975

Fax: 515-294-0975

Fax: 515-294-2299

Email: schnable@iastate.edu

PCR PRimers

FORWARD: TJ (AA TAC CAC TCA TAA G5)

BACKWARD: TJ (AA TAC CAC TCA TAA G5)

Seq primer: primer TJ-1 (AA TAC GAC TCA TAA A6)

Seq primer: primer TJ-1 (AA TAC GAC TCA TAA A6)

Seq primer: primer TJ-1 (AA TAC GAC TCA TAA A6)

Seq primer: primer TJ-1 (AA TAC GAC TCA TAA A6)

Seq primer: primer TJ-1 (AA TAC GAC TCA TAA A6)

Seq primer: primer TJ-1 (AA TAC GAC TCA TAA A6)

Seq primer: primer TJ-1 (AA TAC GAC TCA TAA A6)

Seq primer: primer TJ-1 (AA TAC GAC TCA TAA A6)

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG840383 550 bp mRNA linear EST 29-MAY-2001
MEST12-H11.T7-1 ISUM4-TN Zea mays CDNA clone MEST12-H11 5', mRNA
                                                                                                                                    303
                                           CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGGCGCGCCA---ACCACCA 243
                                                              364 TAACTGAGCCGGCCGGCGCGCGCACCCCGTTCGTGCTTGCCTGCGTGCCTTATG 423
104 GGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGGAGGCGGCGTCCAGCAGCACGT 163
                                                                                                                                                                                                    304 GGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGC 363
                                                                                                                                                                                                                            483
                                                                                                                                                                                                                                                                                                                                                                                          /hote-"Vector: pT773PAC; Site_1: EcoRI; Site_2: NotI; ds-cDNA molecules were generated as follows, First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'
                                                                                                                       244 CCACCACCATGGTCACCACGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                  424 TATGICTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Seedling and silk" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4577"
/clone="MEST12-H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="ISUM4-TN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 ACTAATACCTACATCAAAAAAA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524 AAAAAAAAAAAAAAAAAA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG840383.2 GI:14242676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG640383
                                           187
                                                                                                                                                                                                                                                                                                                                                                                                                                                     484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
BG840383
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                      ογ
                                                                       a
                                                                                                                  ò
                                                                                                                                                       g
                                                                                                                                                                                                                                       g
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
ECORI; Site_2: XhoI; ds-CDNA molecules were generated as
follows. First-strand cDNA was prepared from oligo-dr
selected mRNA by priming with an XhoI oligo-dr primer. The
resulting DNA:RNA hybrid was treated with RNASE H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-CDNAS were digested with XhoI and size-selected. The
resulting molecules were directionally cloned into the
ECORI and XhoI sites of the HybriZAP lambda vector
(Stratagene) and excised as pAD-GAL4 phagemids."
                                                                                                                                                                                                                          AA779839
MEST2-B7.TW1412.Seq ISUM2 Zea mays cDNA clone MEST2-B7 5', mRNA
    Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldee; Andropogoneae; Zea.

1 (bases 1 to 546)
Wen,T.J., Ashlock,D.A. and Schnable, P.S.
Expressed Sequence Tags from B73 Maize Seedlings
Unpublished (1997)
Contact: Schnable, PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGAGGTCGGTCGCCCGGCCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGT 186
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.7%; Score 464.6; DB 9; Length 546; 96.6%; Pred. No. 9.38-42; Live 0; Mismatches 14; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="ISUM2"
//Lisua_Lyppe="above ground tissues"
/dew_stage="Two-leaf-stage green seedling"
/lab_host="Xi1-MFR Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
Plate: WEST2 row: B column: 7
Seq primer: tw1412 (5'-GAAGATACCCACCAAACC-3')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iowa State University
G405 Agronomy, Ames, IA 50011, USA
Tel: (515)-294-0975
Fax: (515)-294-2299
Email: Schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:4577"
/clone="MEST2-87"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .546
/organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
                                                                                                                                                                                                                                                                                                        AA979839.1 GI:3157217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                     sequence.
                                                                                                                                                                                                                                                                                                                                                   Zea mays.
                                                                                                                                                                                                                                                                                                                                                                         2ев шаув
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
                                                                                                                                                                                 RESULT 12
AA979839
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
ö
                                  g
                                                                                                              g
                                                                           ò
```

õ . අ ò

```
/note="Organ: tassel, kernal, silk, husk, root, leaf; vector: pGAD10; Site_1: ECORI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A linear EST 16-MAY-2000 from Walbot lab, same as 707
                                                                                                                                                                            Zea mays.

Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

( (bases 1 to 500)

Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCAACACCTGCACGGCGAGGTCCACGAGGGCAGGGAGGCTTCCTCGCCAGGGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCACCATGGTCACCACGGCCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCCGGCGCCCAACCACCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .500

/organism="zea mays"
/outhivar="W23"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 500;
                                                                                                                                                                                                                                                                                                                Maize ESTS from various cDNA libraries sequenced at University
                                                                                                                                                                                                                                                                                                                                                                                              Department of Biological Sciences
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USi
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945002 row: E column: 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 470.6; DB 1-
Pred. No. 2.2e-42;
                                                                tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 69.6%; Score 470.6; al Similarity 99.2%; Pred. No. 2.2e 473; Conservative 0; Mismatches
                                                                       (SK) Zea mays CDNA, mRNA sequence.
                                            500 bp
adult t
                                                                945002E06.X3 945 - Mixed
                                                                                                                               AW787732.1 GI:7844510
                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                 LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
COMMENT
                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
        RESULT 11
AW787732
                                                                                                                  ACCESSION
                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGCACCGGCGAGGICCACGAGGCGCAGGAGGCTICCTCGCCAGGGCTAACTGAGCGGCC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCCGGCCGGCTTCGGCCGCCGCCGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 TCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAATACTAATACCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CTCGGAGGACACACCAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCGAGGAGGTCGACACGGTATCACGCGCCGGCGCCA---ACCACCACCACCATGGT
                                                                            οĘ
                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/db_xref="MaizeDB:637271"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone="PCO124784"
/clone="pCO124784"
Library"
           1 (bases 1 to 553)
Hainey, C.F., Dolan, W., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Anthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design overgo Probes
Unpublished (2002)
C. (bases 1 to 553)
                                                                                                                                                                                                           ŏ
                                                                                                                                                                                     Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1 . 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 474.2; DB 11; Length
Pred. No. 8.5e-43;
0; Mismatches 23; Indels
clade; Panicoideae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GCAGCAATCCACACAAGCACTTCGAAGGACCACTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mapping Project'
173 c 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cch 70.1%;
al Similarity 94.3%;
516; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAAAA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
Matches 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427
                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                      JOURNAL
                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                            FEATURES
                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

δ

ö

186 132 246

72

306

366

adult tissues from Walbot lab

0

```
/organism="Zea mays"
//cultivar="W23"
//db_xref="taxon:4577"
//clone_lib="707 - Mixed")"
      Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707009 row: E column:
Location/Qualiflers
1. 524
                                                                                                                                                                                                     / Match 71.2%;
Local Similarity 96.5%;
Nes 503; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY104409.1
                                                                                                                                                                           ಥ
                                                                                                                                                                          107
                                                                                                                                                                                                    Query Match
Best Local S
Matches 503
                                                                                                                                                                                                                                                                                                                  140
                                                                                                                                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                             320
                                                                                                                                                                                                                                                                                                                                                                                                                                               304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
AY104409
LOCUS
                                   FEATURES
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                            å
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
/note="Organ: tassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: EcoR1; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA linear EST 16-JAN-2000
tissues from Walbot lab (SK) 2ea
                                                                                                                     GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 126
                                                                                                                                                              186
                                                                                                                                                                                145
                                                                                                                                                                                                                                        306
                                                                                                                                                                                                                                                                           366
                                                                                                                                                                                                                                                                                                                426
                                                                                                                                                                                                                                                                                                                                385
                                                                                                                                                                                                   246
                                                                                                                                                                                                                     205
                                                                                                                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; PACC clade; Panicoldees; Andropogoneae; Zea. (bases 1 to 524)
Walbot,V.
Walbot,V.
Marze ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                        247 CCACCATGGTCACCACGCCGCCACGCCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGA
                                                                                                                                                                                                                                           Gaps
                                                                                                       ö
                                                                                  Score 492.6; DB 10; Length 552;
Pred. No. 8.9e-45;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     AATACCTACATCAAAAAAAAAAAAAAAAAAAA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                              707009E07.x4 707 - Mixed adult t. mmays cDNA, mRNA sequence.
                                                                                  72.9%;
llarity 97.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW288876.1 GI:6695663
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
Zea mays
                                                                                  Local S.
501;
                                                                                                                     67
                                                                                                                                                          127
                                                                                                                                                                          98
                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   446
                                                                                                                                                                                                                                                                                                                            326
                                                                                                                                                                                                                                                                                                           367
                                                                                                                                                                                                                                                                                                                                             427
                                                                                                                                                                                                                                                                                                                                                                                  487
                                                                                                                                                                                                                                                                                                                                                                                                                      547
                                                       COUNT
                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
AW288876
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                     ð
                                                                                                                                    8
                                                                                                                                                        ò
                                                                                                                                                                     유
                                                                                                                                                                                           ò
                                                                                                                                                                                                           g
                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                               윱
                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                     윱
```

```
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="bul08"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
liferentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/21/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."

a 170 c 157 g 89 t l others
                                                                                                                                                                                                                                                      139
                                                                                                                                                                                                                                                                              123
                                                                                                                                                                                                                                                                                                        199
                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                          259
                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                             319
                                                                                                                                                                                                                                                                                                                                                                                                                                                              379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                               ACCGGCGAGGTCCACGAGGGAGGGAGCTTCCTCGCCAGGGCTAACTGAGCGCCCGG
                                                                                                                                                                                               CGCAGCAATCCACACAAGCACTTCGAAGGACCACTGCTCGGAG----GACACACCAAGCG
                                                                                                                                                                                                           GCCCCGGCCGGCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCGTCAAGGAAAG
                                                                                                                                                                                                                                                                                                                  200 ITCGAGGAGGTCGACACGGTATCACGCGCGGCGCCAACCACCACCACCACCATGGTCAC
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTC
                                                                                                                                                DB 10; Length 524;
                                                                                                                                             Score 481.2; DB 10; Length
Pred. No. 1.5e-43;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY104409 553 bp
Zea mays PC0124784 mRNA sequence.
AY104409
```

g

à g ·δ QQ ŏ q δ ద

à

```
BE025302
945028B09.Yl 945 - Mixed adult tissues from Walbot lab, same as 707
(SK) Zea mays cDNA, mRNA sequence.
BE025302.1 GI:8318737
                                                                                                                                                                                                                                                                                                        486
                                                                                                                                                                                                                                                                                                                              432
                                                                                                                                                                                                                                                                                                                                                        546
                                                                                                                                                                                                                                                                                                                                                                                 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                  426
                                                                                                                                                                                                                                                                             372
                                                                                                                                                    306
                                                                                                                                                                          252
GACACACCAAGGGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 126
                                                                                                    246
                                                                                                                 186
                                                                          132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
                                                                                                                                                    CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCGGCGCGCCAACCACCA
                                                  GGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGGCGGCGGCGCGTCCAGCACGT
                                                                Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                          University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
B55 California Ave, Palo Alto, CA 94.
Tel: 650 723 227
Fax: 650 725 821
Email: Walbot estanford.edu
Plate: 945028 row: B column: 09.
1. 552
1. 552
/organism="Zea mays"
/cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 552)
Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                             427
                              13
                                                        127
                                                                                                         187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
BE025302
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                        ζŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                              g
                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                            ò
                                                                                                                             g
                                                                                                                                                         ò
                            셤
                                                      ò
                                                                              8
                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                707049E04.x1 707 - Mixed adult tissues from Walbot lab (SK) Zea mays CDNA, mRNA sequence.
AW331212
AW331212.1 GI:6627569
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1...523
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: tassel, kernel, silk, husk, root, leaf; vector: pGAD10; Site_1: ECORI; cDNA library from fully differentiated malze tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; 2ea.
                                                                                                                                                          424 TATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCA 483
                                                                                                                         TAACTGAGCCGCCCGGCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCCTTATG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 498.2; DB 10; Length 523;
Pred. No. 2.3e-45;
); Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 728 8221
Email: walbotestanford.edu
Plate: 707049 row: E column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                707049 row: E column: 04 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.7%;
ilarity 98.4%;
Conservative
                                                                                                                                                                                                                                                                  604 AAAAAA 610
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 503; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                        ESI.
                                                              364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                            AW331212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                 RESULT 7
```

	REBURY SOURCE  DEFINITION  BOG19390  DEFINITION  ROSED/3900  ROSED/3900  SERVINE CONSERVABLE SAIL STEES DE MRNA Linear EST 27-JUN-2002  ROSENIES CONSERVABLE SAIL SAIL STEES DE MANA LINEARY Zea mays rocts CDNA Library Zea sequence.  REPERENCE  BOG19390  DEFINITION  BOG19390  CARLOCACACACACACACCACACCACCACCACCACACCAC	
90 00 00 00 00 00 00 00 00 00 00 00 00 0	RESULT 6 BO619390 LOCUS DEFINITIO VERSION VORGILIN VERSION VERS	
2002	50   150   119   119   119   179   1	
540 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Ege mays Viridiplantee; Streptophyta; Embryophyta; Tracheoph Subraryots; Magnollophyta; Liliopsida; Poales; Poaceae; Pkoclade; Panicoldeae; Andropogonese; Zea.  [	
Db Db Gy G G G G G G G G G G G G G G G G G G	NICE SEE SEE SEE SOUTH NICE SEE SEE SEE SEE SEE SEE SEE SEE SEE S	

```
TÀACTGAGCCGCCGGCGGCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCTTATG 423
BQ619337 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6E12_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Wang, H. and Bohnert, H.J.
Upublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 CCACCACCATGGTCACCACGCGCCACGCTTCGTGGTGCGCGAGACCAGGGTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                     75.2%; Score 508.6; DB 14; Length 648; 96.9%; Pred. No. 1.5e-46; Live. 0; Mismatches 14; Indels 3;
                                                                                                                                                                                                                                1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                       183 9
                                                                                                                                                                                              Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
                                                                 GI:21621331
                                                                                                                                                                                                                                                                                                                                                                                        193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 96.9
Matches 530; Conservative
                                                       BQ619337
BQ619337.1
                                                                                           Zea mays.
                                               sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
           LOCUS
                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423
                                                                                                                                                                                                                                                                                                                                                                     GACACCAACCAAGCGTCTGCAACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGGCGGCGCGTCCAGCAGCACGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                           179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                         /organism="Zea mays"
/organism="Laxon:4577"
/clone="RNOSEGED01_SK.ab1"
/clone="RNOSEGED01_SK.ab1"
/tissue_type="Roots"
/dev_stage="Roots"
/dev_stage="Loots"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 CICAGCICCIGIACGAAITACGACAATAAGCICGIGACCIGAAIAAAACITCIICGIAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 TAACTGAGCCGCCCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 crcascrcrstacgaarracgacaaraagcrcsrsacrcsaaraaaacrrcrrsaar
                                                                                                                                                                                                                                                                                                                                                                                   187 CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCCGCCGCCCA---ACCACCA
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                          DB 14; Length 648;
                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                                                                                                   USA
                                                  | (bases 1 to 648)
| Wang, H. and Bohnert, H.J.
| Wang, H. and Bohnert, H.J.
| Genomics of plant stress tolerance
| Unpublished (2002)
| Contact: Mark Fredricksen
| Department of Plant Biology
| University of Illinois
| 1201 W. Gregory Dr., Urbana, IL 61801, US
| Tel: 2172655473
| Email: bohnertlab@life.uluc.edu.
| Location/Qualifiers
| Location/Qualifiers
| Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         Query Match 75.2%; Score 508.6; DB 1 Best Local Similarity 96.9%; Pred. No. 1.5e-46; Matches 530; Conservative 0; Mismatches 14
                                                                                                                                                                                                                                                                                        100 t
                                                                                                                                                                                                                                                                                          183 g
                                                                                                                                                                                                                                                                                           193 c
                                                                                                                                                                                                                                                                                mM NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAA 606
                                                                                                                                                                                                                                                                                            172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604
                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304
                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
BQ619337
                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                              à
```

1;

Gaps

3;

186 179 243 239 303 299 363 603

479 543

483

```
University of Illinois
1201 W. Gregory Dr., Urbana, IL.
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
BQ619318
BQ619318.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
                                                                                                                                                                                                    67
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604
                                                      source
                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
BQ619318
                                                                                                                                                                                                    õ
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             윤
                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ619315 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6C06_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6C06_SK.abl similar to No homology, mRNA
                                                                                                                                                     186
                                                                                                                 126
                                                                                                                       243
                                                                                                                                                                                                                             303
                                                                                                                                                                                                                                                            179
                                                                                                                                                                                              423
                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
(Dpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
                                 150
    cDNA library"
                                                                                                                                               67 GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA
                                                                                                                                                                                     CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCCGCGCGCCA---ACCACCA
                                                                                                                                                                                                                        CCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGA
                                                                                                                                                                                                                                                                                                364 TAACTGAGCCGCCCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCCTTATG
                                 at
                                                                                               Gaps
                               Stressed 24 hours
                                                                                              э
;
                                                                            DB 14; Length 648;
/clone_lib="Salt stressed Zea mays roots
/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed
                                                                       Match 75.2%; Score 508.6; DB 14; Length Local Similarity 96.9%; Pred. No. 1.5e-46; les 530; Conservative 0; Mismatches 14; Indels
                                                100
                                              183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:21621309
                                               193 c
                                     mM NaC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    604 AAAAAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 AAAAAA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
BQ619315
BQ619315.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
Zea mays
                                                                        Query Match
Best Local S
Matches 530
                                                                                                                              9
                                                                                                                                                                                     187
                                                                                                                                                                                                                         244
                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
BQ619315
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         }
                                                                                                                            g
                                                                                                            à
                                                                                                                                                                 8
                                                                                                                                                                                                    셤
                                                                                                                                                ò
                                                                                                                                                                                    ö
                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ619318 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6D01_SK.abl Salt stressed Zea mays roots cDNA library Zea .mays cDNA clone RNOSEQ6D01_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                    187 CGTCAAGGAGAAGTTCGAGGAGGTCGACAGGTATCACGCGCGGGGGCGCA---ACCACCA 243
                                                                                                                                                                                                                                                                                                                       1. .648
/organism="zea mays"
/do_ref="taxon:457"
/do_ref="taxon:4577"
/clone="RNSEOGG-6S.abl"
/clone=lib="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_stage="z weeks old"
/note="vector: pBluescript SK+; Stressed 24 hours at 150
mM Nacl"
                                                                                                                                                                                                                                                                                                                                                                  303
                                                                                                                                                                                                                                                                                                                                                                           363
                                                                                                                                                                                                                                                                                                                                                                                                                                           359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA
                                                                                                                                                                                                                                                                                                                                                            244 CCACCACCATGGTCACCACGGCGACACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                              304 GGACATCAACACCTGCACCGGCGAGGTCCACGAGGGAGGAGGGTTCCTCGCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                            TATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CICAGCICCIGIACGAATIACGACAAIAAGCICGIGACCIGAAIAAAACTICITCGIAAI
                                                                                                                                                                                   Gapa
                                                                                                                                                                                  ë.
                                                                                                                                                         648;
                                                                                                                                                       Score 508.6; DB 14; Length Pred. No. 1.5e-46;
                                                                                                                                                                                  14; Indels
                                                                                                                                                                              0; Mismatches
                                                                                                                     ų
                                                                                                                   100
                                                                                                                     ъ
                                                                                                                   183
                                                                                                                                                     75.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:21621312
                                                                                                                   193 c
                                                                                                                                                                   Local Similarity
nes 530; Conservative
```

```
June 16, 2003, 01:23:01; Search time 1439.61 Seconds (without alignments) 7604.943 Million cell updates/sec
                                                                                                                                               32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                  16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         en_gss_mam:*
em_gss_mus:*
em_gss_other:*
em_gss_pro:*
em_gss_pro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_gss_inv:*
em_gss_pln:*
em_gss_vrt:*
                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_gss:*
em_gss_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                              em_estba:*
em_esthum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:*
em_estfun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_estin:*
em_estmu:*
em_estov:*
em_estpl:*
em_estro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est2:
gb_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qb_est1:
                                                                                                                                                                                                                                                                                                                                                                                                                     ESI:*
                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                      Searched:
                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	BQ619167 RNOSEQ4E0	BQ619315 RNOSEQ6C0	BQ619318 RNOSEQ6D0	BQ619337 RNOSEQ6E1	BQ619383 RNOSEQ7B0	BQ619390 RNOSEQ7B0
SUMMARIES		ID	BQ619167	BQ619315	BQ619318	BQ619337	BQ619383	BQ619390
		· DB	14	14	14	14	14	14
		Query ore Match Length DB II	648	648	648	648	648	648
	øР	Query Match	75.2	75.2	75.2	75.2	75.2	75.2
		Score	508.6	508.6	508.6	508.6	508.6	508.6
		Result No.	1	7	m	4	Ŋ	9

1. .648 /organism="Zea mays" /db\_xref="taxon:4577" /clone="RNOSEQ4E05\_SK.abl"

AW331212 707049E04 BE025302 94502B09 AW2B8876 707009E07 AY104409 2ea mays AM714409 2ea mays AM714732 945002E06 AA979839 MEST12-H1 A1855425 603016F02 AW787314 945002E06 BE519299 945007B05 AP5448 496010H04 BE12897 945032C12 AW787315 945002E06 BE12897 945032C12 AW787315 945002E06 BE12897 945002E06 BE12897 945002E06 BE12897 945002E06 AB787315 945002E06 BE12897 945002E06	AW289056 707005607 BW501439 PAC000000 AW745400 WS1_34_H1 BR025503 945028809 BR364814 PIL_16_C0 AW680016 WS1_34_H1 BQ280709 WHE3004_A BQ2807738 PIL_85_F0 BE599123 PIL_85_F0 BW774693 WS1_74_A BW774693 WS1_74_A	A16496 A49245 A49245 A99245 BQ2815 BQ2815 BE5933 S mRNA linear ES ea mays roots CDNA lis	ohyta; Embryoph lopsida; Poales ; Zea. e
212 212 302 409 732 333 3314 225 3314 3314 3315 34	0008 436 436 4400 303 303 303 303 1123 738 882 603 507	49804 288975 288279 281558 593304 ALIGNMENTS 648 bp 648 bp 648 bp	Strepto yta; Lil pogoneae toleranc gy na, IL 6 uc.edu.
AW331 BE0231 AW2088 AW104 AW104 AW187 AW187 AW187 AW187 AW187 AW187 AW187 AW187 AW187 AW187 AW187 AW187 AW187 AW187	BEZZ20UB BMS01439 BM745436 AW745400 BE025303 BE364814 AW680016 BQ2800709 BQ2800709 BC280709 BC280709 BC280709 BC280709 BC280738 BC380709 B	8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	ridiplantae; St.; Magnoliophyta ideae; Andropogo 648) ohnert, H.J. 101 ant stress tol. 2020; Fredricksen Plant Biology Illinois Dr., Urbana, 73 br., Urbana, 73 br., Urbana, 73 br., Urbana, 74 br., Urbana, 74 br., Urbana, 75 br., Urbana, 76 br., Urbana, 77 br., Urbana, 7
100 100 100 100 100 100 100 100	100 110 110 110 110 110 110 110	2011001100 114410	r:21621110 ridiplan ; Magnol ideae; AA obnert,H lant str lant str lant str redric Plant B redric rilinoi ry Dr.,
00000000000000000000000000000000000000	4.4 4.4 4.6 4.6 4.6 4.6 4.6 4.6 4.6 4.6	288 274 234 3338 5512 577 277 28.38	s. S. Yil GI:21621161 S. S. S. Viridiplantae; Stophyta; Magnoliophyta Pantcoideae; Andropod ens 1 to 648) end Bohnert, H.J. S. of plant stress to: Shed (2002) End of Plant Biology ity of Illinois Cregory Dr., Urbana Gregory Dr., Urbana Gregory Dr., Urbana Dohnertlab@life.uiuc Location/Qualifieri 1. 648
723.7 711.2 700.1 700.1 669.6 67.5 666.4 665.3 663.3 603.5	0.0.0.0.4.4.4.4.4.4.4.4.4.4.6.6.6.6.6.6.	31.7 31.4 27.4 27.4 27.2 27.2 27.2 27.2 27.2	and year.  9167. 9167. 9167. 9167. 9167. 9167. 9167. 9167. 9167. 9167. 9167. 917. 917.
46446680466966		2.6 2.12 2.12 2.12 5.4 3.6 BQ612 BQ612 BQ612	sequents of the sequents of th
80440404044	204-404-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3-3	212 212 212 213 185 185 185 183 10N	
20 20 20 20 20 21 21 21 21	33 34 35 37 37 37 37 37 37 37 37 37 37 37 37 37	c 40 2: 41 2 42 11 43 11 44 11 45 11 B0619167 LOCUS DEFINITION	ACCESSION VERYOUS KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCES
ט ט ט	· <b>v</b>	C 44 44 44 44 44 44 44 44 44 44 44 44 44	ACC VEF KEY SOU C C C C C C C

```
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 129, Appl
Sequence 19, Appl
Sequence 3, Appl 1
Sequence 3, Appl 1
Sequence 3, Appl 1
Sequence 31, Appl 2
Sequence 317, Appl 2
Sequence 317, Appl 3
Sequence 117, Appl 3
Sequence 117, Appl 3
Sequence 117, Appl 3
Sequence 11, Appl 3
Sequence 11, Appl 3
Sequence 11, Appl 3
Sequence 201, Appl 3
Sequence 19, Appl 3
Sequence 199, Appl 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGG
                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-090-035-2

Sequence 2, Application US/10090035

Patent No. US20020170089A1

GENERAL INFORMATION:
TITLE DE INVENTION: Nucleic Acids Encoding Defense Inductble
TITLE DE INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/090,035

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 02/28/2001
NUMBER OF SED ID NOS: 25

SOFTWARE: FastSED for Windows Version 4.0

LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Score 510; DB 9; Length 93;
Batches 93; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10090035
| Patent No. US20020170089A1
| GENERAL INFORMATION:
| APPLICART: Simmons, Carl R.
| TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible in TITLE OF INVENTION: Proteins and Uses Thereof
             9 US-09-876-904A-627

10 US-09-824-735-3

10 US-09-824-735-3

11 US-09-821-736-13

12 US-10-925-302-501

10 US-09-937-90-428

9 US-10-108-605-125

9 US-10-108-605-125

9 US-10-108-605-125

9 US-09-932-257A-19

9 US-09-932-257A-19

10 US-09-913-90-8

10 US-09-913-17

9 US-10-108-605-11

9 US-10-044-622-317

9 US-10-044-622-317

9 US-10-044-622-317

9 US-10-108-605-71

10 US-09-731-38-65

9 US-09-975-719-201

9 US-09-75-719-201

10 US-09-75-719-201

9 US-09-975-719-201

10 US-09-975-719-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Zea mays US-10-090-035-2
        RESULT 2
US-10-090-035-4
        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                               June 6, 2003, 12:52:33 ; Search time 29 Seconds (without alignments) 331.081 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Appendix of the property of the pr
                                                                                                                                                                                                US-10-090-035-2
510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 / Ggn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2 / Cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
3 / Cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4 / Cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5 / Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6 / Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
8 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
9 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
12 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
13 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
14 / Cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-090-035-4
US-10-090-035-4
US-10-090-035-8
US-10-090-035-16
US-10-090-035-16
US-10-090-035-16
US-10-090-035-22
US-10-090-035-24
US-10-090-035-14
US-10-090-035-14
US-10-090-035-14
US-10-232-563-7
US-09-879-312-2
US-10-232-563-6
US-09-879-312-2
US-10-232-563-6
US-09-879-312-2
US-10-232-563-6
US-10-052-798-9
                                                                                                                                                                                                                                                                                                                                               392085 seqs, 103240269 residues
                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000.0
1000.0
99.4
97.9
97.9
97.9
97.9
97.9
17.7
115.7
115.3
115.3
115.3
115.3
115.3
                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499.5
499.5
277.5
273.258
245.245
80
80
80
80
77
                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                          Sequence:
                                                                                                                  Run on:
```

Result

Š

9 9

Gaps

```
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/10090035
Patent No. US20020170089A1
                                                                                                                                                   Query Match
Best Local Similarity 98.9%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.99
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Zea mays
US-10-090-035-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                     ; TYPE: PRT
; ORGANISM: Zea mays
US-10-090-035-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-090-035-18
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-10-090-035-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 8
                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                              1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFFEVDTVSRAGANHHHHHGHHGG
                                                                                                                                                                                                                                                                                                                                            1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGG
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10090035

Sequence 6, Application US/10090035

Patent No. US20020170089A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
PRICEING ACIDS Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990

CURRENT APPLICATION NUMBER: US/10/090,035

CURRENT FILING DATE: 202-02-28

PRIOR APPLICATION NUMBER: 60/272,227

PRIOR FILING DATE: 02/28/2001

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10. Application US/10090035
Sequence 10. US20020170089A1
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Mucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REPERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 510; DB 9; Length 93; 100.0%; Pred. No. 5e-45; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     DB 9; Length 93;
                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 510; DB 9; Length <sup>§</sup> Best Local Similarity 100.0%; Pred. No. 5e-45; Matches 93; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR PILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Zea mays
US-10-090-035-6
                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
US-10-090-035-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-090-035-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
```

```
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGAN-HHHHGHHG 59
                                                                                           9
                                                                     1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGHHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/10090035

Sequence 18, Application US/10090035

Patent No. US20020170089a1

GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/242990

FILE REFERENCE: 35718/24299

CURRENT APPLICATION NUMBER: US/10/090,035

CURRENT PILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/272,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 94;
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Simmons, Carl R. Trible of Simmons of Simmons, Carl R. Simmons, Simmons, Carl R. Trible of Invention: Nucleic Acids Encoding Defense Inducible Trible of Invention: Proteins and Uses Thereof File Reference: 35718/242990.
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
Length 93;
                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%; Score 499.5; DB 9;
98.9%; Pred. No. 5.9e-44;
:1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 507; DB 9;
pred. No. 1e-44;
                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
```

m

;

```
1 MAYYQEVDYCSEEVRSVA-PAGFGRHGGGVQQHVVKEKF-EEVDTVSRAGANHHHHHGHH 58
                                                                     1 MAYYQEVDYCSEEVRSVA-PAGFGRHG-GGVQQHVVKEKF-EEVDTVSRAGANHHHHHGH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAYYQEVDYCSEEVRSVA-PAGFGRHG-GGYQQHVVKEKF-EEVDTVSRAGANHHHHHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: NUCLEIC Acids Encoding Defense Inducible TITLE OF INVENTION: Proceeding and Uses Thereof FILE REFERENCE: 35718/742990
CURRENT APPLICATION NUMBER: 05/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 0.022/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SITMONS, Carl R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF. SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 273; DB 9; Length 92;
Pred. No. 7e-21;
2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 HG---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 G---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 258; DB 9;
; Pred. No. 2.4e-19;
14; Mismatches 13
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       Sequence 20, Application US/10090035 Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.6%;
Matches 61; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Triticum aestivum
US-10-090-035-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.6%
Matches 58; Conservative
          Conservative
        :09
                                                                                                                                                                                                                                                    US-10-090-035-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-090-035-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-090-035-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 20
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
          Matches
                                                                              g
                                                                                                                            ð
                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                       1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGYQQHVVKEKFEEVDTVSRAGAN-HHHHHGHHG 59
                                                                                                                                                                1 MAYYQEVDYCSEEVRSVAP-AGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/10090035
FORTHIE OF US/20020170089A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
FRIOR PILING DATE: 02/28/2001
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: FASTEED for Mindows Version 4.0
                                                                 Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 91;
                                                                                                                                                                                                                                                                                                                                                          Sequence 16. Application US/10090035
Patent No. US2002017008941
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/744990
CURRENT FILLING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.8%; Score 295; DB 9; Length 91
Best Local Similarity 60.6%; Pred. No. 4e-23;
Matches 57; Conservative 14; Mismatches · 19; Indels
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 277.5; DB 9;
Pred. No. 2.4e-21;
                                                           Score 499.5; DB 9;
Pred. No. 5.9e-44;
                                                                                                                                                                                                                       60 GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                              61 GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                           Query Match
Best Local Similarity 98.98;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.4%;
61.2%;
; ORGANISM: Triticum aestivum
US-10-090-035-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         US-10-090-035-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-090-035-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 16
LENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                               a
                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

7;

```
Sequence 64, Application US/0988615
Patent No. US20020064856A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: MOD_RES
; LOCATION: (1891)
; OTHER INFORMATION: Any amino acid
US-09-888-615-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 -- INTCTGEVHERRESF 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33,3%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.3 Best Local Similarity 29.9 Matches 23; Conservative
                                                                                                                                                                                         APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
LENGTH: 3353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-232-563-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
49 A---
                                                                                                           US-09-888-615-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-232-563-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HANYQEVDYCEBEVRBYTPTGGFLGRGGVOOQHVVKETFGEIDX----SGSGRXXHNHNHG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAYYQEVDYCSEEVRSVAP-----AGFGRHGGGVQOH-----VVKEKFEEVDTVSRAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAYYQEVDYCSEEVRSVAP-AGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10222563

Publication No. US20030087394A1

GENERAL INFORMATION:

APPLICANT: Sharma, Arun

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 10276-072001

CURRENT APPLICATION NUMBER: US/10/232,563

CURRENT FILING DATE: 2002-08-30

PRIOR APPLICATION NUMBER: US 60/316,453

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                       APPLICANT: SIMMONS, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 80; DB 9; Length 359;
Pred. No. 1.4;
7; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Indels
                     HG---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                           Score 245; DB 9;
Pred. No. 5.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1) ...(99)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-10-090-035-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GHGFVVRETRVEEDINTCTGEVHER 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 NDYXMVRETKXEEDFNTCTGEFRER 82
                                                                                                                                   US-10-090-035-14; Sequence 14, Application US/10090035; Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.0%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 48.0%;
Best Local Similarity 58.8%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT LOCATION: (1)...(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-232-563-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   å
                                                       셤
```

```
21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHGHHG-----FVVRETRVEED 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10232563
Publication No. US20030087394A1
GENERAL INFORMATION:
APPLICANT: Sharma. Arun
TITLE OF INVENTION: INSULIN RELATED TRANSCRIPTION FACTOR AND
TITLE OF INVENTION: USSS THEREOF
FILE REPRENCE: 10276-072001
CURRENT FILIGATION NUMBER: US/10/232,563
CURRENT FILIAG DATE: 2002-08-30
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 GANHHHHHHHHGHHGGH--GFVVRETRVEEDINTCTGEVHERRESFLA 90
175 ADDMGAGHHHGAHHTAHHHHSANHHHHHHHHGGSG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.1;
7; Mismatches
                                                                                                                                                                                             APPLICANT: WHYTE, DAVID
APPLICANT: CARNEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROFESES
TITLE REFERENCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-66-26
NUMBER OF SEQ ID NOS: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 80;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78;
```

Search completed: June 6, 2003, 13:02:10 Job time: 30 secs

		The state of the s		. * ( The state of	*	- ₹ - 1			
						Q.			
				<i>y</i> .					
1									
2									
<b>*</b>									4
3		•							
¥.									
•							.*		
Î	***	in a second of the second of t		• * *				*	
				45					
		a ji	* , *						
			6						right .
	. "							•	
		<u>.</u>							
Å	ν e : ) e								1 .
				·					
									• • •
		· · · · · ·							
			•						
	,								
		× .							*
		an .		• •	•	• (1)			
									of Sa
	*								
		•							
4	· · ·								
•		0		-	* *				
X.							•		
			•						
		*							
L									
				•					4
									.# 
2.5°									
The same of the sa									» · · · · · · · · · · · · · · · · · · ·
504. 504.			. * .	•					•
									2
**	. *	•			•			•	
									į.
į.		5 y		1		3			1

```
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 17, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-09-103-840A-2/C
Sequence 2, Application US/09103840A
Patent NO. 6394328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen C.
TITLE OF INVENTION: TUBERCUICSS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LEMETH OF THE COMMENT OF THE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          positions throughout the sequence g
                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, A
Sequence 5, A
Sequence 96,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2
Sequence 7
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4403765
21
6
6
229
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
               US-10-090-035-2 (1-93) x US-09-103-840A-2 (1-4403765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various
OTHER INFORMATION: represent a, t, c or
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.22e+04
83.00
46.558
36.218
16.278
                                                                                                                                                                                                                                                                                                                                                                                                                                            43280
   1303
21121
22121
123
185
930
930
93120
1970
1970
2066
2066
2066
2066
2066
4131
4131
4334
4131
   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
70.5
70.5
70.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                    0000 000
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Appli
Sequence 25, Appl
Sequence 25, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 1, Appli
                                                                                 % Search time 39 Seconds
(without alignments)
731.306 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl1
Appl1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    US-10-090-035-2
510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
Sequence 1,
Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: /cgr2_6/ptodate/1/ina/5A_COMB.seq:*
2: /cgr2_6/ptodata/1/ina/5B_COMB.seq:*
4: /cgr2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgr2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgr2_6/ptodata/1/ina/pcTr02_COMB.seq:*
6: /cgr2_6/ptodata/1/ina/pcTr02_COMB.seq:*
                                                OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.3 4403765 4 US-09-103-840A-2

15.3 4411529 4 US-09-103-840A-1

15.7 2310 3 US-09-305-987A-25

15.7 2310 4 US-09-305-987A-25

15.6 195 2 US-08-622-740-9

15.6 195 4 US-08-622-740-9

15.6 195 4 US-08-689-9

15.1 2373 4 US-08-440-689-9

15.1 3218 2 US-08-75-1

15.1 3218 2 US-08-75-1

15.1 3218 2 US-08-75-1

15.1 3218 2 US-09-75-5-1

15.1 3218 2 US-09-75-5-1
                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                              441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                         BLOSUM62
Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext 7
Delop 6.0 , Delext 7
                                                                                June 16, 2003, 10:20:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %
Query
Match Length DB
                                                                                                                                                  Perfect score:
                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
80.5
80
79.5
77
77
                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                               Searched:
                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11098765433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٠
ي
```

υυ

QQ à g

à

```
303 GGAGCTGCACGAGATCGAGGTGGAGACCATCCCGGTGGAGACCATCGAGACCACCACGAGGTGGT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGluVa 81 ::: | | | ::: | | | ::: | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 ------AlaAsnHisHisHisHisGlyHisGlyGlyHis--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GlyGlyGlyValGlnGlnHis-ValVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 lLysGluLysPheGluGluValAspThrValSerArgAlaGly-----
                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,623
REFERENCE/DOCKET NUMBER: M-12594 CIP (1570-8)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-2 (1-93) x PCT-US92-06840-1 (1-2353)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06840
FILING DATE: 19920814
                                                                                                                                           CLASSIFICATION: AU 1805
CLASSIFICATION: AU 1805
PRIOR APPLICATION NUMBER: US 07/746,485
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE TYPE: HeLG Cells TISSUE TYPE: Carcinoma CELL TYPE: tumor cells CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GlyPheGlyArgHis-
                                                                                                                                                                                                                                                                                                                                                                                                                              2353 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                               Dennis, Manette
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: D98/AH-2
CLONE: p14-1 or pYY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
241..1485
         READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D98/AH-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
PCT-US92-06840-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3234435 TCCATCGCCGTTCTACATCATGGACGAGGTGGAGGCCGCCCTCGACGTGAACGTGAACCTGCG 3234376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3228651 CCGACTGCTCAGCCTGTTCGAACAGCAGAGCAGTGCGCAGATCATCATCACCCA 3228592
                                |||:::|||
3228711 TCCATCGCCGTTCTACATCATGGACGAGGTGGAGGCCGCCCTCGACGTGAACCTGCG 3228652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerValAlaProAlaGlyPheGlyArgHisGlyGlyValGlnGlnHisValValLys 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3234315 CCAGAAGCCGACGATGGAGGTCGCGGACGCACTGTACGGCGTAACCATGCAGAA 3234262
SerValAlaProAlaGlyPheGlyArgHisGlyGlyValGlnGlnHisValValLys 35
                                                                      36 GluLysPheGluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHis--- 54
                                                                                                                                                                  APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, OOD C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-2007.00
CURRENT APPLICATION WIDHER: US/09/103,840A
CURRENT FILING DAIE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---HisGlyHisHisGlyGlyHisGlyPheValValArgGluThrArgValGlu 71
                                                                                                                                           55 ---HisGlyHisHisGlyGlyHisGlyPheValValArgGluThrArgValGlu 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shi, Yang
APPLICANT: Seto, Edward
APPLICANT: Seto, Edward
APPLICANT: Shows TITLE OF INVENTION: YY1 TRANSCRIPTION FACTOR AND METHODS OF TITLE OF INVENTION: ISOLATING SAME
TITLE OF INVENTION: ISOLATING SAME
WUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALUNESSEE: Ostrolenk, Faber, Gerb & Soffen STREET: 1180 Avenue of the Americas - 7th Floor CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-090-035-2 (1-93) x US-09-103-840A-1 (1-4411529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9206840; GENERAL INFORMATION:
                                                                                                                                                                                                                                                         Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION: APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.22e+04
83.00
46.55%
36.21%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: H37RV US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID
                                                                                                                                                                                                                                              US-09-103-840A-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US92-06840-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
312 GGACATCAGGCCGCCAACCAGTTCGCGGTCGCAGATGTCGCCGCAGACGAA----- 262
                                        27 GlyGlyValGlnGlnHisValValLysGluLysPheGluGluValAspThrValSerArg 46
                                                                                                                             ---AlaAsnHisHisHisHisHis 55
                                                                                                                                                                                                 56 GlyHisHisGlyGlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsn 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 GTAGACCTCGTCGTGGAAACGTGCACGAACTTGCCGATCTCGGCGTCGAGCGC----- 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 ---GGCCTGCAGCAGCACGTTGGTGCCGACCACGTTGGTGATCACGAAGGCGTC---CGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ValAspTyrCysSerGluGluValArgSerValAlaProAlaGlyPheGlyArgH1sGly 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 AlaGly------AlaAsnHisHisHisHis 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyHisHisGlyGlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsn 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GlyGlyValGlnGlnHisValValLysGluLysPheGluGluValAspThrValSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baltz, Richard H
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawfood, Rathryn P
APPLICANT: Crawfood, Rathryn P
APPLICANT: Treadway, Patt1 J
APPLICANT: Waldron, Clive
ITILE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
ITILE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
CURRENT FILING DATE: 1999-08-09
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 2310
TWODE: NUMBER: NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                              261 CTTCAGCCGGGGTTGTCCGCGACCGGCGCGAG 229
                                                                                                                                                                                                                                                                              76 ThrCysThrGlyGluValHisGluArgArgGlu 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-090-035-2 (1-93) x US-09-370-700-25 (1-2310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Saccharopolyspora spinosa
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09370700 Patent No. 6274350 GENERAL INFORMATION:
                                                                                                                    47 AlaGly------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.24
80.00
41.76%
29.67%
15.69%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1165)..(1992)
US-09-370-700-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (88)..(1077)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                US-09-370-700-25/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                       g
                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
              ---CCGACCCAGGT 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 ValAspTyrCysSerGluGluValArgSerValAlaProAlaGlyPheGlyArgHisGly 26
                                                                                                                                                                                                                  APPLICANT: Baltz, Richard H.
APPLICANT: Baltz, Rathry C.
APPLICANT: Broughton, Mary C.
APPLICANT: Madduri, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
183 GCCCATGATCGCTCTGCAGCCGCTGGTCACCGACGAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPLIGATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-2 (1-93) x US-09-036-987A-25 (1-2310)
                                                                          531 GCACCACCACCAGGAGGTGATCCTGGTGCAG 561
                                      81 lHisGluArgArgCluSerPheLeuAlaArg 91
                                                                                                                                                           Sequence 25, Application US/09036987A Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: USTERN CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION UNDER: 28,479
REFERENCE/DOCKET NUMBER: 50,6(
TELECOMMUNICATION INFORMATION:
TELEFAX: (317)337-4816
TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 2310 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2310 base pair
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 88..1077
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                      US-09-036-987A-25/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-09-036-987A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
a
                                      ð
                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
```

```
Sequence 9, Application US/09122399
Sequence 9, Application US/09122399
Patent No. 6329574
GENERAL INFORMATION:
APPLICANT: Lundquist, Ronald C.
APPLICANT: Matters, David A.
APPLICANT: Kirihara, Julie A.
APPLICANN: Kirihara, Julie A.
APPLICANN: Richara, Julie A.
APPLICANN: Rich
                                                                                                                                                                                                                        APPLICANT: Kirihara, Julie A. TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants TITLE OF INVENTION: and Cells Thereof NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 SerValAlaProAlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 GluLysPheGluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCH COMPATIBLE
CONFINES: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: NC-DOS/MS-DOS
SOFTWARE: PATENT: NC-MAY-1995
FILING DATE: 15-MAY-1995
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WOOSENEY, WAITEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 350,410
TELECHANTON TO NUMBER: 350,013US2
TELECHANTON FORMATION:
TELECHANTON FORMATION FORMATION:
TELECHANTON FORMATION FORMAT
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3500 IDS Center CITY: Minneapolis STATE: AN COUNTY OF THE COUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 TCTGGAGGACCGGCGGCGACGGGGAGGCTGGCGGTGGACTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 gAGCCCTGGAACGGAGGGCGGTGGCCGACGAGGC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-2 (1-93) x US-08-440-689-9 (1-195)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 Gly-HishisGlyGly---HisGly 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GGTTCATCACGGTGGGCGCCCATGGC 39
9, Application US/08440689
                                                                                                                                                                    APPLICANT: Lundquist, Ronald
APPLICANT: Walters, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.50
48.98%
46.94%
15.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                          Patent No. 6025545
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-122-399-9/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-440-689-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lundquist, Ronald C.
APPLICANT: Walters, David A.
APPLICANT: Walters, David A.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
TITLE OF INVENTION: and Cells Thereof
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 GluLysPheGluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHis 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ServalAlaProAlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLys 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                     262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----CATCATCAC
                                     312 GGACATCAGGCCGCCAACCAGTTCGCGGTCGCAGATGTCGCCGCAGACGAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Schwegman, Lundberg, Woessner & Kluth, P.A.: 3500 IDS Center
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GAGCCCCTGGAACGGACGACGGCGGTGGCCGACGAGGC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 TCTGGAGGACGGCGGCGACGAGGCTGGCGGTGGACTT-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/622,740 FILING DATE: 27-WARCH-1996 CLASSIFCATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                         261 CTTCAGCCGGGGTTGTCCGCGACCGGCGCAG 229
                                                                                                                                         76 ThrCysThrGlyGluValHisGluArgArgGlu 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-2 (1-93) x US-08-622-740-9 (1-195)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 Gly-HisHisGlyGly---HisGly 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GGTTCATCACGGTGGGCGCCCATGGC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,440
REGISTRATION NUMBER: 30,440
REPRENCE/DOCKET NUMBER: 950.(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08622740 Patent No. 5990390 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.50
48.98%
46.94%
15.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Minne
STATE: MN
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-08-440-689-9/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                  .08-622-740-9/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-622-740-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                             셤
                                                                                                                                                                    ò
```

```
US-10-090-035-2 (1-93) x US-08-789-275-1 (1-2373)
                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T96-005/A63613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1918 CATCACCACCATGGA 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78-08-677-862-1
; Sequence 1, Application US/08677862
; Patent No. 5874230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: T96-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 38-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3218 base pairs
STADE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 HisHisGlyGlyHisGly 62
                      CURRENT FILING DATE: 1997-01-28 UNDMER OF SEQ ID NOS: 6 SEQ ID NO 1 LENGTH: 2373
                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                          US-08-789-275-1
                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                      ..
Q
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ServalalaProalaGlyPheGlyArgHisGlyGlyGlyValClnGlnHisValValLys 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 GluLysPheGluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHis 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GAGCCCCTGGAACGGAGCGACGGCGGTGGCCGACGAGGC------CATCATCAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Palleja, Estivill Xavier
APPLICANT: Palleja, Melanie.
APPLICANT: Vilaro, Jordi Guimera
TITLE OF INVENTION: Human Gene Sequence of the Down Syndrome Critical
TITLE OF INVENTION: Region of Human Chromosome 21, Coding for A Serine-
TITLE OF INVENTION: Threonine Protein Kinase (MNB), Expressed in the
TITLE OF INVENTION: Neuronal Regions Affected in Down Syndrome
FILE REPERENCE: U 011114-4
CURRENT APPLICATION NUMBER: US/08/789,275A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 TCTGGAGGACCGGCGGGGAGGCTGGCGGCGGCGTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195
23
1
13
12
                      NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
STREET: 3500 IDS Center
                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/09/122,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-090-035-2 (1-93) x US-09-122-399-9 (1-195)
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.13US01
TELECOMMUNICATION INPORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-0361
: INFORMATION FOR.SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
ITLE OF INVENTION: and Cells Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/112,245
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08789275A Patent No. 6251664
                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.50
48.98%
46.94%
15.59%
                                                                                                                                                        ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                  Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity;
Query Match:
                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-122-399-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-08-789-275-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

```
1858 CAGAATGCATTGCATCATCACCATGGTAACAGTTCCCATCATCACCACCACCACCACCACCAC 1917
                                                                                                                                                                                                                                ||| :::|||||||
|1738 AGTCCCCAGGTCAGCATTTCCTGCTCCTCTTGGTCGTCAGGCACTGAAGCTCCT | 1797
                                                                                                                                                                                                                                                                                                                                         1798 ACACAGGICACIGITGAAACICCATCCTGITCAAGAAACAACCITICAIGIAGCCCCTCAA 1857
                                                                                                                                                                                                                                                                                                                        44
                                                                                                                                                                                                                                                                                                     28 ------GlyValGlnGlnHisValValLysGluLysPheGluGluValAspThrVal
                                                                                                                                                                                                                                                                                                                                                                                                             45 SerArgAla-------GlyAlaAsnH18H18H18H18Gly
                                                                                                                                                                                             11 SerGluGluValArgSerValAlaProAlaGlyPheGlyArgH18GlyGly----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOTUMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,862
FILING DATE:
CLASSIFICATION: 435
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: SONG, HO YEONG
APPLICANT: SONG, HO YEONG
APPLICANT: ROTHE, MIKE
TITLE OF INVENTION: TRAF2-ASSOCIATED Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & H
STREET: 4 Embarcadero Center, 34th floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ILP: 94111
COMPUTER READABLE FORM:
```

```
1843 ACACAGGICACIGITGAAACICAICCIGITCAAGAAACAACCIITCAIGIAGCCCCICAA 1902
                                                                                                                                                                                                                                                                                                                         1903 CAGAAIGCAIIGCAICAICACCAIGGTAACAGIICCCAICACCAICACCACCACCACCAC 1962
                                                                                                                                                                                                                                                                                                      45 SerArgAla---------GlyAlaAsnHisHisHisHisGly 56
                                                                                                                                                                                                                                 28 ------GlyvalGlnGlnHisValvalLysGluLysPheGluGluValAspThrVal 44
                                                                                                                                                                11 SerGluGluValArgSerValAlaProAlaGlyPheGlyArgHisGlyGly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INPORMATION:
APPLICANT: SONG, HO Yeong
APPLICANT: ROTHE, Mike
TITLE OF INVENTION: TRAF2-Associated Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, 34th floor
         3218
22
4
4
14
14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                US-10-090-035-2 (1-93) x US-09-252-571-1 (1-3218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REJERENCE/DOCKET NUMBER: T96-005/A63613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 781-1989
TELEFAX: 415 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/434,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/677,862
                                                                                                                                                                                                                                                                                                                                                                                                         1963 CATCACCACCATGGA 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09434065
Patent No. 6107074
                                                                                                                                                                                                                                                                                                                                                                                    57 HisHisGlyGlyHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:, 3218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415 398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                  39.39%
33.33%
15.10%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linea
                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-434-065-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                      Pred. No.:
                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                          1903 CAGAATGCATTGCATCATCACGATGGTAACAGTTCCCATCACCATCACCACCACCAC 1962
                                                                                                                                                                                                                                                                                                                            28 ------GlyValGlnGlnHisValValLysGluLysPheGluGluValAspThrVal
                                                                                                                                                                                                                                                                                                                                                                         45 SerArgAla----------GlyAlaAsnHisHisHisGly
                                                                                                                                                                                                                                 11 SerGluGluValArgSerValAlaProAlaGlyPheGlyArgHisGlyGly--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROTHE, Mike
APPLICANT: ROTHE, Mike
TITLE OF INVENTION: TRAF2-Associated Kinase
TUTHE OF INVENTION: 2
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,571
                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                 US-10-090-035-2 (1-93) x US-08-677-862-1 (1-3218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T96-005/A63613
                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/677,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT
NAME: Brezner, David J
REGISTRATTON UNDRER: 24,774
REFERENCE/DOCKET NUMBER: T96-(
TELECOMMUNICATION INFORMATION:
TELEPAN: 415,398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-571-1
; Sequence 1, Application US/09252571
; Patent No. 5981250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1963 CATCACCACCACCATGGA 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                57 HisHisGlyGlyHisGly 62
                                                                                4.58
77.00
39.39%
33.33%
15.10%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE:
US-09-252-571-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
             ; MOLECULE TYPE:
US-08-677-862-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                  ò
```

Percent Similarity: 39.39% Conservative: 4 Best Local Similarity: 33.33% Mismatches: 26 Query Match: 15.10% Indels: 14 DB: 2	Percent Similarity: 45.61% Conservative: 8 Best Local Similarity: 31.58% Mismatches: 25 Query Match: 14.90% Indels: 6
US-10-090-035-2 (1-93) x US-09-434-065-1 (1-3218)	.10-090-035-2 (1-93) x IIS-09-086-010-1 (1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-
Oy 11 SerGluGluValArgSerValAlaBroAlaGlyPheGlyArgHisGlyGly 27	11
Oy 28GlyvalGinGlnHisvalvaliyeGluLysPheGluGluValAspThrVal 44	Db 403 GCGCAGCAGCGGGGGGGGGGGGCAGCTGCGGCGCCTTGGGCGCAGCGGC 462 Qy 31 GlnH18
1843 ACACAG	463 GAGGAGATGGGCCCCGCCGCGC
45	SCCCCCA6
27 - 77 HISHINGLY 62   11   1   1   1   1   1   1   1   1	RESULT 14 US-09-329-234A-6
RESULT 13 US-09-086-010-1	; Sequence 6, Application US/09329234A ; Patent No. 6331416 ; GENERAL INFORMATION:
; Sequence 1, Application US/09086010 ; Patent No. 6274338	; APPLICANT: Shan1, Ziv ; APPLICANT: Shoseyov, Oded
<pre>; GENERAL INFORMATION: ; APPLICANT: Glimcher, Laurie H. et al.</pre>	; TITLE OF INVENTION: PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND R ; TITLE OF INVENTION: PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSIES OF CHITCHE
TITLE OF INVENTION: Human c-Maf Compositions and	FILE REFERENCE: 00/20274  CURRENT APPLICATION NUMBER: US/09/329,234A
CORRESPONDENCE ADDRESS:	NUMBER OF SEQ ID NOS: 8
ADDRESSEE: LAHIVE & COCKFIELD, LLP	; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 6
CITY: Boston ; STATE: Massachusetts . Commun. no.	TENGTH: 1305 TOPOSHICS: NAME 66.063
ZIP: 02109	FEATURE:
ᅜᇤ	; OTHER INFORMATION: Construct containing Protein L, fused to CBDcex sequence US-09-329-234A-6
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS	
CURRENT APPLICATION DATA:	3.2/ Length: 74.00 Matches:
APPLICATION NUMBER: US/09/086,010 ; FILING DATE:	larity: 40.91% Conservative: 2 imilarity: 36.36% Mismatches: 2
AFFLICATION NUMBER: 09/030,579 ; FILING DATE: 2-FEB-1998 ; ATTORNEY ARCHITETED	US-10-090-035-2 (1-93) x US-09-329-234A-6 (1-1305)
NAME: Kars. Cathellon: ; REGISTRATION NUMBER: 41,106	
; REFERENCE/DOCKET NUMBER: HUI-027CP; TELECOMMUNICATION INFORMATION:	Db 1173 CCGGGGGGGCGCACCGCGCAGTTCGGCTTCAACGGCTCGCACCGGGCACCAACGCCGCG 1232
; TELEPHONE: (617)227-7400 ; TELEFAX: (617)742-4214	35
; INFORMATION FOR SEQ ID NO: 1: . SEQUENCE CHARACTERISTICS:	Db 1233 CGACGGCGTTCTCGCTCAACGGCACGCCTGCACGGTCGGCGTCGAGCACCACCAC 1292
LENGTH: 1203 base pairs	Qy 55 H1sG1yH1sH1s 58
STRANDEDNESS: single	Db 1293 Caccaccaccac 1304
~	RESULT 15 US-08-240-783B-1/c
NAME/KEY: CDS   LOCATION: 11203   US-09-086-010-1	Direction by
Alignment Scores: Pred. No.: 1.65 Length: 1203 Score: 76.00 Matches: 18	Smith, Kelli Borden, Laurence A. Branchek, Theresa Hartig, Paul R.
	; AFFLICANT: Weinshank, Richard L.

```
64 ValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGluValHisGlu 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 ValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGlyGlyHisGlyPhe 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 ------GlyGlyValGlnGlnHisValValLysGluLysPheGluGluValAspThr 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 CysSerGluGluValArgSerValAlaProAlaGlyPheGlyArgHisGly-----
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET UNMER: 1795/39875-A-PCT-US
TELECHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
STELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-090-035-2 (1-93) x US-08-240-783B-1 (1-2121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,783B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SERSE: N
ORIGINAL SOURCE:
ORGANISM: RAT GLYCINE TRANSPORTER
CELL TYPE: MAMMALIAN
CELL LINE: COS7
IMMEDIATE SOURCE:
CLONE: rB20a
FEATURE:
                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 62..1975
; OTHER INFORMATION:
US-08-240-783B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknowr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                    STATE: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                CITY: Nev
STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           å
```

```
Search completed: June 16, 2003, 12:40:53
Job time : 1414 secs
                          g
 ŏ
DNA ENCODING A GLYCINE TRANSPORTER AND USES THEREOF
```

```
Sequence 17, Appl Sequence 15, Appl Sequence 21, Appl Sequence 23, Appl Sequence 23, Appl Sequence 13, Appl Sequence 13, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 1, Appl Sequence 213, Appl Sequence 1, Appl Sequence 213, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1, Appl Sequence 143, Appl Sequence 143, Appl Sequence 143, Appl Sequence 143, Appl Sequence 144, Appl Sequence 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Appli
Sequence 7, Appli
Sequence 15, Appl
Sequence 457, App
Sequence 6480, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10090035
Fatent No. US/20020170089A1
Fatent No. US/20020170089A1
Fatent No. US/20020170089A1
FILE NEPALCANT: Simmons, Carl R.
FILE REFERENCE: STABS/42499
CURRENT APPLICATION NUMBER: US/10/090,035
FILE REFERENCE: 35718/242990
CURRENT FILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: 60/272,227
FRIOR APPLICATION NUMBER: 60/272,227
FRIOR APPLICATION NUMBER: 60/28/2001
NUMBER OF SEQ ID NOS: 25
SOFWWARE: FastSEQ for Windows Version 4.0
FERGINAL STABS/4001
FERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574
93
0
      Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3e-58
510.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (96)...(374)
US-10-090-035-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                         295
277.5
258
258
251
251
213
92.5
92.5
88.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                              78.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-090-035-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 574
Command line parameters:

"MODEL-frame+_p2n.model -DEV-x1h
-0-Yegn2_1VSPTO_spool_VS10090035/runat_06062003_105507_11116/app_query.fasta_1.526
-0-Yegn2_1VSPTO_spool_VS10090035/runat_06062003_105507_11116/app_query.fasta_1.526
-1DB-published_Applications_NA -OFFNT-fastap -SUFFIX-rnpb -MINNATCH-0.1
-TRANS-humand.cd. -UIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-TRANS-humand.cd. -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-MAXLEN-2000000000 -USER-US10090035_GCN -1_176_grunat_06052003_105507_1116
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS=1 -XGAPOP=10 -XGAPEXT-0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                     (without alignments)
1077.357 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, P
Sequence 5, P
Sequence 1, P
Sequence 9, P
                                                                                                                                                                                                                                                                                                         510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US01_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
                                                                                                                                                             June 16, 2003, 11:41:43 ; Search time 125 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                 OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1029858 seqs, 724030393 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-3
US-10-090-035-5
US-10-090-035-1
US-10-090-035-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                   Xgapop 10.0 , Xgapext (Ygapop 10.0 , Ygapext (Fgapop 6.0 , Fgapext Delop 6.0 , Delext ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0, Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                   US-10-090-035-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0
100.0
100.0
99.4
                                                                                                                                                                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Satabase :
                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
```

```
1.59e-58
510.00
100.00%
100.00%
                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (89)...(367)
US-10-090-035-1
                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                  ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-090-035-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329
                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                  ..
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                à
                                   ò
                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                                                                                      Sequence 5, Application US/10090035
; Sequence 5, Application US/10090035
; Patent No. US20020170089A1
; GENERAL INFORMATION:
    TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: NUMBER: US/10/090,035
    CURRENT FILING DATE: 2002-02-28
    PRIOR FILING DATE: 2022-02-28
    NUMBER OF SEQ ID NOS: 25
    SOFTWARE: FastSEQ for Windows Version 4.0
    LENTH: 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577
93
0
0
                                                                                                                                                                                                            000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
             Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-090-035-2 (1-93) x US-10-090-035-5 (1-577)
                                                US-10-090-035-2 (1-93) x US-10-090-035-3 (1-574)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.31e-58
510.00
100.00%
100.00%
              100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)...(377)
US-10-090-035-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
                 Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ored. No.:
                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                             g
                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                  ద
                                                                                                          ð
                                                                                                                          셤
                                                                                                                                            à
                                                                                                                                                           g
                                                                                                                                                                               à
```

```
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; sequence 1. Application US/10090035
; Sequence 1. Application US/10090035
; Patent No. US/2002017008941
; GENERAL INFORMATION:
; APPLICANT: Simonons, Carl R.
; TTLE OF INVENTION: Mucleic Acids Encoding Defense Inducible
; TTLE OF INVENTION: Proteins and Uses Thereof
; TTLE REPRENCE: 35718/242990
; CURRENT APPLICATION UNBER: US/10/090,035
; CURRENT PILING DATE: 2002-02-28
; PRIOR FILING DATE: 00/28/2001
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10090035

Patent No. US20020170089A1

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Proteins and Uses Thereof

FILE REFERENCE: 35718/742990

CURRENT APPLICATION NUMBER: US/10/090,035

CURRENT FILING DATE: 2002-02-28

CURRENT FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           676
93
0
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-2 (1-93) x US-10-090-035-1 (1-676)
```

m

```
21 GlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGluGlu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                                                MetAlaTyrTyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
TITLE OF INVENTION: Proteins and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 202-228
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARRE: FastSED for Windows Version 4.0
                                                                                                                                                                                                                                                     580
0 0 1 1
               011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
            Mismatches:
Indels:
Gaps:
                                                   US-10-090-035-2 (1-93) x US-10-090-035-17 (1-524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-2 (1-93) x US-10-090-035-7 (1-580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.24e-57
499.50
98.94%
98.94%
97.94%
            98.94%
97.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: CDS
) LOCATION: (99)...(380)
US-10-090-035-7
            Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580
                                                                                                                                                                                                                                                                                                             US-10-090-035-7
                                                                          П
           Best Local S
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                          à
                                                                                             g
                                                                                                                                        ద
                                                                                                                     ò
                                                                                                                                                                ò
                                                                                                                                                                                     ద
                                                                                                                                                                                                           à
                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                 US-10-090-035-17
Sequence 17, Application US/10090035
Fatent No. US20020170089A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/24299
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,227
FRIOR FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PASSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 524
                                                                                                                                                 529
92
1
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                      524
93
                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                    US-10-090-035-2 (1-93) x US-10-090-035-9 (1-529)
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SEQTYARE: PastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 529
                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA

GRANISM: Triticum aestivum
FRATURE:
NAME/KEY: CDS

NAME/KEY: misc_feature

LOCATION: (1)...(524)

GOTHER INPORMATION: n = A,T,C or G
                                                                                                                                           2.93e-58
507.00
100.00%
98.92%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.85e-57
499.50
98.94%
                                                                                     ) NAME/KEY: CDS
) LOCATION: (53)...(331)
US-10-090-035-9
                                                       TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                      Ouery Match:
DB:
                                                                             FEATURE
                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                  음
                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-090-035-19
                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 AACGACTACCTGATGGTGCGCGAGAGAAGAGGAGGAGGAGGACGACTTCAACACCTGCACCGGC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLySGluLySPheGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGly 59
                                                                                                                                | Sequence 15, Application US/10090035 | Sequence 15, Application US/10090035 | Sequence 15, Application US/10090035 | Patent No. US200201700834 | Sequence 15, Application: Sequence 15, TITLE OF INVENTION: NUCLEIC Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/242990 | CURRENT APPLICATION NUMBER: US/10/090,035 | CURRENT FILING DATE: 2002-02-28 | PRIOR APPLICATION NUMBER: 60/272,227 | PRIOR FILING DATE: 02/28/2001 | NUMBER OF SEQ ID NOS: 25 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 15 | LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-21
| Sequence 21, Application US/10090035
| Padent No. US2002017008941
| GENERAL: INFORMATION:
| APPLICANT: Simmons, Carl R.
| TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof
| FILE REFERENCE: 35718/242990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 GAGTICCGCGAGCGCAAGCAGCTICCTGCTCAAGTCCGAC 333
                                               80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-090-035-2 (1-93) x US-10-090-035-15 (1-591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - A, I, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4e-30
295.00
75.53%
60.64%
57.84%
                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (61)...(333)
; NAME/KEY: misc_feature
; LOCATION: (1)...(591)
; OTHER INFORMATION: n = A
US-10-090-035-15
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                US-10-090-035-15
                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                         g
                                                                                    g
                                                       à
```

```
165 CAGGAGTTCGACACCTCCGGCCGC-----CGCCACGGTCACCACGGTCACCAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 Gly------GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsn 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AlaglyPheclyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPhe--- 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 GluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 ThrCysThrGlyGluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-028
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 2002-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                        436
60
12
13
13
                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-090-035-2 (1-93) x US-10-090-035-21 (1-436)
                                                                                                                                                                                                                                                                                                            Length:
Matches:
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/10090035
Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  = A,T,C or
                                                                                                                                                                                                                                                                                                        5.68e-28
277.50
73.47%
61.22%
54.41%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Triticum aestivum
                                                                                                                                                              TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (46)...(321)
NAME/KEY: misc_feature
                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (54)...(326)
US-10-090-035-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(584)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-090-035-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
```

Ŋ

```
111111 | 111111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
                                                                                                              58 HisGly------GlyHisGlyPheValValArgGluThrArgValGluGluAspile 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 GAGATCGACANG-----TCCGGCTCCGGCGANCANCACAACAACCAGGC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                         39 --- GluGluValAspThrValSerArgAlaGlyAlaAsnH1sH1sH1sH1sH1sGlyH1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGly
                                                                                                                                                                                                                                                             RESULT 11
US-10-090-035-13
Sequence 13, Application US/10090035
Fatent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-8
FRIOR APPLICATION NUMBER: 60/272,227
FRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARR: FRASERE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-090-035-2 (1-93) x US-10-090-035-13 (1-348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-923-876-2788
; Sequence 2788, Application US/09923876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.39e-24
251.00
70.59%
60.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 | 111 | 111111 | 183 GAGTTTCGCGAGCGC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 GluValHisGluArg 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (52)...(348)
NAME/KEY: misc_feature
LOCATION: (1)...(348)
COCATION: (1)...(348)
COCATION: (1)...(348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 13
LENGTH: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                               QQ
                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                               1 MetalaTyrTyrGlnGluValAspTyrCysSerGluGluValArgSerValAla---Pro 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 ---GluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/10090035

Patent No. US20020170089A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990

CURRENT APPLICATION UNMBER: US/10/090,035

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/272,227

PRIOR APPLICATION NUMBER: 60/272,227

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 584
        584
58
14
13
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584
58
14
13
7
      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                US-10-090-035-2 (1-93) x US-10-090-035-19 (1-584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-090-035-2 (1-93) x US-10-090-035-23 (1-584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.13e-25
258.00
72.73%
58.59%
50.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.13e-25
258.00
72.73%
58.59%
50.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Triticum aestivum FEATURE:
                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-090-035-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                            à
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

69

```
j.S-vy->>0-v4.A-1000

j. Sequence 1858, Application US/09938842A

j. Patent No. US20020160378A1

j. GENERAL INFORMATION:

APPLICANT: Wang, Xun

APPLICANT: US AME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND WETHODS OF USE

TITLE OF INVENTION: SAME, AND WETHODS OF USE

TITLE OF INVENTION UNMBER: US 60/227,866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 GGAGGAGGAGTGAACGGTGGTGGAGATATGTCGGCGGCGTATATAAGGAGAAAAGCGGCG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg 69
                                                                                                                                                                                                                                                                                                 GlyPheGlyArgHisGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GlyPheGlyArgHisGlyGlyGlyGly---ValGlnGlnHisValValVaSluLysPheGlu
||| ||| ||| ||| ||| |||| |||| ||||
                                                                                                                                                                                               40 Glu-------AsnHisPhrvalSerArgAlaGlyAla------AsnHisHis
                                                                                                                                                                                                                                                                                                                                                                    53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 Glu-----ValAspThrValSerArgAlaGlyAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-090-035-2 (1-93) x US-09-938-842A-1858 (1-591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 ValGluGluAspileAsnThrCysThrGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
                            Mismatches:
Indels:
                                                                                                                         US-10-090-035-2 (1-93) x US-09-924-035A-17 (1-328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OKGANISM: Arabidopsis thaliana
US-09-938-842A-1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.50
50.70%
33.80%
18.14%
     50.70%
33.80%
18.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-938-842A-1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Laura Y. (Ito)
APPLICANT: Sharman, Bradla Y. (Ito)
APPLICANT: Sherman, Bradla Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700161180H1
; NAME/KEY: unsure
; LOCATION: 125-146, 202
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GTACA, Jrn
APPLICANT: GTACA, Jrn
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIOR PILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237
48
1
11
2
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-090-035-2 (1-93) x US-09-923-876-2788 (1-237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/09924035A Patent No. US20020142319A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.24e-20
213.00
81.67%
80.00%
41.76%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.00126
                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-924-035A-17/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-924-035A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

----AsnHisHis 52

3

```
Sequence 417. Application US/09728445

Patent No. US20020102543A1

GENERAL INFORMATION:

APPLICANT: Eriedrich, Glenn

APPLICANT: Sambrowicz, Brian

APPLICANTON: No. US20020102543A1e1 Mutated Mammalian Cells and

TITLE OF INVENTION: Animals

FILE REFERENCE: LEX-0102-USA

CURRENT FILING DATE: 2000-11-30

PRIOR PLICATION NUMBER: US 60/168,358

PRIOR FILING DATE: 1999-12-01

NUMBER OF SEQ ID NOS: 891

SEQ ID NOS: 891

LENGTH: 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 AsnHisHisHisHisHisHisHisHisGlyGlyHisGlyPheValValArgGluThrArg 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
475 ATTAATGATGATGTTATGGAGTGTAGTAGTAAA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-090-035-2 (1-93) x US-09-728-445-817 (1-546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 16, 2003, 13:51:16
Job time : 132 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 GGCACATTCATAGAACAAGCC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 ---SerPheLeuAlaArgAla 92
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(546)
GTHER INFORMATION: n = A,T,C or G
US-09-728-445-817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.00804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.50
51.06%
40.43%
17.35%
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                RESULT 15
US-09-728-445-817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

Walter Control	ing the second s	(m)	\.			<b>₹</b> 5	***	
	4					e i		
	3 - 0 2 - 0 4 - 0				18 Mg			
	in a second of the second of t	- A					· • · · .	7
1		\$						
1		·			No.			
*	* :	*			in the second			
		* *					÷.	
				·		· ·		
	· · · · · · · · · · · · · · · · · · ·	4.				· * · · · · · · · · · · · · · · · · · ·	- 1 i - 1 i	1
		•			9 4			÷ .
		v • • • • • • • • • • • • • • • • • • •			y in			,
						v		
	•	÷4.			**/ ** *			. *
P.	* *				: '			
				3.				
								V <sub>2</sub> 0
					*			
		9	•					
B								
	*	. *						a simmer
	0 4				. *			:
								,
	•							5
	*		•					* ***
1		· ·					70	y
								4.
					•			
						*. *		. *
			·	n.			•	-
					•			
			•					
					. *			
					and the second s			
								•
		•						
9								• (1)
				•				
47°		. *						
3					•			
,								
<u>;4.</u>	•							
			•.					<u>.</u> 2
								*
2.3								45
								<b>r</b>
hite.								•
A.							4-2	
		1 1	4 4 1 1 1		se les care en mante de mando les al			

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

June 6, 2003, 12:48:33 ; Search time 25 Seconds (without alignments) 357.620 Million cell updates/sec Run on:

US-10-090-035-2 510 1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 1: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			dolts www wm-m	delta/iii/NF-E1/UC	쿹.			nypornetical prote	grycine/proline-ri		nypornetical prote	•	environmental stre		protein corA, cold	transcription repr	Down-syndrome-crit	hypothetical prote				transactive of for	transforming moto	cranstorming proce	probable limonene	dve protein - frui	CRAG protein - fru	hypothetical prote		ء ,	hypothetical prote	
SUMMARIES	ID	G85435	152619	A48273	T49815	733997	D96591	T45059	151469	531223	T16437	A42844	20000	00001	100338	70001	440330	JC4898	T16436	C83682	T30119	100080	JH0710	TVFVAF	727123	10 11 11 11 11 11 11 11 11 11 11 11 11 1	110011	T13/1/	1.26/57	T16435	JC7089	133594	
	DB		· ~	N	~		(7	~				٠,	، د	۱ ر	۹ ۲	۹ (	۹ (							-		-							
	Length	196	259	414	1245	471	473	735	173	495	86	191	i e e	1273	700	7 7	7 1	104	77	332	102	1560	425	369	909	000	101	1	4 10	83	895	1891	
æ	Query Match	18	18.1	18.0	17.5	17.0	16.5		16.1	16.0	15.9	15.9		15.7				1.01					14.8	•	14.7	14.7			,,,	14.5	14.5	14.5	
	Score	92.5	92.5	92	83	86.5	84	82.5	82	81.5	81	81	80	80	62	4.0		, ,	76.5	76.5	16	16	75.5	75	75	7.5	7.0	, , , ,	; [	4	74	74	
	Result No.	г	7	e	4	S	9	7	8	O	10	11	12	13	14	15	4	3 6	7,	20	, L	20	21	22	23	24	25	2 2	2 5	7	58	5.5	

hypothetical prote probable AT-hook D	hypothetical prote hypothetical prote gamma aminobutyric	hypothetical prote hypothetical prote homeotic protein o	phosphopyruvate hy histidine rich cal hypothetical prote cation effilm fami	female sterile hom kakapo gene protei environmental stre
T16440 E84766	509880 T02702 A41145 A26030	T31611 S39406 A56446	C75251 A54660 A82890 F87286	A43742 T13714 T09610
000	700-	000	0000	000
147 285	439 776 606 633	1585 354 268	499 699 338 361	2038 2396 59
14.4	1 4 . 4 . 4 . 4 . 4 . 4 . 4 . 4 . 4 . 4	14.2 14.1	14.0 14.0 13.9	13.9 13.9 13.8
73.5	73.5	72.5	71.5 71.5 71	71 71 70.5
30	, w w w 4 w 4 w	38 38 38	39 41 42	4 4 4. ይ 4 ሺ

## ALIGNMENTS

```
TINY-like protein [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C; Accession: G84435
R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp Nature 402, 769-777, 1999
A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A85001; MUID:20083488; PMID:10617198
A; Accession: G88435
A; Molecule type: DNA
A; Residues: 1-196 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:NC_001268; NID:97270639; PIDN:CAB80356.1; GSPDB:GN00140 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 4
RESULT 1
```

Query Match 18.1%; Score 92.5; DB 2; Length 196; Best Local Similarity 33.8%; Pred. No. 0.012; Matches 24; Conservative 12; Mismatches 24; Indels 11; Gaps

5

21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R 69 ò g

::|: |:: 159 INDDLMECSSK 169 70 VEEDINTCTGE 80 à 

RESULT 2

Tive protein (imported) - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (any first cress)
C;Accession: T52619
R;Terryn, N.; Heijnen, L.; De Keyser, A.; Van Asseldonck, M.; De Clercq, R.; Verbakel ueller, C.; Mayer, K.; Dehals, P.; Rombauts, S.; Van Montagu, M.; Rouze, P.; Vos, P.
FEBS Lett. 445, 237-245, 1999
A;Title: Evidence for an ancient chromosomal duplication in Arabidopsis th aliana by A;Recession: T52619
A;Title: Evidence for an ancient chromosomal duplication in Arabidopsis thaliana by A;Accession: T52619
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-259 - TERsA;Cross-references: EMBL:AJ002598; PIDN:CAA05630.1

A; Map position: 4

18.1%; Score 92.5; DB 2; Length 259;

Query Match

ő

Gaps

ö

Indels

Length 1245;

DB 2; 0.21;

```
A Molecule type: DNA **

A Molecule type: DNA **

A Residues: 1-471 cAPAD: A MOSCI.5

A STOOMS - references: EMBL:AF125964; PIDN:AAD14753.1; GSPDB:GN00022; CESP:W03GI.5

A; Experimental source: strain Bristol N2; clone W03GI

A; Genetics:

A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GVQQHVVKEKFEEVDTVSRAGANHHHHG---- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Caenorhabditis elegans
|Date: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
|Accession: T33997
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1245 <SCH>
A;Cross-references: EMBL:AL356815; GSPDB:GN00116; NCSP:B24H17.10
A;Experimental source: BAC clone B24H17; strain OR74A
C;Genetics:
A;Gene: NCSP:B24H17.10
A;Map position: 6
A;Introns: 6/2; 1141/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Pauley, A.; Scheet, P.; Harper, M. submitted to the EMBL Data Library, February 1999 A; Description: The sequence of C. elegans cosmid W03Gl. A; Reference number: Z21454 A; Accession: T33997 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%; Score 86.5; DB 2; 34.8%; Pred. No. 0.14; Live '4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein W03G1.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                               Score 89;
Pred. No. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                   17.5%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 SRAGANHHHHHGHHGGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 RSVAPAGFGRHGG---
                                                                                                                                                                                                                                                                                                                                                      Query Match 17.5
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 РРННGНННF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 --HHGGHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-473 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: D96591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: Awa6423 multiple and Ag873 multiple and accession: Ay8873 multiple and accession: Ay8874 multiple and accession: Ay8874 multiple and accession: Ay8874 multiple and accession: Ay8874 multiple and accession: Ay8854 multiple and accession: Ay874 multiple and accession: Ay874 multiple and accession: Ay874 multiple and accession: Ay101 multiple accession: Ay800 multiple ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related to multifunctional cyclin-dependent kinase PHO85 [imported] - Neurospora crassa NyAlternate names: protein B24H17.10 C; Species: Neurospora crassa C; Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 C; Accession: T49815 R; Schulte, U.; A49015 R; Schulte, U.; A4901, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000 A; Reference number: 225022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiDate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
CiAccession: A48273; A42055; A56418
Risafrany, G.; Perry, R.P.
Risafrany, G.; Perry, R.P.
A;Title: Characterization of the mouse gene that encodes the delta/TY1/NF-E1/UCRBP trans
A;Title: Characterization of the mouse gene that encodes the delta/TY1/NF-E1/UCRBP trans
A;Reference number: A48273; MUID:93296177; PMID:8516301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                             21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGGHGFVVRETRVEEDINTCTGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                     21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: mRNA
A; Cross-references: GB:M74590; NID:9192940; PIDN:AAA37521.1; PID:9192941
C; Genetics:
A; Introns: 227/1; 281/2; 301/3; 354/3
C; Keywords: transcription factor; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.0%; Score 92; DB 2; Length 414; llarity 31.0%; Pred. No. 0.031; Conservative 7; Mismatches 26; Indels
              0.016;
---- 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delta/YY1/NF-E1/UCRBP transcription factor - mouse
                            Pred. No. 0.01
                                                                12;
                            33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GGGDHGGGGGGH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :| | :
99 VHHHQEVILVQ 109
                                Similarity 33.8
24; Conservative
                                                                                                                                                                                                                                                                                                                                    222 INDDLMECSSK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 VHERRESFLAR 91
                                                                                                                                                                                                                                                                    70 VEEDINTCTGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T49815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                       ద
```

4

25; Gaps

Indels

16;

Length 471;

```
hypothetical protein T24C10.10 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 (Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 % Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hundrer, J.C.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.Authors: Hunter, J.L.; Jahn, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia R.Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A.Authors: Salzberg, S.L.; Schwartz, J.C.; Davis, R.W. A.M.; Wu, D.; Yu, G.; Fraser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Wu, D.; Yu, G.; Fraser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Fraser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Fraser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Mu, D.; Yu, G.; Praser C.M.; Ventler, J.C.; Davis, R.W. A.M.; Sun, H.; Tallo A.M.; Su
```

ä

Gaps

; 10;

```
A,Cross-references: EMBL:U23523; NID:9746551; PID:9746557; PIDN:AAC46561.1; CESP:F53A
A,Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                            Transcription factor Brn-1 - mouse

NyAlternate names: class III POU domain protein brain-1

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Species: O2-bec-1993 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999

R;Harar, Y; Roveesalll, A.C.; Kim, Y; Nirenberg, M.

Britle: Structure and evolution of four POU domain genes expressed in mouse brain.

A;Reference number: S31223; MUID:92228768; PMID:1565620

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule Lype: DNA
A; Residues: 1-495 cHAR>
A; Residues: 1-495 cHAR>
A; Residues: 1-495 cHAR>
A; Residues: 1-495 cHAR>
A; Cross-references: EMBL:M88299; NID:9200444; PIDN:AAA39960.1; PID:9200445
C; Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C; Superfamily: transcription factor Brn-1; homeobox in capulation
F; 27-49/Region: glycine-rich
F; 101-112/Region: alanine-rich
F; 186-201/Region: alanine-rich
F; 186-201/Region: alanine-rich
F; 186-201/Region: glycine-rich
F; 236-247/Region: glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F53A9.6 - Caenorhabditis elegans
C;Spocies: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Şep-1999 #text_change 20-Sep-1999
C;Accession: Ti6437
                                                                                                                                                           Length 495;
                                                                                                                         19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGA----NHHHHHHHHGHHGGHGF
                                    Length 173;
                                                                                 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81; DB 2; Length 86;
Pred. No. 0.089;
5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Miller, N. submitted to the EMBL Data Library, March 1995
A;Description: The sequence of C. elegans cosmid F53A9.
A;Reference number: Z18513
A;Accession: T16437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHH-
                               Score 82; DB 2;
Pred. No. 0.15;
7; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-86 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPGLNSHDPHSDEDTPTSDDLEQFAKQFKQRR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 -----FVVRETRVEEDINTCTGEVHERR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.0%; Score 81.5; Di
26.1%; Pred. No. 0.5;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <P00/>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F)236-247/Region: glycine-rich
F)267-291/Region: histidine/proline-rich
F)316-383/Domain: POU domain homology <POI
F)402-458/Domain: homeobox homology <HOX>
                       Query Match
Best Local Similarity 34.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 29.5%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 16.0%
Best Local Similarity 26.1%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP: F53A9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                q
                                                                                                                           ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                         RESULT 7
745059
hypothetical protein Y39B6B.gg [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Date: 21-Jan-2000
R;Milson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns
B; O'Callaghan, M.; Parsons, J.; Percy, C.; Riffken, L.; Roopra, A.; Saunders, D.
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; S
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; S
A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A;Reference number: S45531; MUID:94150718; PMID:7906398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycline/proline-rich protein - Arabidopsis thaliana
NiAlternate names: protein K10A8_130
CiSpeciaes: Arabidopsis thaliana (mouse-ear cress)
CiSpeciaes: Arabidopsis thaliana (mouse-ear cress)
CiDate: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
CiAccession: T51469
SiSato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew A; Reference number: Z25394
A; Accession: T51469
A; Accession: T51469
A; Status preliminary
A; Molecule type: DNA
A; Residues: 1-173 <SAT>
A; Molecule type: DNA
A; Residues: 1-173 <SAT>
A; Cross-references: EMBL:AL391151
A; Experimental source: cultivar Columbia; BAC clone K10A8
                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:96434440; PIDN:CAB60938.1; PID:96434473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005173; NID:99857523; PIDN:AAG00878.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                          8 DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGH----HGGH 61
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 735;
                                                                                                                                         Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ė,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                   ; Score 84; DB 2;
; Pred. No. 0.26;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 GRHGGGVQQHVVKEKFEEVDTVSRAGANHH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.2%; Score 82.5; D
26.4%; Pred. No. 0.6;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: DNA
A; Residues: 1-735 <WIL>
A; Cross-references: EMBL:AL132896; N
A; Experimental source: clone Y39B6B
                                                                                                                           16.5%;
36.8%;
                                                                                              Query Match
Best Local Similarity 36.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11111111
563 SLAHHGHHGGHG 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 ---ннсниссис 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69/1
                     C;Genetics:
A;Gene: T24C10.10
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 3
A;Introns: 18/1; 6
A;Note: Y39B6B.gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 5
A; Introns: 97/1
A; Note: K10A8_130
                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
```

ä

25;

----- 6ннсенс- 62

ä

56;

-----GVQQHVVKEKFEEVDTVS 45

1 MAYYQEVDYCSEEVRSVAPAGFGRHGG------

ô

```
Transcription repressor protein XYI - human Nialternate names: transcription repressor/activator protein NF-E1 Nialternate names: transcription repressor/activator protein NF-E1 C;Species: Homo sapiens (man) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 08-Oct-1999 C;Accession: A40390; S78494; S33712; A56419 F;Shi, Y; Seto, E; Chang, L.S.; Shenk, T. Cell 67, 377-388, 1991 A;Title: Transcriptional repression by XYI, a human GLI-Krueppel-related protein, and A;Title: Transcriptional repression by XYI, a human GLI-Krueppel-related protein, and A;Title: Transcriptional repression by XYI, PMID:1655281
                                                                                                                                                         genes. IX. The comp
                                                                                              Nomura, N.; Ohara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: 170338
R;Magase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; C
DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. Th
A;Reference number: Z14086; MUID:98290545; PMID:9628581
A;Recession: T00338
A;Recenter number: Z14086; MUID:9820545; PMID:9628581
A;Recenter number: Z14086; MUID:9820545; PMID:9628581
A;Recenter number: Z14086; MUID:9820545; PMID:9628581
A;Residues: 1-1273 <NAG>
A;Residues: 1-1273 <NAG>
A;Residues: 1-1273 <NAG>
A;Residues: L1273 <NAG
A;Residues: L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein corA, cold- and drought-regulated - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:L03708; NID:9289122; PIDN:AAA99833.1; PID:9289123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: A40350
A, MoLecule type: mRNN
A, Residues: 1-414 <SHI>
A, Cross-references: GB:M77698; NID:9186767; PIDN:AAAS9467.1; PID:9186768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Laberge, S.; Castonguay, Y.; Vezina, L.P.
Plant Physiol. 101, 1411-1412, 1993
A;Title: New cold- and drought.regulated gene from Medicago sativa.
A;Reference number: 216754; MUID:94143496; PMID:8310076
A;Accession: T09592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 1273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 204;
0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 GANHHHHHHHHHGH--GFVVRETRVEEDINTCTGEVHERRESFLA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GFGRHGGGVQQHV-VKEKFEEVDTV-----SRAGANH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: KIAA0570
C; Superfamily: human hypothetical protein KIAA0570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: corA
C;Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 2;
Pred. No. 2;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.5%; Score 79; DB 30.4%; Pred. No. 0.37 tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 GGHGGHGGHGAVQTEDNTQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 HHHGHHGGHGFVVRETRVE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.7%;
ilarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A: Residues: 1-204 <LAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T09592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                        Associate acid-and environmental stress-inducible protein - alfalfa (fragment)
c) Species: Medicago sativa (alfalfa)
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Accession: Ad2844
B; Luo, M; Liu, J.H.; Mohapatra, S.; Hill, R.D.; Mohapatra, S.S.
J Biol. Chem. 267, 15367-15374, 1992
J; Biol. Chem. 267, 15367-15374, 1992
J; Biol. Chem. 267, 15367-15374, 1992
J; Richerence number: A42844; MUID:92348382; PMID:1379227
A; Reference number: A42844
A; Molecule type: MRNA
A; Residues: 1-191 < Luo
A; Molecule type: MRNA
A; Residues: 1-191 < Luo
A; Cross-references: GB:S40947; NID:g252396; PIDN:AAB22713:1; PID:g252397
A; Note: sequence extracted from NCBI backbone (NCBIN:109886, NCBIP:109889)
C; Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T09608
R; Luo, M.; Mohapatra, S.; Hill, R.
submitted to the EMBL Data Library, February 1992
A; Bescription: Nucleotide sequence analysis of a environmental stress and ABA inducible A; Reference number: 216770
A; Accession: T09608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFGRHGGGVQQHV-VKEKFEEVDTV-----SRAGANH------HHHHGHH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----H 52
                                environmental stress-induced protein - alfalfa (fragment)
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21. GFGRHGGGVQQHV-VKEKFEEVDTV------SRAGANH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-133 <LUO>
A; Residues: 1-133 <LUO>
A; Cross-references: EMBL:M74190; NID:g166373; PID:g166374
A; Experimental source: cultivar Anik
C; Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGHGGTVDTVLTKLRTTLKTDHNDIIMHALFLS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGHGFVVRE--TRVEEDINTCTGEVHERRESFLA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81; DB 2;
Pred. No. 0.21;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80; DB 2
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 GGHGGHGADQTEDNTQNDHN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 HHHGHHGGHGFVVRETRVEEDIN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T00338
hypothetical protein KIAA0570 - human
                                                                                                                                                                  46 RAGANHH--НННGНHGGH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.9%;
Best Local Similarity 30.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 28.7
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                              g
                                                                                                                                        ö
                                                                                                                                                                                                ద
```

```
A:Experimental source: HeLa cells
A:Note: the authors translated the codon CGC for residue 371 as Lys, CGA for residue 375
R:Whitson, R.H.; Huang, T.; Dang, J.; Itakura, K.
submitted to the EMBL Data Library, July 1992
A:Description: Observed and predicted DNA binding of a zinc finger protein which recognia A:Reference number: $78494
                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-195, G',197-414 <WHI>
A; Cross references: EMBL:214077; NID:938010; PIDN:CAA78455.1; PID:938011
R; Park, K.; Atchison, M.L.
Proc. Natl. Acad. Sci. U.S.A. 88, 9804-9808, 1991
A; Title: Isolafichn of a candidate repressor/activator, NF-E1 (XY-1), delta, that binds
A; Accession: S33712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GFGRHGGGVQQHVVKEKFEEVDIVSRACANHHHHHGHHGGH-GFVVRETRVEEDINTCTG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: mRNA A Molecule type: mRN 6541; NID:9189173; PIDN:AAA59926.1; PID:9189174 C; Keywords: DNA binding; transcription regulation; zinc finger CCHH motif F:298-320/Region: zinc finger CCHH motif F:327-347/Region: zinc finger CCHH motif F:355-377/Region: zinc finger CCHH motif F:385-407/Region: zinc finger CCHH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 79; DB 2; Length 414;
Pred. No. 0.78;
6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 6, 2003, 12:53:24 Job time : 26 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.2%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| :| :
96 QVHHHQEVILVQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 EVHERRESFLAR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

June Run on:

6, 2003, 12:42:32 ; Search time 13 Seconds
 (without alignments)
 296.715 Million cell updates/sec

US-10-090-035-2 510 1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		Q00899 mus musculu	_	rattu		Q07202 medicago sa	homo	homo	mus m	0			P31366 brachydanio		P23091 avian miscu				P50439 caenorhabdi					didel		homo	droso	_	P80205 mus musculu			P10180 drosophila	_	843 1
SUMMARIES	. qI		TYY1_MOUSE	BENT MOUSE	DENT_KAT	DAMI_HOMAN	CORA_MEDSA	TITT BOWAN	DI KA_HUMAN	DIKA MOUSE	DI KA_KAT	MAF_HUMAN	CBX4_MOUSE	POUL_BRARE	CBX4_HUMAN	TMAF_AVIS4	CSUP_DROME	Z281_HUMAN	CCAD_CHICK	YV59_CAEEL	EP84_HCMVA	GAB_DROME	SNF1_YEAST	OTX1_HUMAN	A2AC_DIDMA	ZIC2_HUMAN	SRCH_HUMAN	FSH_DROME	SALA_DROSI	OTX1_MOUSE	OTX1_RAT	CCT1_HORSE	HMCU_DROME	HUNB_DROCR	MAF_MOUSE
	DB	١.	٦,	٦.	٦.	٠,	٦,	٠,	٦,	٦.	٠,	٦,	٠,	٠,	٠,	٦.	Н,	<b>-</b>	٦,	н,	-	Н	-	-		Η,	н.	٦.	-	-		Η.	-	⊣,	-
	Length		4 4	40.4	ָר ער היים היים	200	* -	. 42	7 0		0 0	, i	100	0 C	200	305	440	S 6 6 6	2190	147	684	909	633	354	469	532	669	2038	139	322	355	727	2175	190	370
æ	Ouery Match		ש מ	v	ď	ď	7 5	ď	ď	1.5	٠,	· -	· -	•		٠	•	٠	•	•	٠	٠	•	•	•	٠.	٠,		უ,	·,	÷.	m.,	÷.	13.7	m.
	Score		81 22	2.18	. 0		66	77	77	7.7			٠,		) ) ) (		4 .	4 .	,	0.55		٤/	7 C	7	1.5	7.1.0	(T.)	, c	0.00	0.07	0.00	20.5	0.0	200	2
	Ø	-	10	m	4	ď	φ	7	· cc	0	10,	] [	12	- 1	3 -	1 -	ר ז ר	ָרָבְּ	, c	9 6	4 6	0 5	7 (	77	2 6	7 0	7 6	9 6	7 6	9 0	<b>N</b> (	2 .	J C	2 6	'n

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/

caenorhabdi drosophila homo sapien sarcophaga mus musculu caenorhabdi zea mays (m homo sapien mus musculu homo sapien drosophila plasmodium
Q9xtq7 P51025 060563 008617 P40764 018879 013934 099593 099593
KE4L_CAEEL PNT1_DROME CCT1_HUMAN ANTE_SAREE DLX2_MOUSE CAV2_CAEEL HKN1_MAIZE BR3B_HUMAN BR3B_HUMAN RX_DROME HRPX_PLALO
515 623 726 85 1332 1351 1351 1410 1410 1410 1351 1351 1351 1351
133.66 133.66 133.66 133.66 133.66 133.66 133.66 133.66 133.66
699.55 699.55 699.59 699.59 68.59
4444 444 50 4444 444 444 444 444 444 444

## ALIGNMENTS

```
POLY-ALA.
POLY-ALA.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                  ношеорох
                                                                                                                                                                                                               Principal Pro0046; homeobox; 1. Pfam; Pr00157; pou; 1. PRINTS; PR01028; POUDOMAIN. ProDom; PD0100101; Homeobox; 1. SMART; SM00389; HOX; 1. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                          PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                         HSSP; P14859; IOCT.
MGD; MGI:102564; Pou3f3.
MGI:102564; Pou3f3.
InterPro; IPR001356; Homeobox.
InterPro; IPR00327; POU_domain.
                                                                                                                                                                                                                                                                                                                                                                                                          50012 MW;
                                                                                                                                                                                                                                                                                                                         PROSITE; PS00465; POU_2; 1.
Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                              16.0%;
26.1%;
                                                                                                                                                   EMBL; M88299; AAA39960.1; -.
                                                                                                                                                                                                                                                                                                               PROSITE; PS00035; POU_1; 1. PROSITE; PS00465; POU_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                 S31223.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           495 AA;
                                                                                                                                                                  PIR; S31223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wegner M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRN1_RAT
Q63262;
                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRN1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     %TTTTTTT¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGGHGFVVRETRVEEDINTCTGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
MEDLINE-92228768; PubMed-1565620;
MEDLINE-92228768; PubMed-1565620;
MEDLINE-92228768; PubMed-1565620;
MEDLINE-STRUCTURE and evolution of four POU domain genes expressed in mouse brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                             TRANSFAC; T00865; -

TRANSFAC; T00865; -

ROT; MGI:99150; Yyl.

R InterPro; IPR000822; Znf_C2H2,

R Ffant; PP00066; zf_C2H2; 4.

R PRINTS; PR00048; ZINCFINGER.

R PRODOM; PD000003; Znf_C2H2; 1.

R PRODOM; PS000089; ZINC_FINGER_C3H2; 4.

R PROSITE; PS00028; ZINC_FINGER_C3H2; 4.

DR PROSITE; PS050157; ZINC_FINGER_C3H2_2; 4.

KW Transcription regulation; Repressor; Activator; Nuclear protein; KW Zinc-finger; Metal-binding; DNA-binding; Repeat.

KW Zinc-finger; Metal-binding; DNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                           INVOLVED IN NUCLEAR MATRIX ASSOCIATION (BY SIMILARITY).
INVOLVED IN REPRESSION OF ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                            INVOLVED IN MASKING TRANSACTIVATION
INVOLVED IN MASKING TRANSACTIVATION
DOMAIN (BY SIMILARITY).
F -> S (IN REF. 3).
R -> G (IN REF. 3).
CO12378288E984F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 1 (BRN-1 protein).
POUJST3 OR OTF8.OR BRN1 OR BRN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92; DB 1; Length 414; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 AA
                                                                                                                                                                                                                                                        POLY-HIS.
GLY/SER-RICH.
ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
    email to license@isb-sib.ch).
                                   EMBL; L13966; AAA40477.1; JOINED.
EMBL; L13966; AAA40477.1; JOINED.
EMBL; L13967; AAA40477.1; JOINED.
EMBL; M74590; AAA37521.1; JOINED.
HSSP; P25490; JUBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                  44717 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 31.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || :| |:
99 VHHHQEVILVQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 VHERRESFLAR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                          375 ... 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                          371
                                                                                                                                                                                                                                                                                                                                                       333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRN1_MOUSE
P31361;
       an
                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                DOMAIN
ZN_FING
ZN_FING
ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
      send
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRN1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

```
5
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wise by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHH-------GHHGGHG- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ς;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98070400; PubMed-9405434;
Schreiber J., Enderich J., Sock E., Schmidt C., Richter-Landsberg
Proc. Natl. Acad. Sci. U.S.A. 69:3280-3284(1992).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
CLASS-3 SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-UUL-1998 (Rel. 36, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 1 (BRN-1 protein).
POUJF3 OR BRN1 OR BRN-1 OR RHS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Redundancy of class III POU proteins in the oligodendrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMEOBOX.
77B802E890C9A014 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 81.5; DB 1;
Pred. No. 0.26;
7; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 GPGLNSHDPHSDEDTPTSDDLEQFAKOFKORR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 -----FVVRETRVEEDINTCTGEVHERR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497 AA
```

```
[1]
SEQUENCE FROM N.A.
MEDLINE-96359175; PubMed-8703082;
MEDLINE-96359175; PubMed-8703082;
MEDLINE-96359175; PubMed-8703082;
MEDLINE-MALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WALAND-WA
                                                                                                          Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                          He X., Treacy M.N., Simmons D.M., Ingraham H.A., Swanson L.W., Rosenfeld M.G.;
                 01-NOV-1997 (Rel. 35, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/FOU domain protein 1 (BRN-1 protein).
POUJF3 OR BRNI OR OTF8.
                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
MEDLINE-89295573; PubMed-2739723;
                                                                                                                                                  NCBI_TaxID-9606;
                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSITE;
                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     le Moine C., Young W.S.;
"RHS2, a POU domain-containing gene, and its expression in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHH-----------GHHGGHG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 89:3285-3289(1992).
-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
-1- TISSUE SPECIFICITY: BRAIN.
-1- DEVELOPMENTAL STAGE: EXPRESSED FROM EMBRYONIC DAY 11.5 INTO
                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY. CLASS-3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00640505E343ABC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 GPGLNSHDPHSDEDTPTSDDLEQFAKOFKORR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.1%; Pred. No. 0.26; ive 7; Mismatches
                                                                                                                                                                                                                                                                                               -1- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 -----FVVRETRVEEDINTCTGEVHERR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA.
POLY-GLY.
POLY-HIS.
POLY-GLY.
               Biol. Chem. 272:32286-32293(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMEOBOX
                                                                           TISSUE-Hypothalamus;
MEDLINE-92228769; PubMed-1348858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO0028; POUDOMAIN.
PD000010; Homeobox; 1.
PD000583; POU_domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
InterPro; IPR001327; POU_domain.
Pfam; PP001046; homeobox; 1.
Pfam; PP00157; Pou; 1.
PRINTS; PR001028; POUDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSITE; PS00027; HOMEOBOX_1; 1.
ROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ001641; CAA04893.1; -. EMBL; M84644; AAA42041.1; -. HSSP; P14859; loct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 HC
50226 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO0035; POU_1; 1.
PROSITE; PSO0465; POU_2; 1.
Nuclear protein; DNA-binding; PA 49
                                                       SEQUENCE OF 325-449 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 26.1 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389; HOX; 1
SMART; SM00352; POU; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.ch).
-> S (IN REF. 2).
E536EFFFA5212319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POU.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY.
POLY-ALA.
POLY-PRO.
POLY-PRO.
POLY-ALA.
POLY-GLY.
HIS-RICH
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000010; Homeobox; 1.
ProDom; PD000583; POU_domain; 1.
SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00035; POU_1; 1.
                                                                                                                                                                                                                                                                                   EMBL; AB001835; BAA19459.1; -. PIR; S05042; S05042.
HSSP; P14859; 10CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POUDOMAIN.
                                                                                                                                                                                                                                                                                                                                TRANSFAC; T04469; -.
Genew; HGNC:9216; POU3F3.
MIM; 602480; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281
304
388
465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433
500 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
```

DB 1; Length 500;

Score 80.5;

¥.

200

PRT;

STANDARD;

BRN1\_HUMAN

BRN1\_HUMAN

RESULT

P20264; P78379; 01-FEB-1991 (Rel. 17, Created)

```
53 HHHGHHGGHGFVVRETRVE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                               initiator
                                                      TYY1_HUMAN
                                             RESULT 6
                                                                       ò
                   g
                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | | | | GHGGHGGAESVAVQTEEKTNEVNDAKYGGGSNYNDGRGGYNHGGGGHGGHGGH | 184
             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                        --- СКНССКС 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H----
                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
             Gaps
                                                                                                                                                                                                                            Laberge S., Castonguay Y., Vezina L.-P.;
"New cold- and drought-regulated gene from Medicago sativa.";
"Plant Physiol. 101:1411-1412(1993).
--- FUNCTION: MAY BE INVOLVED IN RESISTANCE OF THE PLANT TO
ENVIRONMENTAL STRESS.
--- INDUCTION: BY COLD, ABSCISIC ACID (ABA) AND DROUGHT STRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
             15;
                                                                                                                                                                                                                                                                                                                                                                            6 AA REPEATS OF Y-N-H-G-G-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79; DB 1; Length 204;
Pred. No. 0.19;
3; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GFGRHGGGVQQHV-VKEKFEEVDTV------SRAGANH-----
                               19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AA REPEATS OF H-G-G.
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8A2C082359FCC17F CRC64;
              22;
                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Cold and drought-regulated protein CORA.
                                                                                          204 AA
       Pred. No. 0.34
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              11 x :
2-1.
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-4.
2-5.
2-6.
2-8.
                                                                                                                                                                                                                 STRAIN-cv. Apica;
MEDLINE-94143496; Pubmed-8310076;
               3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19599 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.5%;
       ilarity 33.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                            EMBL; L03708; AAA99833.1;
                                                                                                                                                      (Alfalfa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                       Repeat
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AA;
       Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                         85
164
171
98
                                                                                                                                                                                     NCBI_TaxID=3879:
                                                                                                                                                       Medicago sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                           CORA_MEDSA
Q07202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                    CORA_MEDSA
                                                                             RESULT
                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                   셤
                                   ò
```

```
J. MOL. BIOL. 279:973-986(1998).

J. MOL. BIOL. 279:973-986(1998).

J. MOL. BIOL. BIOL. THE TRANSCRIPTION FACTOR THAT EXHIBITS
POSITIVE AND NEGATIVE CONTROL ON A LARGE NUMBER OF CELLULAR AND VIRAL GENES BY BINDING TO SITES OVERLAPPING THE TRANSCRIPTION START SITE. MAY PLAY AN IMPORTANT ROLE IN DEVELOPMENT AND DIFFERENTIATION. THE FUNCTION OF YYL AS AN ACTIVATOR OR A REPRESSOR IS SPECIFIED BY THE PRESENCE OF OTHER PROTEINS. FOR EXAMPLE IT A GYS AS A REPRESSOR IN ABSENCE OF ADENOVINGS ELA PROTEIN BUT AS AN ACTIVATOR IN ITS PRESENCE.

SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.

SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C242-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98152931; PubMed-9493912; McDLINE-98152931; PubMed-9493912; McDLINE-98152931; Stein J.L., Lian J.B., Bushmeyer S., Seto E., Atchison M.L., Penman S., van Wijnen A.J., Stein G.S., "Targeting of the YII transcription factor to the nucleolus and the nuclear matrix in situ: the C-terminus is a principal determinant for nuclear trafficking.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98308000; PubMed-9642075;
MEDLINE-98308000; PubMed-9642075;
Wiles J.H., Patel S.U., Mitchell J.B.O., Moody C.M., Justice D.E., Uppenbrink J., Doyle P.M., Harris C.J., Sadler P.J., Thornton J.M.;
"Design, synthesis and structure of a zinc finger with an artificial
                                                                                                                                                                                                                                            TYYI HUMAN STANDARD; PRT; 414 AA.
P25409; 041935;
01-MAY-1992 (Rel. 22, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-CAT-2001 (Rel. 40, Last annotation update)
17-CAT-2001 (Rel. 40, Last annotation update)
18-CAT-2001 (Rel. 40, Last annotation update)
19-CAT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation of a candidate repressor/activator, NF-El (YY-1, delta), that binds to the immunoglobulin kappa 3' enhancer and the immunoglobulin heavy-chain mu El site."; Proc. Natl. Acad. Sci. U.S.A. 88:9804-9808(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97098436; PubMed-8942976; Houbaviy H.B., Usheva A., Shenk T., Burley S.K.; "Cocrystal structure of YY1 bound to the adeno-associated virus P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nouso Sapirons, deracami, chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Merania; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-92005716; PubMed-1655281;
Shi Y., Seto E., Chang L.-S., Shank T.;
"Transcriptional repression by YX1, a human GLI-Kruppel-related protein, and relief of repression by adenovirus ElA protein.";
Cell 67:377-388(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whitson R.H., Huang T., Dang J., Itakura K.;
Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 93:13577-13582(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 304-414.
                                                                                                                                                                                                                                       414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell. Blochem. 68:500-510(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Foreskin;
MEDLINE-92052179; PubMed-1946405;
STRUCTURE BY NMR OF 353-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Park K., Atchison M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
```

```
NCBI_TaxID=9606;
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GFGRHGGGVQQHVVKEKFEEVDIVSRAGANHHHHGHHGGH-GFVVREIRVEEDINICTG 79
                                                                                                                                                              R Genew.

R MM; 600013;

R MM; 600013;

R MM; 600013;

R PRINTS; PRO00642; ZINCEINGER.

DR PRINTS; PRO00648; ZINCEINGER.

DR PROSTE; PRO0003; ZnC_CZH2; 1.

DR SWART; SW00355; ZnC_CZH2; 1.

DR PROSITE; PS00028; ZINC_FINGER_CZH2_1; 4.

DR PROSITE; PS50157; ZINC_FINGER_CZH2_1; 4.

DR PROSITE; PS50157; ZINC_FINGER_CZH2_1; 4.

KW Transcription regulation; Repressor; Activator; Nuclear protein; XM Zinc-finger; Metal-binding; DNA-binding; Repeat; 30-structure.

ASP/GIU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Gaps
                                                                                                                                                                                                                                                                                                                                                       INVOLVED IN NUCLEAR MATRIX ASSOCIATION.
INVOLVED IN REPRESSION OF ACTIVATED
TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                  INVOLVED IN MASKING TRANSACTIVATION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYRALHUMAN STANDARD; PRT; 763 AA.
013627; 092810; 092582; 090NM5;
01.NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Dual-specificity tyrosine-phosphorylation regulated kinase la (EC 2.7.1.-) (Protein kinase minibrain homolog) (MNBH) (HP86)
DYRKIA OR DYRK OR WNBH OR MNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                       15.5%; Score 79; DB 1; Length 414; 29.2%; Pred. No. 0.4; Live 6; Mismatches 7.5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      058C05A0AD2D04E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     -> R (IN REF. 2).
                                                                                                                                                                                                                                                                              GLY-RICH,
POLY-HIS,
GLX/SER-RICH,
ZINC FINGERS,
C2H2-TYPE,
C2H2-TYPE,
C2H2-TYPE,
C2H2-TYPE,
                                                                                         EMBL; M77698; AAAS9467.1; -.
EMBL; M76541; AAAS9926.1; -.
EMBL; Z14077; CAA78455.1; -.
PIR; A40350; A40350.
PDB; 1UBD; 23-DEC-96.
PDB; 1ZNM; Oll-APR-98.
                                                                                                                                                                                                                                                                                                                                                                                                                        ¥
                                                                                                                                                                                                                                                                                                                                                                                                                       44712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| :| | :
QVHHHQEVILVQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Conservative
                                                                                                                                                             Genew; HGNC:12856; YY1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 EVHERRESFLAR 91
                                                                                                                                                                                                                                                                                      80
170
407
320
347
                                                                                                                                                    TRANSFAC; T00915; -.
                                                                                                                                                                                                                                                                                                                                                                                                 65
196
414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     DOMAIN
2N_FING
2N_FING
2N_FING
2N_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYRA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                        Song W.J., Sternberg L.R., Kasten-Sportes C., van Keuren M.L., Chung S.H., Slack A.C., Miller D.E., Glover T.W., Chiang P.W., Lou L., Kurnit D.W.;

"Isolation of human and murine homologues of the Drosophila minibrain gene: human homologue maps to 21q22.2 in the Down syndrome 'critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., VARIANTS F-415; H-681, AND ALTERNATIVE SPLICING. MEDLINE=99263503; PubMed=10329007; Gulmera J., Casas C., Estlvill X., Pritchard M.; Human minibrain homologue (MNBH/DYRKI): characterization, alternative splicing, differential tissue expression, and overexpression in Down
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning of a human homolog of the Drosophila minibrain/rat Dyrk gene from 'the Down syndrome critical region' of chromosome 21."; Blochem. Blophys. Res. Commun. 225:92-99(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; A LONG FORM (SHOWN HERE), 1, 2, 3 AND 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN SKELETAL MUSCLE, TESTIS, FETAL LUNG AND FETAL KIDNEY.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING CENTRAL NERVOUS
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE-97026291; PubMed-8872470;
Guimera J., Casas. C., Pucharcos C., Solans A., Domenech A.,
Planas A.M., Ashley J., Lovett M., Estivill X., Pritchard M.A.;
"A human homologue of Drosophila minibrain (MNB) is expressed in the neuronal regions affected in Down syndrome and maps to the critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1- FUNCTION: MAY PLAY A ROLE IN A SIGNALING PATHWAY REGULATING NUCLEAR FUNCTIONS OF CELL PROLIFERRATION. PHOSPHORYLAYES SERINES, THREONINES AND TYROSINES RESIDUS IN ITS SEQUENCE AND IN EXOGENOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96332410; PubMed-8769099;
Shindoh N., Kudoh J., Maeda H., Yamaki A., Minoshima S., Shimizu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
Miki O., Masahira H., Yasufumi M., Naohiko S., Takahiro N.,
Hitoshi I., Nobuo N., Toshihiko E., Yoshiyuki S., Misao O.,
Ohira M., Seki N., Nagase T., Suzuki E., Nomura N., Ohara O.,
Hattori M., Sakaki Y., Eki T., Murakami Y., Saito T., Ichikawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- PTM: AUTOPHOSPHORYLATED ON TYR RESIDUES.
-i- DISEASE: OVEREXPRESSED 1.5-FOLD IN FETAL DOWN SYNDROME BRAIN.
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MNB/DYRK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region.";
Hum. Mol. Genet. 5:1305-1310(1996).
SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE-97131512; Pubmed-8975710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1). TISSUE-Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U58496; AAC50939.1; -.
EMBL; U52373; AAB18639.1; -.
EMBL; D85759; BAA12866.1; -.
EMBL; D86550; BAA13110.1; -.
                                                                                                                                                                                                                                                                                                                 Genomics 38:331-339(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 57:407-418(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimizu N
                                                                                                                                                                                                                                                                                   region,
```

```
763 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NP_BIND
BINDING
ACT_SITE
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                              region'
. 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHG 56
                                                                                                                                                                                                                                                                   GGSSGTSNGGRARSDPTHOHEHSGG -> VECHWMPGAFRM
TVSFTLEVHDVPV (IN ISOFORM 3).
MISSING (IN ISOFORM 3).
                                  MINI, 000030;
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000290; Ser_thr_pkinase.
InterPro; PR00069; pkinase; 1.
Probom; PD000001; Euk_pkinase; 1.
SWART; SW00220; S_TKC; 1.
SWART; SW00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_LOM; Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; Transferase; Serine/threonine-protein kinase; APP-binding; Nuclear protein; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                           SSHVVHLLVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Gaps
                                                                                                                        BIPARTITE NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                    PHOSPHORYLATION (AUTO-) (BY SIMILARIT PHOSPHORYLATION (AUTO-) (BY SIMILARIT MISSING (IN ISOFORM 1).

GGSSGTSNSGRARS -> GASAISCSSWLVRH (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
16-UUL-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dual-specificity tyrosine-phosphorylation regulated kinase lA
                                                                                                                                                                                                                                                                                            ROOFPAPLGWSGTEAPTOVIVETHPV -> S
AILRWSSTGCOVPLE (IN ISOFORM 4)
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77; DB 1; Length 763;
Pred. No. 1.2;
4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                   -> N (IN REF. 1).
-> G (IN REF. 1).
-> P (IN REF. 1).
7C3A52A3CBB04FB5 CRC64;
                                                                                                                                                                                                               PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                             MISSING (IN ISOFORM 4)
                                                                                                                                                                                                                                                            MISSING (IN ISOFORM 2)
                                                                                                                                       PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                            /FTId=VAR_009395.
                                                                                                                                                                                                                                                                                                                                             FTIG=VAR_009396
                                                                                                                                                                                               SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                    -> S (IN
-> P (IN
                                                                                                                                                                                                                                                        ISOFORM 2
                                                                                                                                                                          POLY-SER
                                                                                                                                                                                                         POLY-SER
                                                                                                                                                                                                                                                                                                                                      -\
H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . PRT;
                                                                                                                                                                                                                                                                                                                                                                     ^ ^
                                                                                                                                                                                                                                                                                                                                                                                                            85584 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%;
33.3%;
   EMBL, AF108830; AAD31169.1;
HSSP; Q00534; 1B18.
Genew; HGNC:3091; DYRK1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                     32
47
57
1123
397
592
679
                                                                                                                                                                                                                                                                                       763
                                                                                                                                                                                                                                                                                                              763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | | HHHHHG 620
                                                                                                                                                                                                                                                                                                                                                                                     397
592
679
763 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ннеснс 62
                                                                                                                                                                                                                                                                                                                                      681
                              MIM; 600855; -
                                                                                                                   Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYRA_MOUSE
Q61214;
                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                 MOD_RES
VARSPLIC
VARSPLIC
                                                                                                                                                                   ACT_SITE
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                 MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                 /ARSPLIC
                                                                                                                                                                                                                                                                         ARSPLIC
                                                                                                                                                                                                                                                                                         ARSPLIC
                                                                                                                                          DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                       /ARIANT
                                                                                                                                                                                                                                                                                                                        /ARIANT
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYRA_MOUSE
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * DE DE DE
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding; Nuclear protein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION, AND SUBUNIT.

SUBCINE-97224401; PubMed-9070862;
Song W.J., Chung S.H., Kurnit D.M.;
Song W.J., Chung S.H., Kurnit D.M.;
"The murine Dyrk protein maps to chromosome 16, localizes to the nucleus, and can form multimers.";
Blochem. Blophys. Res. Commun. 231:640-644(1997).

Blochem. Blophys. Res. Commun. 231:640-644(1997).

HOSPHOTION: MAY PLAY A ROLE IN A SIGNALING PATHWAY REGULATING FARMAY REGULATING FARMAY REGULATING PATHWAY 
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-Swiss Webster / NIH;
MEDLINE-97131512; PubMed-8975710;
Song W.J., Sternberg L.R., Kasten-Sportes C., van Keuren M.L.,
Chung S.H., Slack A.C., Miller D.E., Glover T.W., Chiang P.W., Lou L.,
Kurnit D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation of human and murine homologues of the Drosophila minibrain gene: human homologue maps to 21q22.2 in the Down syndrome 'critical
(EC 2.7.1.-) (Protein kinase minibrain homolog) (MNBH) (MP86) (Dual specificity YAK1-related kinase).
DYRKIA OR DYRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation.
BIPARTITE NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Nuclear.
-i- PTM: AUTOPHOSPHORYLATED ON TYR RESIDUES (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MNB/DYRK SUBFAMILY.
                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E117DDD6C5E8C74F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-SER.
POLY-HIS.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77; DB 1;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; WGD: 12103029; Dyrkla.
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
Prom; PP000069; pkinase; 1.
SWART; SW00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ar protein; 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U58497; AAC52994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 38:331-339(1996).
```

~

```
ä
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration the Ewes the Swiss Institute of Bloinformatics and the EWES outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.ch).
                                                      11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence characteristics, subcellular localization, and substrate specificity of DYRK-related kinases, a novel family of dual specificity protein Kinases."

J. B101. Chem. 273:25893-25902(1998).

-I. FUNCTION: MAY PROLE IN A SIGNALING PATHWAY REGULATING NUCLEAR FUNCTIONS OF CELL PROLIFERARATION. PHOSPHORYLATES SERINES, THREONINES AND TYROSINES RESIDUES IN ITS SEQUENCE AND IN EXOGENOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dual-specificity tyrosine-phosphorylation regulated kinase 1A
EC 2.7.1.7 (Protein kinase minibrain homolog) (MNBH) (RP86) (Dual
Specificity YAK1-related kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Nuclear.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORNS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARREPRODUCTS BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- PTM: AUTOPHOSPHOYLATED ON TYR RESIDUES (BY SIMILARITY).
-1- SIMILARITY: BELLONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND MUTAGENESIS OF TYR-219.
TRAIN-Spraque-Dawley; TISSUE-Brain;
MEDLINE-96216443, PubMed-8631952;
Rentrup H., Becker W., Heukelbach J., Wilmes A., Schuermann A.,
Huppertz C., Kahnulainen H., Joost H.-G.;
Dyrk, a dual specificity protein kinase with unique structural
features whose activity is dependent on tyrosine residues between
Subdomains VII and VIII.";
J. Biol. Chem. 271:3488-3495(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98421512; Pubmed-9748265;
Becker W., Weber Y., Wetzel K., Elrmbter K., Tejedor F.J.,
Joost H.-G.;
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kentrup H.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                          763 AA.
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X79769; CAA56164.1; -.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNB/DYRK SUBFAMILY.
                                                                                                                                                                                                                                                615 нинин 620
                                                                                                                                                                                   57 HHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                DYRA_RAT
Matches
                                                                                                                                                                                                                                                                                                                                            RESULT 9

DYRA_RARA

TO 0634

DT 16-0

DE 0636

DE 0636

DE 0636

OC EUKA

                                                             ò
                                                                                                                   g
                                                                                                                                                                                   ð
                                                                                                                                                                                                                                             a
```

```
ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHHG 56
       Fromis Founds: parimage; 1.

Problem: Probooo; Sarc; 1.

SMART; SM00220; Sarc; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011, PROTEIN_KINASE_DOM; 1.

Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding; Nuclear protein; Phosphorylation; Alternative splicing.

DOMAIN 117 134 BIPARTITE NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glesi M., Bergaggel P.L., Shonukan O.O., Martelli M.L., Brents L.A., Chen T., Schrock E., Ried T., Shonukan O.O., Martelli M.L., Brents L.A., Frequent dysregulation of the c-maf proto-oncogene at 16q23 by Blood 91:4457-4463(1998).

1. SUBCELLUIGAR LOCATION: Nuclear (By similarity).

1. SUBCELLUIGAR LOCATION: Nuclear (By similarity).

1. ALTERNATIVE PRODUCTS: 2 isoforms, a long form (shown here) and a short form; are produced by alternative splicing.

1. DISEASE: Some forms of multiple myeloma (MM) tumors are characterized by a chromosomal translocation t(14;16)(q32.3;q23)
                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostom1;
                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (AUTO-).
PHOSPHORYLATION (AUTO-).
MISSING (IN SHORT ISOFORM).
Y->F: REDUCED AUTOPHOSPHORYLATION (
TYROSINE, BUT NO LOSS OF HISTONE
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that involves MAF and an 19H locus.
-- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                       CBSEC7EC4C1F9A47 CRC64;
                                                                                                                                                                                                                                                 SER/THR-RICH.
POLY-SER.
PHOSPHORYLATION (AUTO-).
                                                                                                                                                             ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-SER.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAR_HUMAN STANDARD; PRT; 403 AA. 07544; 09UP93; 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Transcription factor Maf (Proto-oncogene c-maf).
                                                                                                                                                                                                                                                                                                                                                                                                                Score 77; DB 1;
Pred. No. 1.2;
1; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-98282186; Pubmed-9616139;
                                                                                                                                                  PROTEIN KINASE
                                                                                                                                                                                                                                       POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                    763 AA; 85541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 15.1%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Conservative
Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615 нинин 620
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 HHGGHG 62
                                                                                                                                            159
165
188
188
289
599
607
666
664
664
70
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                         ACT_SITE
DOMAIN
                                                                                                                                                                                                                                                                                           MOD_RES
MOD_RES
VARSPLIC
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                          DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            tches
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alkema M.J., Jacobs J., Voncken J.W., Jenkins N.A., Copeland N.G., Satijn D.P.E., Otte A.P., Berns A., van Lohuizen M.; Mpc2, a new murine homolog of the Drosophila polycomb protein is a member of the mouse polycomb transcriptional repressor complex.", J. Mol. Biol. 273:993-1003(1997).

- FUNDION: INVOLVED IN MINTAINING THE TRANSCRIPTIONALLY REPRESSIVE STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED IN ITS EXPRESSIBILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 SEEVRSVAPAGFGRHGGGVQQH-----VVKEKFEEVDTVSRAGANHHHHHHHHHGHHGGH 61
                                                                                                                                                                                                                                                                                                                                                                                                                               ITEPTRKLEPSVGYATFWKPQHRVLTSVFTK -> M (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                      MBL) ...
jenew, HGNC:67/u,
MIM; 177075; -...
MIM; 177075; -...
InterPro; IPR004827; TF_MAf.
InterPro; IPR004826; TF_MAf.
Pfam; PF03131; bZIP_Maf; 1.
SMART; SM0338; BRLZ; 1.
SNART; SM0338; BRLZ; 1.
Proto-oncogene; Transcription regulation; DNA-binding;
Proto-oncogene; Transcription regulation; Chromosomal translocation.
Proto-oncogene; Transcription Pasic MOITE
LEUCING-ZIPPER.
LEUCING-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Chromobox protein homolog 4 (Polycomb 2 homolog) (Pc2) (MPc2).
CBX4 OR PC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 31.6%; Pred. No. 0.8;
Matches 18; Conservative 8; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHORT ISOFORM).
263D2FF2AF8DFB5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: CONTAINS 1 CHROMO DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                              POLY-HIS.
POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98035734; PubMed-9367786;
                                                                                         EMBL; AF055377; AAC27038.1; -. EMBL; AF055378; AAC27039.1; -. EMBL; AF055376; AAC27037.1; -. Genew; HGNC:6776; MAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 AA; 41961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CBX4_MOUSE
055187;
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CBX4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
phis SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                     ñ
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cygriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chromatin regulator; Nuclear protein; Transcription regulation;
                                                                                                                                                                                                                       8;
                                                                                                                                                                                            / Match 14.9%; Score 76; DB 1; Length 551; Local Similarity 37.8%; Pred. No. 1.1; hes 17; Conservative 2; Mismatches 18; Indels
                                                                                                                                                                                                                                                                    45 SRAGANHHHHHHHHGHHGGH---GFVVRETRVEEDINTCTGEVHERRE 86
                                                                                                                                          11 69 CHROMO.
383 395 POLY-HIS.
551 AA; 60581 MW; 30CEB09A82C58400 CRC64;
                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
POU domain protein 1 (ZFPOUI).
                                                                                                                                                                                                                                                                                                                                         425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D13045; BAA02377.1; -.
PIR; JH0710; JH0710.
HSSP; P14859; 10CT.
ZFIN; ZDB-GENE-990415-209; Poul.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probom; PD000010; Homeobox; 1. probom; PD000583; POU_domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox InterPro; IPR000327; POU_domain
                             MGD; MGI:1195985; Cbx4.
InterPro; IPR000953; Chromo.
Pfam; PP00385; Chromo; I.
PRINTS; PR00504; CHROMODOMAIN.
SMART; SM00298; CHROMO, I.
PROSITE; PS00598; CHROMO, I.
PROSITE; PS00139; CHROMO, 2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00028; POUDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
      EMBL; U63387; AAB96874.1;
HSSP; P23197; 1AP0.
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00389; HOX; 1.
                       HSSP; P23197
                                                                                                                                                                                                                                                                                                                                            POU1_BRARE
                                                                                                                                        Repressor.
                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom;
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                    DOMAIN
                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                   RESULT 12
POU1_BRARE
                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                               qq
CCC
DR
DR
DR
DR
DR
DR
SO
SO
                                                                                                                                                                                                                                                         ò
```

```
TMAF_AVIS4
                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                        DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMAF_AVIS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
      a
                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                    18 APAGF---GRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGH-----HGGHGFVVRET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Fetal brain;
MEDLINE-P64459707; PubMed-9315667;
Satijn D.P.E., Olson D.J., van der Vlag J., Hamer K.M., Lambrechts C., Masselink H., Gunster M.J., Sewalt R.G.A.B., van Driel R., Otte A.P.;
Interference with the expression of a novel human polycomb protein, hPC2, results in cellular transformation and apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Cell. Biol. 17:4105-4113(1997).
FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE
STATE OF GENES. MOIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
IN ITS EXPRESSIBILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 455-558 FROM N.A. MEDLINE-97342649; PubMed-9199346; Satijn D.P.E., Gunster M.J., van der Vlag J., Hamer K.M., Schul W., Alkema M.J., Saurin A.J., Freemont P.S., van Driel R., Otte A.P.; "RING1 is associated with the Polycomb group protein complex and acts as a transcriptional repressor.";
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IN 11S EAFMESSIBILII.
SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            þe
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                regulation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may produced by alternative splicing.
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- SIMILARITY: CONTAINS 1 CHROWO DOMAIN.
                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                            CBX4_HUMAN STANDARD; PRT; 558 AA.
000257; Q96C04;
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
chromobox protein homolog 4 (Polycomb 2 homolog) (Pc2) (hPc2).
                                                                                                                                                        Length 425;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                            5C50C09CEF7EF16D CRC64;
                                                                                                                                                                               33;
                                                                                                                                                       DB 1;
                                                                                                                                                   14.8%; Score 75.5; DB 30.9%; Pred. No. 0.95;
                                                                                                                                                                              5; Mismatches
                 PROSITE; PS00035; PUL, 1
PROSITE; PS00465; POUL2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA-binding; Transcription 1
84 98 ALA-RICH
                                                                                         HIS-RICH.
                                                                                                                 HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Nuclear.
          PS00027; HOMEOBOX_1; 1.
PS00035; POU_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                            45626 MW;
                                                                                                                                                                Local Similarity 30.9
                                                                                                                                                                                                                                                                                235 HSDEDTPT 242
                                                                                                                                                                                                                                                        RVEEDINT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                          425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Colon
                                                                                                                                                                                                                              175
                                                                                                                                                                                                                                                        69
             PROSITE;
                                                                                                                DNA_BIND
                                                                                                                          SEQUENCE
                                                                                                                                                    Query Match
                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                  CBX4_HUMAN
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                      RESULT 13
OF FFF SOR SOR
                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                              셤
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avian musculoaponeurotic fibrosarcoma virus AS42.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90046665; Pubmed-2554284;
Nishizawa M., Kataoka K., Goto N., Fujiwara K.T., Kawai S.;
Nishizawa M., Kataoka K., Goto N., Fujiwara K.T., Kawai S.;
Nuaf, a viral oncogene that encodes a 'leucine zipper' motif.";
Proc. Natl. Acad. Sci. U.S.A. 86:7711-7715(1989).
-!- FUNCTION: MIGHT BE A TRANSCRIPTIONAL TRANS-ACTIVATOR.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- DISEASE: INDUCES MUSCULOAPONEUROTIC FIBROSARCOMA IN CHICKENS.
-!- MISCELLANGOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-MAF
POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS50599; CHROWO_1; 1.
PROSITE; PS50013; CHROWO_2; 1.
Chromatin regulator; Nuclear protein; Transcription regulation;
Repressor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75.5; DB 1; Length 558; Pred. No. 1.3; 4; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7158526991D33463 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> P (IN REF. 2).
-> C (IN REF. 2).
-> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 NHHHHHHHHGHHGGHGFVVRETRVEEDINTCTGEVHERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-LUN-2002 (Rel. 41, Last annotation update)
Transforming protein Maf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-HIS.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHROMO
                                                                                                                                                                                                                                        EMBL; AF013956; AAB80718.1; -.
EMBL; BC014967; AAH14967.1; -.
EMBL; U94344; AAB62734.1; -.
HSSP; P23197; 1AP0.
Genew; HGNC:1554; CBX4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000953; Chromo.
Pfam; PF00385; chromo; 1.
PRINTS; PR00504; CHROMODOMAIN.
SMART; SM00298; CHROMO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M26769; AAA42377.1; -. PIR; B33975; TVFVAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 37.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            456
475
478
558 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAR REPRESENTATION OF THE PROPERTY OF THE PROP
```

```
Search completed: June 6, 2003, 12:50:40 Job time : 14 secs
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA Adams M.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
RA Adams M.D., Scherer S.E., Holf W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandall M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Bogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Briton R.C., Bayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Berman B.P., Bhannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Berman B.P., Bhannkoch C., Bassley E.M.,
RA Borkova D., Botchan M.R., Bourd W., Brokstein P., Brottler P.,
Rockova D., Botchan M.R., Bourd W., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Danlke C., Davenport L.B., Davis S.P.,
RA Cherry J.M., Cawley S., Davlkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Davlkov B.C., Dunn P.,
RA Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernis M.L., Harvey D., Helman T.J., Hernis M.C.,
RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibeqwam C.,
RA Lasko P., Lei Y., Levaltsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levaltsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Lid Y., Lin X.,
Lin X., Mattei B., McIntosh T.C., McLeod M.P., Lid Y., Lin X.,
Lin X., Mattei B., McIntosh T.C., McLeod M.P., Lid Y., Lin Y.,
Lin X., Mattei B., McIntosh T.C., McLeod M.P., Lid Y., Lin Y.,
RA Lin X., Mattei B., McIntosh T.C., McLeod M.P., Lid X., Lid Y., Lin X.,
RA Lin X., Mattei B., McIntosh T.C., McLeod M.P., Lid X., Lid Y., Lin X.,
R. Lin X., Mattei B., McIntosh T.C., McLeod M.P., Lid X., Lid Y., Lid X.,
R. Lin X., McLeon T.C., McLeod M.P., Lid X., Lid Y., Lid X.,
R. Lid X., McLeon T.C., McLeod M.P., Lid X., Lid X.,
R. Lid X., McLeon T.C., McLeod W.P., Lid X.,
R. Lid X., McLeon T.C., Leviker A., Lid X., Lid X.,
R. Lid X., McLeon T.C
                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wright T.R., O'Donnell J.M.;
"The catecholamines up (Catsup) protein of Drosophila melanogaster functions as a negative regulator of tyrosine hydroxylase activity."; Genetics 153:361-382(1999).
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                         Oncogene; Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                    .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99403013; PubMed-10471719;
Stathakis D.G., Burton D.Y., McIvor W.E., Krishnakumar S.,
Wright T.R., O'Donnell J.M.;
                                                                                                                                                                                                                                                                           Score 75; DB 1; Length 369;
Pred. No. 0.93;
2; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                         143 GGSVPAEEMGSAAAVVSAVIAAAAAQGGAPHYHHHHHHHHHHHGGG 187
                                                                                                                                                                                                                                                                                                                                                    26 GGGVQQHVVKEKFEEVDTVSRAGA-----NHHHHHHHHHGHHGGHG 62
                                                                                                                                                                                                     BASIC MOTIF.
LEUCINE-ZIPPER.
F386B220ACE50FF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Catecholamines up protein.
                                                                                                                                                POLY-GLY.
POLY-GLY.
POLY-GLY.
                                                                                                             POLY-ALA.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Berkeley;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                              38892 MW;
       TKANSFAC; TUL440; ...
INTERPRO; IPRO04827; TE_BZIP.
INTERPRO; IPRO04827; TE_BZIP.
PÉBM; PF03131; BZIP_MAÉ; I.
SWART; SMO0338; BRLZ; I.
                                                                                                                                                                                                                                                                           Query Match 14.7%;
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                            369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catsup OR CG10449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muscomorpha; Eph
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSUP_DROME
Q9V3A4;
                                                                                                                                                                      DOMAIN
DOMAIN
DNA_BIND
DOMAIN
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                 DOMAIN
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSUP_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in no way
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Rabue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spice E., Spradling A.C., Stapleton M., Strong R., San B.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Nang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Re J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A. L., Zhong F.M., Zhong W., Zhou S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
--- FUNCTION: NEGATIVELY REGULATES TYROSINE HYDROXYLASE ACTIVITY.
--- SIMILARITY: BELONGS TO THE KE4/CATSUF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstati
the Buropean Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 GANH-HHHHGH-----HGGHGFVVRETRVEEDINTCTGEVHERRESFLARA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
F7111A254C07AB4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74; DB 1; Length 449;
Pred. No. 1.4;
7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (
or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR002395; Kininogen.
Interpro; IPR003689; Zn_trnprt_Zip.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF216584; AAF37226.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0002022; Catsup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00334; KININGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003661; AAF53744.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 32.7*
....has 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395
316
449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEM
```

```
Q20691 Caenorhabdi
Q20699 mus musculu
Q42448 medicago sa
Q9nc84 strongyloce
G9vx61 drosophila
Q9fh24 arabidopsis
Q92712 medicago sa
G00116 homo sapien
Q94189 oryza sativ
Q84189 oryza sativ
G94189 oryza sativ
G94189 oryza sativ
G94180 drosophila
Q8460 drosophila
Q8461 drosophila
Q8471 drosophila
Q9vx16 drosophila
Q9vx16 drosophila
Q9vx16 drosophila
Q9vx16 drosophila
Q9vx16 drosophila
Q9vx16 drosophila
Q9vx18 drosophila
     091f59 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AYYQEVDYCSEEVRSVAP-AGFGRHGGGYQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGG 60
                                                                                                                                                                                                                                                                              O9kg54 bacillus |
O95rh4 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0470A12."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.1%; Pred. No. 4.9e-23;
Matches 54; Conservative 14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003436; BAB90280.1; -.
SEQUENCE 229 AA; 25296 MW; D6ED4AA65FFEF61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0470A12.5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 DYLMVRETKVEEDFNICTGEFRERKQSFLLKSD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                       229 AA
                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                    Q90689
Q90784
Q90784
Q90781
Q90781
Q90189
Q90189
Q90471
Q90181
Q90181
Q90181
Q90181
Q90181
Q90181
Q90775
Q9688
Q90776
Q90776
Q90776
Q90788
Q90788
                                                                                                                                                                                                                                                                 Q20690
Q9KG54
Q95RH4
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                 PRELIMINARY;
5.77.5
5.77.5
5.77.5
7.7.5
                                                                                                                                                                                                                                                               76.5
76.5
76.5
                                                                                                                                                                                                                                                                                                                                                                  Q8S0B1
Q8S0B1;
                                                                                                                                                                                                                                                                                                                                                RESULT 1
 RESULT
Q9SM40
                                                                                                                                                                                                                                                                                                                                                         Q8S0B1
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q880bl oryza sativ
Q9sm40 sporobolus
Q850b2 oryza sativ
Q92x6 arabidopsis
Q9w63 arabidopsis
Q4443 arabidopsis
Q9p44 neurospora
Q8y219 homo sativ
Q9y219 homo sativ
Q9y219 arabidopsis
Q9447 arabidopsis
Q9x342 arabidopsis
Q9x342 drosophija
                                                         June 6, 2003, 12:47:53 ; Search time 50 Seconds (without alignments) 383.248 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90wv0 petromyzon
Q9nes7 caenorhabd1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           510
1 MAYYQEVDXCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                671580
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                     671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                         protein search, using sw model
                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9SM40
Q8SOB2
Q93ZA6
Q9SW63
Q24643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9P543
Q8S0B4
                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             094407
09F233
09W3D2
09VWM5
090WV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09UAY0
09Y2L9
                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_unclassified:*
                                                                                                                                                                                                                                                                                                                           sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                            sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                 sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                   US-10-090-035-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                    SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                          sp_mhc: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.6
18.1
18.1
18.1
10.1
10.0
10.9
10.9
10.5
116.3
116.2
                                                                                                                                                                                                                                                                                                                                               6:
7:
10:
110:
112:
113:
115:
116:
                                                                                                         Perfect score:
                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274
1777
141
992.5
992.5
86.5
86.5
86.8
84
84
84
83
                                      OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.
                                                                                                                     Sequence:
                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                   Database
                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
```

```
-JUN-2002 (TrEMBLrel. 21, Last annotation update)
             AT4g36900/C7A10_460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09SW63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9SW63
                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95W63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                             1 MAYYQE-VDYCSEEVRSVAPAGFGRH-GGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHH 58
                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Putative glycine-rich protein.
Sporobblus stapfianus (Ressurection grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Chloridoideae; Eragrostideae; Sporobolus.
                                                                                                                                                                                                                                                                                                         3 YYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGHHGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 YYSEVDHCAEEMNRPP------HAGGEHYAVRRESYEEVDEWARAGRGHHHGNGGGGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                       Neale A.D., Blomstedt C.K., Bronson P., Le T.N., Guthridge K., Evans J., Gaff D.F., Hamill J.D.;

Evans J., Gaff D.F., Hamill J.D.;

"The isolation of lowly-transcribed genes which are induced during dessication of the resurrection grass Sporobolus stapfianus.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ242802; CAB61838.1;

SEQUENCE 95 AA; 10668 MW; D756DCE2B68DDBSB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
9
                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 27.6%; Score 141; DB 10; Length 102; Local Similarity 45.8%; Pred. No. 2e-08; nes 27; Conservative 8; Mismatches 18; Indels
                                                                                                                                                                                                                                                   Length 95;
                                                                                                                                                                                                                                                 Score 177; DB 10; Length 9:
Pred. No. 1.5e-12;
8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone:P0470A12.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003435; BAB90279.1; -
SEQUENCE 102 AA; 11214 WW; 6FF1266B1CDE7768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel, 21, Created)
01-JUN-2002 (TrEMBLrel, 21, Last sequence update)
01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           102 AA.
         95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                  Created
                                                                                                                                                                                                                                                                                                                                                           S8 GNQCHGSGHFQARETKFE 75
                                                                                                                                                                                                                                                                                                                                             59 G--GHG---FVVRETRVE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TremBLrel. 19, (TremBLrel. 19,
                                                                                                                                                                                                                                                    ch 34.7%;
1 Similarity 57.7%;
45; Conservative
                                   (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
             PRELIMINARY;
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 45; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P0470A12.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=39947;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=56623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          093ZA6;
093ZA6;
01-DEC-2001 (01-DEC-2001)
                                  01-MAY-2000 (
01-MAY-2000 (
01-MAR-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P0470A12
                                                                                                                                                                                                                                                                                                                                                                                                                                          08S0B2;
                                                                                                                                                                                                                                                                                                                                                                                                                               Q8S0B2
             Q9SM40
Q9SM40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
Q93ZA6
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                    Q8S0B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25F
                                                                                                                                                                                                                                                                                                                                                                                                                               ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                      g
               ò
                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                 ö
```

```
21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R 69
                                                                                                                                                                                                                        Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Namann G.,
Kawai J., Lam B., Lee J.M., Lin J., Lilu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TINY-like protein.
C7Al0.460 OR A14636900.
Arabidosis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Mayer K.F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 299707; CAB16766.1; -.
EMBL; AL161590; CAB80356.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ecker J.R.;

Arabidopsis cDNA clones.";

Arabidopsis cDNA clones.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AND57683; ANL15314.1;

InterPro; IPR001471; TF_ERF.

Pfam; PF00847; AP2-domain; 1.

ProDom; PD001423; TF_AP2; 1.

ProDom; PD001423; TF_AP2; 1.

ProDom; PD001423; TF_AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schueller C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.1%; Score 92.5; DB 10;
33.8%; Pred. No. 0.013;
iive 12; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; 080337; 2GCC.
Interpro; IPR001471; TF_ERF.
Pfam; PR00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMYT.
ProDom; PD001423; TF_AP2; 1.
SMART; SM00380; AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.8%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|::|::
159 INDDLMECSSK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 VEEDINTCTGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
```

```
12 EEVRSVAPAGFGRH----GGGVQQHVVKEKFEEVDTVSRAGA-----NHH------ 52
                                                                                                                                                                                  Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spérmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                              Neurospora crassa.
Eukaryota; Fuugi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0470A12."
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003436; BAB90277.1; "... F7E0297877F6DE9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1245;
                       Related to multifunctional cyclin-dependent kinase PHO85 824H17.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
ANK_repeat; Cyclin; Kinase; Repeat.
SEQUENCE 1245 AA; 137798 MW; 16BD0F6A04596A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                     German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; ALJS6815; CAB92623.1;
HSSP; P42773; LIHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0470A12.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89; DB 3;
Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11:
259 HHYGGATAAAYGNASNKQHFTAAAAGHHSSGGH 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 SRAGANHHHHHHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.58;
72.28;
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002110; ANK.
InterPro; IPR004129; GDPD.
InterPro; IPR004331; SPX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.5
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.9%
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         fam; PF00023; ank; 6.
fam; PF03009; GDPD; 1
fam; PF03105; SPX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00248; ANK; 3
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P0470A12.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8S0B4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8S0B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
Q8S0B4
                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCOCCOS SEL REL REL REL SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                              5
                                                                                                                                              21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHHH-HGGHGFVVRET--R 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R 69
                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
TINY-11ke protein (Fragment).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                        18.1%; Score 92.5; DB 10; Length 196;
33.8%; Pred. No. 0.013;
Live 12; Mismatchès 24; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okamuro J.K., Caster B., Villarroel R., van Montagu M., Jofuku K.D.;
"The AP2 domain of APETALA2 defines a large new family of DNA binding
proteins in Arabidopsis.";
Proteins Lin Arabidopsis.";
EMBL: AGOGS AST. U.S.A. 94:7076-7081(1997).
EMBL: AF003103; AAC49776.1;
HSSP: 080337; 2GCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%; Score 92.5; DB 10; Length 259; 33.8%; Pred. No. 0.018; Live 12; Mismatches 24; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
    21362 MW; 0023D5571345C6A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 259
259 AA; 28615 MW; 0464949DB6C619DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TINY-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                        .259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1245
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97338147; PubMed-9192694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHKSPELEMNT
ProDom; PD001423; TF_AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR001471; TF_ERF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 15, C
(TrEMBLrel. 15, I
(TrEMBLrel. 21, I
                                                        Local Similarity 33.8 hes 24; Conservative
                                                                                                                                                                                                                             ::|::|
159 INDDLMECSSK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.19
Best Local Similarity 33.89
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                      70 VEEDINTCTGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00380; AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 INDDLMECSSK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 VEEDINTCTGE 80
      Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09P543;
09P543;
01-OCT-2000 (
01-OCT-2000 (
  SEQUENCE
                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                024643
                                                                                 Matches
                                                                                                                                                                                                                                                                                                     RESULT (

43 AC  

024 643  

024 643  

024 643  

025 AC  

027 AC  

027 AC  

027 AC  

028 AC  

029 AC  

020 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    099543
ID 099
AC 099
DT 011
DT 01
S
                                                                                                                      ò
                                                                                                                                                        q
                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

Gaps

ő

ŝ

Gaps

43;

```
Ecker J.R.;
"Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 RSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRAGANHHHHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BRISTOL NO.

SETRAIN=BRISTOL NO.

MEDINE-94150718; PubMed-7906398;

Wilson R., Adnacough R., Anderson K., Baynes C., Berks M.,

Wilson R., Alanscough R., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durinn R., Favello A., Fulton L.,

Jones M., Kershaw J., Kirsten J., Lister M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latraille P.,

Lightning J., Lloyd C., McMurray A., Mortinnore B., O'Callaghan M.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Sluston J.,

Phomas K., Waudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.0%; Score 86.5; DB 5; Length 471; 34.8%; Pred. No. 0.17; Live 4; Mismatches 16; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pauley A., Scheet P., Harper M.;
"The sequence of C. elegans cosmid W03G1.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125964; AAD14753.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14753.1; -.
50885 MW; BDF30B59A64A985B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  793 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                    Created)
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIAA1016 protein (Fragment) KIAA1016.
                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, W0321.5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans.";
Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | | 427 PPHHGHHHF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 24; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --HHGGHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09Y2L9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9Y2L9
                                                                                                                                                                                                                        W03G1.
                                                                                               O9UAYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20972L9
11D 209
11D 209
10D 200
10D 20
                                                                           29UAY0
                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
6 EVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEE----VDTVSRAGA-----NHHHHH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Cheuk R., Chen H., The J.M., Goldsmith A.D., Hayashizaki Y.,

Bowser L., Carninch P.X., Jones T., Kamiya A., Karlin-Neumann G.,

Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Marusaka M.,

Nguyen M., Onodera C.S., Palm Ç.J., Pham P.K., Quach H.L., Sakurai T.,

Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
          Magase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miagase T., Ishikawa R., Suyama M., Ohara O.;
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:63-70(1999).
EMBL; AB023233; BAA76860.1;
InterPro; IPR001715; Calpoinf-like.
InterPro; IPR001114; HPL-SerP_site.
InterPro; IPR001611; LAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
41-154-990/F14C21_5.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eurosids 11; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGH---HGGH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 ELPFSPRGERCDPPAGAAGRGGGAREKMATPGSEPQPFVPALSVATLHPLHHPHHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 16.9%; Score 86; DB 4; Length 793; Best Local Similarity 32.8%; Pred. No. 0.37; Matches 22; Conservative 7; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF424608; AAL11602.1; -
SEQUENCE 441 AA; 48816 MW; 520163FE0A8DE447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0BE99CC48C3BB37C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.5%; Score 84; DB 136.8%; Pred. No. 0.31; Live 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSS0021; CH; 1.
PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           793 AA; 87801 MW;
                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR003592; LRR_out.
Interpro; IPR003591; LRR_typ.
Pfam; PF00307; CH; 1.
Pfam; PF00560; LRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PRO0019; LEURICHRPT.
SMART; SM00033; CH; 1.
SMART; SM00370; LRR; 3.
SMART; SM00369; LRR_TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 36.8%
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 ОННССТС 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 синсенс 62
```

409 DYISEFV-SLLPKSIRR----VAEEPIPEEVQKVLEEAKAGDDHDHHGHGHAHAGY 460

377 DYISEFV-SLLPKSIRR----VAEEPIPEEVQKVLEEAKAGDDHDHHHGHGHAHAGY 428

```
CTRAIN-CV. COLUMBIA,

WATCHING-21016719; PubMed-11130712;

WHITE-21016719; PubMed-1117; PubMer R.F., Chin C.W.,

WHITE-21016719; PubMed-1117; PubMer R.F., Hughes B., Huizar L.,

WHITE-21016719; PubMed-1117; PubMer N.F., Hughes B., Huizar L.,

WHITE-21016719; PubMed-1117; PubMer M.F., Liu S., Khaykin E.,

WHITE-21016719; PubMed-1117; PubMer M.F., Liu S., Khaykin E.,

WHITE-21016719; PubMer M., William M.C., Osborne B.I.,

WHITE-21016719; PubMer M., Wuyen M., Nierman W.C., Osborne B.I.,

Sakano H., Zalzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

WHITE-21016719; PubMer S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Ramiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Rawiya R., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
Davis R.W., Ecker J.R., Theologia A.;
Submitted (JAN-2002) to the EMBL/Genbank/DDBJ databases.

EMBL; AC068440; AAG5115.1;
REMBL; AC069144; AAG5115.1;
REMBL; ALCOSI A., ALCOSI A.,
REMBL; ALCOSI A.,
REMB
                                                                                                                                                                                                                                                  T24C10.10 OR F14C21.51 OR AT1G54990.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen.N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Chol E., Gonzalez A., Lenz G., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.5%; Score 84; DB 10; Length 473; 36.8%; Pred. No. 0.34; vative 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .l protein.
473 AA: 52419 MW; D09124A11565BB23 CRC64;
                                                                                                                  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
T24C10-10 protein (Hypothetical 52.4 kba protein).
T24C10.10 OR F14C21.51 OR AT1G54990.
                                                                        473 AA.
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                          09FZ33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
RESULT 12
```

8 DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHH---HGGH 61

ö

<del>::</del> ----

```
A Machine-Loughoub, tubbed-lu/31132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Fabiurer M., Hedderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburere M., Hedderson S.N.,

RA Baradon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Baradon R.C., Baterer E.G., Helt G., Champe M., Pfeiffer B.D.,

RA BADII J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Basendale J., Barkataroly B. Bolshakov S.

RA BOTKOVA D., Botchan M.R., Bouck J., Bandari D., Bolshakov S.,

RA BOTKOVA D., Botchan M.R., Bouck J., Bandari D., Bolshakov S.,

RA BOTKOVA D., Botchan M.R., Bouck J., Bandari D., Bolshakov S.,

RA BOTKOVA D., Botchan M.R., Bouck J., Bandari D., Bolshakov S.,

RA BOTKOVA D., Botchan M.R., Bouck J., Broketein P., Brottler P.,

RA BURLIS K.C., Busam D.A., Buller H., Cadleu E., Center A., Chadra I.,

RA Gepablos B., Delcher A., Deng Z., Mays A.D., Davies P.,

RA Dodson K.J., Evangeliste G.C., Ferraz C., Ferriarca S., Pletz S.,

RA Dodson K.J., Evangeliste G.C., Ferraz C., Ferriarca S., Pletz S.,

RA BALLIN M., Roush F., Gorrell J.H., Gu Z., Genbart W.M., Classer R.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Harris M.,

RA Liu X., Mattel B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattel B., Morincoh T.C., Moreno D.A., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.C.,

RA Balazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M. A.

RA Blascon D.R., Nelson K.A., Li J., Li Z., Liang Y.,

RA Blascon D.R., Nelson K.A., Li S., Palazoleb J.W.,

RA Blascon D.R., Woy M., Murphy B., Murphy L., Muzny D.M., Welssenbach J.,

RA Blascon D.R., Woy M., Murphy B., Murphy L., Welsenbach J.,

RA Blascon D.R., Woy M., Murphy B., Murphy L., Welsenbach J.,

RA Blascon D.R., Woy M., Murphy R., Supple C., Stan J., San D., San J., San J., San J., San J., San J., San J., San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 16.5%; Score 84; DB 5; Length 1561; 1.Similarity 23.9%; Pred. No. 1.4; 28; Conservative 17; Mismatches 30; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1561 AA; 174616 MW; 10BFD38A3DD4FC4E CRC64;
                                                                            (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                         PRT; 1561 AA
                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003444; AAF46397.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0025864; Crag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001194; DENN.
InterPro; IPR005113; uDENN.
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03455; dDENN; 1.
Pfam; PF02141; DENN; 1.
Pfam; PF03456; uDENN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                         CRAG protein.
CRAG OR CG12737.
                                                                              01-MAY-2000
                                                                                                01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                       Q9W3D2
RESULT 13
                 Q9W3D2
```

g ð

```
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     090WV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  090WV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
  SORBERS
                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-20196006; PubMed-1073132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B Sutton G.G., Wortman J.Y., Mandeall M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Bogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Basu A., Barendal M.D., Basoley E.M.,
Ballew R.M., Basu A., Barman B.P., Bhankoch C., Baldwin D.,
RA Ballew R.M., Cawley S., Derman B.P., Bhankoch C., Basaley E.M.,
Bartis R.C., Busam D.A., Butler H., Cadieu E., Center P., Bolsakov S.,
Borkova D., Botchan M.R., Bouck J., Broxstein P., Brottier P.,
Borkova D., Botchan M.R., Doug E., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Bullke C., Davenport L.B., Davies P.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Fosler C., Gabrielian A.E., Garrel J.H., Gu Z., Guan P., Harris M.,
R. Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibogwam C.,
A Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D.L.,
RA Mont S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Rainer K., Ramington K.A., Mixon K., Mixon K., Marker D., Puri V., Rese M.
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.
Shue B.C., Siden Kiamos T., Simpson M., Skupski M., P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Yang S., Yao O.A.,
Wayang Z.-Y. Wassamman D.A., Weinstock G.M., Wang A.H., Wang S., Yao O.A.,
Wayang Z.-Y. Wassamman D.A., Weinstock G.M. Wang A.H., Wang S., Yao O.A.,
Wayang Z.-Y. Wassamman D.A., Weinstock G.M. Wang S., Yao O.A.,
Wayang Z.-Y. Wassamman D.A., Weinstock G.M. Wang S., Yao O.A.,
Wang Z.-Y. Wassamman D.A., Weinstock G.M. Wang S., Yao O.A.,
Wang Z.-Y. Wang S., Wang S., Wang S., Yao O.A.,
Wang Z.-Y. Wa
                          | : | : : | : | : | : | : | : | 1090 ENISSISPSLTGKKSNELIQGSLSSIKSAANSLTKKFDEIKGVISANSTPTKTNNGHHPH 1149
12 EEVRSVAPAGFGRHGGGVQQ------HVVKEKFEEVDTVSRA-----------47
                                                                                                     Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., Gorge R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                48 GANH-----HHHHGHHGGHGFVVRE------TRVEEDINTCTGEVHERRES
                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                        UI-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-UNN-2002 (TrEMBLrel. 21, Last anno
CG7406 protein (RE04580p).
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The genome sequence of
                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                             Q9VWM5
                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                             Q9VWM5
                                                                                                                                                                                                                                셤
```

```
3 YYQEVDYCSEEVRS---VAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHG 59
                                                                                                                                                                                                                                                                                     46 VKVISEE-----AGHGGWAGGYSGGYAH-APEEVKIVKVISEAGHSHGHDYGHSHGHGS 98
                                                                                                                                                                                                                                                             7 VDYCSEEVRSVAPAGFGRHGGGVQ---QHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGGHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homeobox protein hox4x (Fragment).
Petromyzon marinus (Sea lamprey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Force A., Amores A., Postlethwait J.;
"Hox cluster organization in the jawless vertebrate, Petromyzon marinus, and the evolution of the vertebrate Hox clusters.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AVD56469; AAL17914.1;
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 381;
                                                                                                                                                       16.3%; Score 83; DB 5; Length 168; 32.9%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                           34; Indels
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003511; AAF48913.1; -.
EMBL; AY089569; AAL90307.1; -.
FlyBase; FBgn0030980; CG7406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA; 43860 MW; 4FD20E59DC48E636 CRC64;
                                                                                                        168 AA; 16791 MW; B14DF461A0AB0F40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 16.2%; Score 82.5; DB 13; Local Similarity 29.0%; Pred. No. 0.38; hes 18; Conservative 9; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 AA
                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodom; PD000010; Homeobox; 1.
PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
PROSITE; PS000027; HOMEOBOX_1; UNKNOWN_1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEODOX; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6, 2003, 12:52:27
                                                                                                                                                                                                                                                                                                                                                                                                              99 DVKIIKVIQEEGHSHGHGH 117
                                                                                                                                                                                                                                                                                                                                                                           64 VVRETRVEEDINTCTGEVH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homeobox;
                                                                                                                                                                  Query Match 16.3
Best Local Similarity 32.9
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June
Job time : 52 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 DH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GH
```

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

```
Command line parameters:

WODEL frame+_p2n.model -DEV-x1h
-Q-Cgn2_1VSF0_spool_VSI090035/runat_06062003_105504_10970/app_query.fasta_1.526
-Q-Cgn2_1VSF0_spool_VSI0090035/runat_06062003_105504_10970/app_query.fasta_1.526
-UNITS-bits -STARR-1 - END--1 -MATRIX-blosum62 - TRANS-human40.cdi -LIST-45
-DCCALIGN-200 -TRR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15 -MDE-LCCAL
-USER-VS10090035_eCGN_11_1_2463_erunat_06062003_105504_10970 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT-120 -WARR_TIMEOUT-50 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP=6 -DELEXT-7
                                             June 16, 2003, 10:02:07; Search time 1293.5 Seconds (Without alignments) 1164.422 Million cell updates/sec
                                                                                                                                                      US-10-090-035-2
510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32308132
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                          16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                            0.5
0.5
0.7
                                                                                                                                                                                                                                                                                    Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                   Run on:
                                                                                                                                                      Title:
```

em\_gss\_other:\* em\_gss\_mam:\* em\_gss\_mus:\* em\_gss\_pro:\* em\_gss\_rod:\* ew\_gss\_hum: em\_gss\_inv:\* em\_gss\_pln: em\_gss\_fun:\* em\_estfun:\* em\_esthum:\* em\_estin:\* em\_estmu:\* em\_estom:\* em\_gss\_vrt em\_estpl:\* gb\_htc:\*
gb\_est3:\*
gb\_est4:\*
gb\_est5:\* em\_estba:\* em\_estov: \* gb\_estl:\* 4:ssb\_db gb\_est2 em\_htc:\* EST:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

:	Score	Query Match	Length	82 : 5	QI	Description
H (2) EV	510 505 505	100.0 99.0 99.0	417 465 500	13	BM501439 BE129897 AW787732	1439 PACO( 9897 9450: 7732 9450
4 W /		99.0 99.0	523 524	100	AW331212 AW288876	AW331212 707049E04 AW288876 707009E04
	ᢐᢐ	97.9	466	თ თ	AI964534	A1964534 496013D01
ထတ	499.5	97.9	539	000	AI855425	A1954458 496010H04 A1855425 603016F02
	900	9.60	550	112	BG840383	AA979839 MEST2-B7. BG840383 MEST12-H1
	۱ O 1	97.9	648	14	AY104409 BQ619167	AY104409 Zea mays BO619167 RNOSEO4E0
	თ თ	97.9	648 648	14	BQ619315	BOG19315 RNOSEQGCO
	000	97.9	648	14	BQ619337	BQ619318 RNOSEQ6D0 BQ619337 RNOSEQ6E1
	<b>TO CO</b>	97.9	648 648	7,	BQ619383	BQ619383 RNOSEQ7B0
		97.6	326	101	BE025303	BQ619390 RNOSEQ7B0 BE025303 945028809
19	496	97.3	443	10	BE129644	BE129644 945027E06
21	494	96.9	476	9 0	BE025302 BF510200	BE025302 945028B09
. 55	492	96.5	496	10	AW787314	AW787314 945007E06
23	482	94.5	433	25	BE225008	BE225008 945042F02
	N	83.0	360	13	AW/8/315 BM318672	AW787315 945002E06
	N C	83.0	466	2	BE597738	BE597738 PII_16_C0
	70	93.0	485	2,	BE599123	BE599123 PII_85_F0
	10	83.0	516	10	BC280/09 BE364814	BO280709 WHE3004_A
	20	83.0	519	10	AW680016	AW680016 WS1_34_H1
32.	70	83.0	522	99	AW679969	AW679969 WS1_34_B0
	~	83.0	541	10	AW745436	AW/45400 WS1_34_H1 AW745436 WS1_34_B0
	12	81.9	348	10	BE593507	BE593507 WS1_100_B
	, (°)	77.5	401	10	BQ280894 AW289056	BQ280894 WHE3006_B
37	96	72.3	274	101	AW288875	AWZ89036 /0/005E07 AWZ88875 707009E07
	6	72.1	311	175	BF729420	BF729420 1000077C0
40	308	60.4	5 5 5 5 5 4	92	AW923922 AW679915	AW923922 WS1_30_A1
41	308	60.4	560	20	AW924079	AW6/9915 WS1_33_G0 AW924079 WS1 49_G0
4.	308	60.4	266	10	AW677917	AW677917 WS1_12_D0
4 4 4 4	308	60.4	566	10	AW746383	AW746383 WS1_49_G0
45	308	60.4	572	20	AW6/9/13 AW925014	AW679713 WS1_30_A1 AW925014 WS1_74_D0
					ALIGNMENTS	
RESULT 1 BM501439						
LOCUS	BM5014	501439	ć		•	linear
ACCESSION	BM501	439	j J	Pionee	r AF-1	
VERSION KEYWORDS	BM501	.439.1	GI:18661	6151	7.	
		mays.				
ORGANISM	Eukar Sperm	zea mays Eukaryota; V Spermatophut		lant	ae; Streptoph	mbryophyt
PEFEBENCE	clade	clade; Panicoi		Y A	deae; Andropogoneae; Zea.	Poales; Poa
AUTHORS	un	ဲ့ဗ	Beatty	χ, Σ,	, Singletary, G	G., Hamaker, B., Larking a A.
	Jung,	₹.				TOTAL STREET, CO. D. C.

```
Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                   160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                            Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                             FEATURES
                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE129897 465 bp mRNA linear EST 21-JUN-2000 945032C12.X1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
BE129897.1 GI:8577260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 465)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                              Trait and Technology Development, Food and Feed Research Proneer Hi-Bred International, Inc. 7300 NM 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA Tel: 515 270 5934 Fax: 515 254 2619 Email: rudolf.jung@pioneer.com.
                                                                                                                                     /organism="Zea mays"
/db_xref="taxon:4577"
/clone_11b="Pioneer AF-1 array"
/note="Vector: pSprt1; Site_1: Sal1; Site_2: Not!"
150 133 9 53 t
            넊
Maize opaque endosperm mutations create extensive changes patterns of gene expression Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University
Unpublished (1999)
Contact: Walbot V
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Fat: 650 723 222
                                                                                                                                                                                                                     417
93
0
0
0
                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                             US-10-090-035-2 (1-93) x BM501439 (1-417)
                                                                                                                                                                                                                       5.6e-47
510.00
100.00%
100.00%
                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays.
                                                                                                                                                                                  ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST.
                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
COMMENT
                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
BE129897
                                    JOURNAL
                                                                                                                      FEATURES
                 TITLE
                                               COMMENT
                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                        硆
                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
AW787732 500 bp mRNA linear EST 16-MAY-2000 945002E06.X3 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
AW787732 GI:7844510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays.
Zea mays
Zea mays
Zea mys
Ze
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: tassel, kernal, silk, husk, root, leaf;
/ector: pGADIO. Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="fully-grown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465
92
0
1
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: .
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Email: walbot@stanford.edu
Plate: 945032 row: C column: 12.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-2 (1-93) x BE129897 (1-465)
                                                                                                                                                     /organism="Zea mays"
                                                                                                                                                                                         /cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.26e-46
505.00
98.92%
98.92%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
```

m

```
2.58e-46
505.00
98.928
98.928
99.028
                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                           Scores:
                                                                                                                                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                          Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
AW288876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                      à
                                     mRNA linear EST 31-JAN-2000
tissues from Walbot lab (SK) Zea
                                                                                                                                                                                                                                                                                214
                                                                                                                                                                                                                                                                                                                                         Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 523)
Walbot, V.
                                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                  CDNA libraries sequenced at Stanford
                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945002 row: E column: 06.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                  AW331212 523 bp 707049E04.x1 707 - Mixed adult t mays CDNA, mRNA sequence. 4W331212 GI:6827569
                                                                                                                                                                                                                                   US-10-090-035-2 (1-93) x AW787732 (1-500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize ESTs from various
                                                                                                                                                                                  2.45e-46
505.00
98.92%
98.92%
99.02%
                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
                                                                                                                                                                           Alignment Scores:
                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
AW331212
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
COMMENT
                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                   ö
```

```
(SK
                                                                                                                                                          /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
/note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1: cDNA library from fully
differentiated malze tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA linear EST 16-JAN-2000 tissues from Walbot lab (SK) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                                   1. .523
/organism="2ea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
                                                                                                                                                                                                                                                                                                                                                                                                           00100
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 222
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707049 row: E column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW288876 524 bp
707009E07.x4 707 - Mixed adult the mays cDNA, mRNA sequence.
AW288876 GI:6695663
                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-2 (1-93) x AW331212 (1-523)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
COMMENT
```

```
EST.
                                                                                                                                                                                                                                                                     Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A1964458/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                      source
                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                 ..
9
                                                                                                                                                                                                                                                                     Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
COMMENT
                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1964534 496 - stressed shoot cDNA library from Wang/Bohnert lab zea mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .524
/organism="zea.mays"
/oultivar="wu2"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"
)"
                                                                                                                                                           /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="bHl0B"
/note="organ: tassel, kernel, silk, husk, root, leaf;
/note="organ: tassel, kernel, cDNA library from fully
vector: pGADIO; Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
plant, root, leaf). Glafietionally cloned."

**A 170 c 157 g 89 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524
0
0
0
0
              Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Tes: 650 725 8221
Email: walbotestanford.edu
Plate: 707009 row: E column: 07.
                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
    Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-2 (1-93) x AW288876 (1-524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walbot,V.
Maize ESTs from various
University
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1964534.1 GI:5757247
EST.
                                                                                                                                                                                                                                                                                                            2.58e-46
505.00
98.92%
98.92%
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
                                                                                                                                                                                                                                                                107
                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI964534/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δý
```

ė\*

```
A1964458 481 bp mRNA linear EST 20-AUG-1999 496010H04.x1 496 - stressed shoot cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence.
A1964458 A1964458.1 G1:5757171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib=%496 - stressed shoot cDNA library from
Wang/Bohnert lab"
//tssue_type="seedling"
/dev_stage="salt stress"
/dev_stage="salt stress"
/lab_host="E_coli XL Gold"
/note="Organ: shoot; vector: pBluescriptII SK(+) XR;
/note="organ: shoot; vector: BBluescriptII SK(+) XR;
/note="organ: shoot; vector: b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466
93
0
1
Contact: Walbot V
Department of Biological Sciences
Stanford University
815 California Ave, Palo Alto, CA 94304, US
Tel: 650 723 2227
Fax: 650 725 8221
Email: Walbot@stanford.edu
Plate: 496013 row: D column: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                   1. .466
/organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-2 (1-93) x AI964534 (1-466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 481)
Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2e-46
499.50
98.94%
98.94%
97.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
```

```
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 603016 row: F column: 02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Town State University G405 Agronomy, Ames, IA 50011, Tel: (515)-294-0975 Fax: (515)-294-2299 Email: schnable@lastate.edu
                                                                                                                                                                                                                                                                                                                          US-10-090-035-2 (1-93) x AI855425 (1-539)
                                                                                                                                                                                                                                              1.08e-45
499.50
98.94%
97.94%
                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays.
Zea mays
                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
AA979839
                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1855425 603016702.X1 603 - stressed root cDNA library from Wang/Bohnert lab A1855425 GI:5499558
                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                        /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:1577"
/dboxne=11b=496 - stressed shoot cDNA library from
%nany/Bohnert lab.
/tissue_type="seedling"
/dev_stage="seedling"
/dev_stage="seedling"
/dev_stage="seedling"
/dev_stage="salt stress"
/lab_host="E.coli XL Gold"
/note="Organ: shoot; Vector: pBluescriptII SK(+) XR;
Wang/Bohnert"
2 a 148 c 154 g 97 t
                                                                                                                                                                                                                                                                                                                                                             Walbet, V. Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fex: 650 725 821
Email: walbotestanford.edu
Plate: 496010 row: H column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                      US-10-090-035-2 (1-93) x A1964458 (1-481)
                                                                                                                                                                                                                                                         9.53e-46
499.50
98.94%
97.94%
                                                                               .481
                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays
                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
AI855425/C
LOCUS
DEFINITION
                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ç
```

```
1. .539

/cultivar="sea mays"
/cultivar="bx;
/db_xref="taxon:4577"
/clone_lib="603 - stressed root cDNA library from
Wang/Rohnert_lab"
//tissue_type="sealit stress"
/dev_stage="sealit stress"
/lab_host="s. coli XL Gold"
/note="Organ: root; Vector: pBluescriptII SK(+) XR;
Seedling stressed root cDNA library from Wang/Bohnert lab"
91 a 157 c 172 g 119 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA979839
MEST2-B7.TW1412.Seq ISUM2 Zea mays CDNA clone MEST2-B7 5', mRNA
AA979839.1 GI:3157217
                                                                                                                                                                                                                                                                                                                                                                                                             418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 546)
Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Unpublished (1997)
Contact: Schnable,P.S.
Schnable laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                           80 GluValH1sGluArgArgGluSerPheLeuAlaArgAlaAsn
                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
Indels:
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
AY104409
                            TITLE
JOURNAL
COMMENT
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                      / ALONG THE ALL WAR DELICATION OF THE ALL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG840383 550 bp mRNA linear EST 29-MAY-2001
MEST12-H11.T7-1 ISUM4-TN Zea mays CDNA clone MEST12-H11 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="ISUM2"
/tissue_type="above ground tissues"
/tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
             PCR PRimers
FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGC-3')
Plate: MEST2 row: B column: 7
Seq primer: tw1412 (5'-GAAGATACCCACCAAACC-3').
Location/Qualiflers
1.546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546
93
0
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                   /db_xref="taxon:4577"
/clone="MEST2-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-090-035-2 (1-93) x AA979839 (1-546)
                                                                                                                                                                                                                 /cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:14242676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1e-45
499.50
98.94%
98.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG840383.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG840383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG840383
                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
FUCK PKINDETS
FORMARD: T7-1 (AA TAC GAC TCA AG)
BACKWARD: T7 (ATT AC CCT TAA AG)
BACKWARD: T3 (ATT AC CCT TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TCA CTA TAG).

1. .550
Cultivar="M973"

(cultivar="M973"

(clone=lib="SEGUM4-TN"

(clone=lib="SE
Cour, F., Cui, F., Guo, L., Ashlock, D.A, Wen, T.J. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14206705.
Contact: Patrick S. Schnable
Schnable Laboratory
I constant: Patrick S. Schnable
Schnable Laboratory
Tous State University
G405 Agronomy, I owa State University, Ames, IA 50011-1010, USA Tel: 515-294-0975
Fax: 515-294-0975
Fax: 515-294-2299
Email: schnablediastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      550
93
0
1
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-2 (1-93) x BG840383 (1-550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.11e-45
499.50
98.948
97.948
```

^

```
Zea mays.

Sea mays.

Clade; Panicoideae; Andropogoneae; Zea.

Sea 1 (bases 1 to 648)

Sea Mandy.

Sea mays.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ619315 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6C06_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6C06_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .648 ...
/organism="zea mays"
/do_xref="taxon:657"
/do_xref="taxon:657"
/clone="RNCSE05_SK.abl"
/clone=lib="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
mM NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648
00011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 t
                                                                                                                                                                                                                                                                                                                                                                Email: bohnertlab@life.uiuc.edu
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-2 (1-93) x BQ619167 (1-648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 g
                                                      GI:21621161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.33e-45
499.50
98.94%
98.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 c
            sequence.
BQ619167
BQ619167.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ619315
BQ619315.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
BQ619315
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                  SM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mannoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (basea 1 to 553)

S Halney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

Malze Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes

IAL Unpublished (2002)

ACCO, E.C.

Coo, E.C.

JISS Coo, E.C.

Missouri, Columbia, MO 65211, USA

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         10.553
/Organism="Zea mays"
/Organism="Zea mays"
/Ob_xref="taxens:4577"
/Clone="PCO124784"
/Clone="this sequence is part of a project of Est assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project.

Naping Project

Naping Project

Naping Project of ST a collaboration for the overgo addressing of BACs in conjunction with the Maize Naping Project.
      HTC 25-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ619167 5K.abl Salt stressed Zea mays rocts cDNA library Zea mays cDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlyPheGlyArgH1sGlyGlyGlyValGlnGlnH1sValValLySGluLysPheGluGlu 40
    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            553
0
1
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
        Zea mays PCO124784 mRNA sequence.
AY104409
ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-090-035-2 (1-93) x AY104409 (1-553)
                                                    AY104409.1 GI:21207487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.11e-45
499.50
98.948
97.948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                           cea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                               source
            DEFINITION
                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
BQ619167
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SASE COUNT
                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                   172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST.
                                                                                                                                                                                                                                                          Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                        source
                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                     . No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
BQ619337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                          Alignment
    JOURNAL
                                                                                         FEATURES
             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ619318 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6D01_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6D01_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 648)

Genomics of plant stress tolerance
L unpublished (2002)

Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
1. 648
//ab. w.cf=#1=con./Apr.#77#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GlyHisGlyPhevalValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                                                                                        /db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone="RNOSE06C06_SK.abl"
/clone=lib="Salt stressed Zea mays roots cDNA library"
/tissue_lyp="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
      Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaTyrTyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648
93
0
1
                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                   100 t
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-090-035-2 (1-93) x BQ619315 (1-648)
                                                                                                                                                                                                                                                                                                    183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ619318.1 GI:21621312
                                                                                                                                                                                                                                                                                                                                                     1.33e-45
499.50
98.94%
98.94%
97.94%
                                                                                                                                                                                                                                                                                                       193 c
                                                                                                                                                                                                                                                                                         mM NaCl"
                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ619318
                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
BQ619318
                                                            AUTHORS
TITLE
JOURNAL
COMMENT
                                                REFERENCE
                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             å
```

```
EST 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beamars

Bea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 ValaspThrValSerArgAlaGlyAlaAsn---HisHisHisHisHisGlyHisHisGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ619337 EST 27-JUN-2
RNOSEQ6E12_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                        //organism="Zea mays"
/db_xref="taxon:457"
/db_xref="taxon:457"
/clone="RNOSEGD01_SK.abl"
/clone="last stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_stage="Z weeks oid"
/dev_stage="Z weeks oid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stressed 24 hours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   648
93
0
1
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2772655473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK+;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ىد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100
                                                                                                                                                                                                                       Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-2 (1-93) x BQ619318 (1-648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ619337
BQ619337.1 GI:21621331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.33e-45
499.50
98.94%
98.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mM NaCl"
                                                                                                                                                                                                                                                                                       1. .648
```

FEATURES

```
1. .648
/Organiam="Zea mays"
/Ob_xref="taxon:4577"
/Clone="RNOSED(6E12_SK.ab1"
/Clone_llb="Galt stressed Zea mays roots cDNA library"
/Clone_ltpe="Roots"
/Clone_lib="alt stressed Zea mays roots cDNA library"
/Clone_lib-"
/Clone_lib-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Email: bohnertlab@life.uluc.edu.
Locatlon/Qualifiers
1. .648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-2 (1-93) x BQ619337 (1-648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 16, 2003, 12:16:33
Job time: 1303.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.33e-45
499.50
98.94%
98.94%
97.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

	A Commence of the contract of	The state of the s	
*4			No. of the second secon
J.			
			•
	• •		,
4.5	**		N. S.
		*	1
*			
			7
			. *-•
s h			¥.
	*		
	÷		*
1			1
do-	*	* *	. "
drus -			
200	•	•	* * *
	· "		
			•
			*
<b>k</b>	*, * *		
		· .	
1			
	v " v		
C A			
			• • • • • • • • • • • • • • • • • • • •
	· · · · · · · · · · · · · · · · · · ·		
1		n .	•
	P.		•
	*		
			•
ř.			
1			
<u>-</u>			
k F			7
No.	·		ta .
***			* ************************************
	· ·		
ē			
é			
		u,	
- as .	No.	of many and the state of the st	

OM nucleic - nucleic search, using sw model

Run on:

June 16, 2003, 04:03:20 ; Search time 1684.8 Seconds (without alignments) 9915.101 Million cell updates/sec

Title: Perfect score: Sequence: Scoring table:

OLIGO\_NUC Gapop 60.0 , Gapext 60.0

2054640 seqs, 14551402878 residues Searched:

0 Word size :

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

GenEmbl:\* Database :

gb\_p1:\*
gb\_pr:\*
gb\_sr:\*
gb\_sr:\*
gb\_sr:\*
gb\_un:\*
gb\_u1:\*
em\_ba:\*
em\_tun:\* gb\_ba:\* gb\_htg:\* gb\_in:\* gb\_om:\* gb\_ov:\* gb\_pat:\* gb\_ph:\*

em\_in:\*

em\_or: \* em\_ov: \* em\_pat: \* em\_ph: \* em\_mu: \*

em\_pl:\* em\_ro:\* em\_un:\* em\_sts

em\_htg\_hum:\* em\_htg\_inv:\* em\_v1:\*

em\_htg\_other:\*

em\_htg\_pln: \* em\_htg\_rod: \* em\_htg\_mam: \* em\_htg\_vrt:\* em\_htg\_mus:\*

em\_htgo\_other:\* em\_htgo\_hum: \* em\_htgo\_mus: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

A Score Match Length DB ID  44 7.7 173699 B AP003416  44 7.7 174218 2 AC091071  44 7.7 174218 2 AC091071  44 7.7 185095 B AP003436  44 7.7 185095 B AP003436  45 7.7 185095 B AC0190716  51 185095 B AC0190716  52 5.1 1318 9 AC0192756  52 5.1 1158 9 BC015542  52 5.1 1158 9 BC015559  52 5.1 172823 9 AC115592  53 8 4.9 AC11823  54 9 AC118233 AC114323  55 1 172823 9 AC115592  56 4.9 AC118233 AC114323  57 4.9 1418 AF467129  58 4.9 AC11823  58 4.9 BC015065  58 4.9 BC016067  58 4.9 BC01	No.   Score   March Length DB   ID	Res	Result		& Query				
C 1 44 7.7 173699 B AP003416 A	C 1 44 7.7 173699 8 AP003316 AP003416 AP003416 Oryza 4 4 7.7 185092 8 AP003436 AP003436 AP003436 Oryza 4 4 7.7 1865092 8 AP003436 AP003436 Oryza 4 4 7.7 1865092 8 AP003436 AP003436 Oryza 4 4 7.7 1865092 B AP003436 AP003436 Oryza 4 4 7.7 1865092 B AP003436 AP003436 AP003436 Oryza 4 1 1 29 5.1 12759 AP003436 AP003436 AP003436 AP003436 AP003436 AP003436 AP003436 AP003436 AP003436 AP003439 AP003436 AP003434 A		8	Scor	Match	Leng	DB	G.	ptio
2 44 7.7 174218 2 AC091071 2 44 7.7 185095 8 AP003435 AC091071088 2 9 5.1 1275 8 AV102542 AC091071 2 9 5.1 1275 8 AV102542 AC019718 2 9 5.1 1275 8 AV102542 AC019718 3 134 9 AC012959 AC019595 AC019595 3 1 12226 9 AC0199486 AC012959 AC019595 3 1 12226 9 AC0199486 AC019595 AC019595 3 1 12226 9 AC0199486 AC01959 AC019595 3 1 12226 9 AC0199486 AC019595 AC019595 3 1 12226 9 AC0199486 AC019595 AC019595 3 1 12226 9 AC0199486 AC01959 AC019595 3 1 12226 9 AC0199486 AC019595 AC019595 4 9 41 8 AF467129 BC010519 BC010519 2 1 12226 9 AC019593 AC019565 3 1 12226 AC019593 AC019593 AC019595 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2         44         7.7 174218         2         AC091071         AC0910710         AC091070         AC0910710         AC0910710	U	г	44	7 7	1736		ADA03416	
c         3         44         7.7 185095         8         AP003436         AP003436           4         44         7.7 185095         8         AP003436         AP003436           5         29         5.1         185481         2         AC091088           6         29         5.1         1373         9         AC091088           1         29         5.1         1275         8         AC115592         AC115592           1         29         5.1         17223         9         AC115592         AC115592           1         29         5.1         17223         9         AC115592         AC115592           1         29         5.1         17223         AC1167129         AC1467129	c         3         44         7.7 189395         6         AP003436         AP003486         AP003436         AP003466			44		1747		A70004	Oryza sa
4         7.7 18259 2         AC003108         AP003435           5         31         5.4 18548 1         AC119716         AC109108           6         29         31         5.4 18548 1         AC109108         AC109108           1         29         5.1 1375 8         AC102542         AC109108         AC109108           10         29         5.1 1226 9         AC09286         AC109108         AC105510           11         29         5.1 13226 9         AC01552         AC115592         AC115592           12         29         5.1 13226 9         AC015592         AC115592         AC115592           13         29         5.1 13226 9         AC015592         AC115592         AC115592           14         29         5.1 13226 9         AC015592         AC115592         AC115592           15         28         4.9         411         B AF467129         AC114323         AC1441323           16         28         4.9         411         B AF467129         AC1044134         AC1441323           16         29         5.1 172226         AC01636         AC164134         AC16411323         AC16411323           17         29         29	4         7.7         182543         2         AC010316         AC051086         OFYza           6         29         5.1         182481         2         AC119716         Ratu           7         29         5.1         1125         B         AC012359         AC010376	U	m	44		100		T/015000	Oryz
Colored Book	Colored Borner   Colo	)	۰ <	* *		0 0		AP003436	Oryza sa
Colored Fig. 1975   ACTIGNTS	Colored Colo		* 10	* *		100		ACOSTORS	Oryza sa
10	7         29         5.1         509         AA400832         AA4067161         AA467161	C	י נ	7 6		1021		AC119/16	Rattus n
Name	29	)	٦ ٢	N C	-i -	n ;		AX400832	AX400832 Sequence
10   29   29   11450   29   29   29   29   29   29   29   2	11   25   5.1   1475   8   AY102242   AY10254   AY10254   AY10254   AY10254   AY10254   AY10251   AY1025		۰ ٥	7 (	7.0	7;		BC032756	BC032756 Homo sap1
10 29 5.1 1450 5 AF295407 AF295407 10 29 5.1 1450 5 AF295407 11 29 5.1 1450 5 AF295407 11 29 5.1 30523 2 AC015592 AC015592 AC012958 BC012958 BC012959 BC008075 BC012958 BC0129	10		0 0	7 0	T.C	77		AY102542	AY102542 Arabidops
10 29 5.1 2879 10 BC012559 BC01255519 13 29 5.1 30523 2 AC115529 AC015519 AC105519 AC105519 AC105519 AC105519 AC105519 AC105519 AC105519 AC105519 AC105519 AC105195 A	10   29   5.1   2879   10   BC012959   BC0		٠,	67	5.1	14		AF295407	Danio
13   29   5.1   3194   9   AK025519     12   29   5.1   13226   9   AC015592   AC0115592     13   29   5.1   13226   9   AC016519     14   29   5.1   13226   9   AC014323     15   28   4.9   411   8   AF467161   AF467129     18   28   4.9   411   8   AF467129   AF467121     19   28   4.9   411   8   AF467129   AF467129     19   28   4.9   4136   9   BC015653     20   28   4.9   1436   9   BC015653     21   28   4.9   1849   9   BC015653     22   28   4.9   1849   9   BC010519   BC016519     23   28   4.9   185   9   BC010519   BC016519     24   28   4.9   185   9   BC010519   BC016568     25   28   4.9   13919   6   AX346988   AX346988     28   4.9   13919   6   AX346988   AX346988     29   28   4.9   130010   2   AC022292   AC0160759     30   28   4.9   130010   2   AC01655     31   28   4.9   13808   2   AC016625   AC010769     32   4.9   15545   2   AC010769   AC010769     34   28   4.9   15545   3   AC010769   AC010769     35   28   4.9   15545   3   AC010769   AC010769     36   28   4.9   15545   3   AC010769   AC010769     37   4.9   176827   3   AC010559   AC010769     38   28   4.9   15545   3   AC010769   AC010769     39   28   4.9   15657   3   AC010769   AC010769     41   28   4.9   176827   3   AC010769   AC010769     42   28   4.9   176827   3   AC010769   AC010769     43   28   4.9   176827   3   AC010769   AC010769     44   27   4.7   336   3   AC010769   AC010769     45   28   4.9   176827   3   AC010769   AC010769     46   27   4.7   336   3   AC010769   AC010769     47   28   4.9   176827   3   AC010769   AC010769     48   4.9   176827   3   AC010769   AC010769   AC010769     49   40   176827   3   AC010769   AC01	11         29         5.1         3194         9         AK025519         AK025519         AK025519         AK025519         AK025519         AK025519         AK025519         AK025519         AK025519         AK0025519         AK0025619         AK0025519         AK00205519         AK00205519         AK00205519         AK00205519		2	53	5.1	28			) i
12   29   5.1   30523   2   ACI15592     13   29   5.1   112226   9   AC099486     14   29   5.1   112226   9   AC099486     15   28   4.9   411   8   AF467129     16   28   4.9   411   8   AF467129     17   28   4.9   411   8   AF467129     18   28   4.9   411   8   AF467129     19   28   4.9   1416   9   AF467129     20   28   4.9   1436   9   BC015055     21   22   28   4.9   1849   9   BC016519     22   28   4.9   1845   9   BC016519     23   28   4.9   1845   9   BC016519     24   28   4.9   1845   9   BC016519     25   28   4.9   1845   9   BC016519     25   28   4.9   1845   9   BC016519     26   28   4.9   2115   10   BC007136     22   28   4.9   2315   9   AX34588     24   28   4.9   13919   6   AX3548     25   28   4.9   13200   2   AC01655     26   29   28   4.9   13200   2   AC116098     27   4.9   15958   9   AC10698     28   4.9   13200   2   AC116098     29   29   4.9   13200   2   AC116098     31   28   4.9   13388   2   AC107591     32   28   4.9   13388   2   AC107591     34   28   4.9   168127   3   AC107591     35   28   4.9   168127   3   AC107591     36   28   4.9   168127   3   AC10527     37   28   4.9   168127   3   AC10527     38   28   4.9   168127   3   AC10527     39   28   4.9   168127   3   AC10527     41   28   4.9   17627   3   AC022306     42   27   4.7   330   11   G41182     43   28   4.9   216250   3   AC099731     44   27   4.7   336   3   AF401182     45   27   4.7   336   3   AF401182     45   27   4.7   336   3   AC001868     45   27   4.7   336   3   AC001868     46   27   4.7   336   3   AC001868     47   27   4.7   336   3   AC001868     48   20   20   20   20   20     49   20   20   20   20   20   20     40   20   20   20   20   20   20     41   28   4.9   20   20   20   20     42   27   4.7   336   3   AC001868     43   24   24   24   24   24     44   27   4.7   336   3   AC001868     45   27   4.7   336   3   AC001868     45   27   4.7   336   3   AC001868     46   27   4.7   336   3   AC001868     47   27   4.7   336   3   AC001868     48   20   20   20   20   2	12   29   5.1   30523   2   AC015592   AC019592   AC099486   AC0		11	29	5.1	31			
13 29 5.1 112226 9 ACO99486 15 28 4.9 411 8 AF467129 18 28 4.9 411 8 AF467129 18 28 4.9 411 8 AF467129 19 28 4.9 881 3 AV044834 20 28 4.9 1635 9 BC015065 21 28 4.9 1849 9 BC015065 22 28 4.9 1865 9 BC015065 23 28 4.9 1865 9 BC015065 24 28 4.9 1865 9 BC015065 25 28 4.9 1865 9 BC015065 26 28 4.9 1865 9 AX346888 27 4.9 13919 6 AX346888 28 4.9 13919 6 AX346888 28 4.9 13919 6 AX346888 29 28 4.9 13919 6 AX346888 20 28 4.9 130010 2 AC025392 20 28 4.9 130000 2 AC025392 20 28 4.9 130000 2 AC025392 20 28 4.9 130000 2 AC025392 20 28 4.9 152472 9 AC09762 20 28 4.9 152472 9 AC09762 20 28 4.9 100652 2 AC116098 20 20 4.9 152672 9 AC010769 20 20 4.9 152672 9 AC010769 20 20 4.9 152672 9 AC010769 21 22 4.9 152672 9 AC010769 22 28 4.9 152672 9 AC010769 23 28 4.9 152672 9 AC010769 24 28 4.9 152672 9 AC010769 25 28 4.9 152672 9 AC010769 26 28 4.9 152678 9 AC010769 27 4.1 28 4.9 176827 9 AC022306 28 4.9 17	13         29         5.1 112226         9 AC099486         AC014333         Homo as AC114323         AC114323         AC014433         AC014433         AC014433         AC014483         AC04484         AC044834         AC000000000000000000000000000000000000	U	12	29	5.1	305		AC115592	Dining sai
14 29 5.1 172823 9 ACI14323 ACI14328 15 15 28 4.9 410 8 AF467161 AFA67161 AFA6711 AF	14   29   5.1   172823   9   AC114323   AC114423   AC114423   AC144124   AC467146   AC1467146   AC167146		13	29	5.1	1122		AC099486	ACTIONS DICLYOSEE
15   28   4.9   4.10   8   AF467161     16   28   4.9   411   8   AF467129     17   28   4.9   411   8   AF467129     18   28   4.9   411   8   AF467129     19   28   4.9   411   8   AF467129     19   28   4.9   411   8   AF467129     20   28   4.9   1635   9   BC0105065     21   22   28   4.9   1645   9   BC0105065     22   28   4.9   1865   9   BC0105065     23   28   4.9   1865   9   BC0105067     24   28   4.9   1865   9   BC0105067     25   28   4.9   1865   9   BC0105067     26   28   4.9   1865   9   BC0105667     22   28   4.9   13919   6   AX346898   AX346398     23   28   4.9   13919   6   AX356480   AX345390     24   28   4.9   13000   2   AC0070625     25   28   4.9   13000   2   AC0070625     26   4.9   13000   2   AC0070625   AC010769     31   28   4.9   133200   2   AC116098   AC116098     32   28   4.9   133898   2   AC107591     33   28   4.9   15344   2   AC107591     34   28   4.9   15958   3   AC104062   AC1050769     35   28   4.9   15958   3   AC104062   AC1050769     36   4.9   176227   3   AC022306   AC022306     37   28   4.9   176227   3   AC022306   AC1050769     38   28   4.9   176227   3   AC022306   AC022306     39   209764   0   AC069731   AC022306   AC1069731     44   27   4.7   330   1   G41782   AC009731     45   27   4.7   3369   3   AC0099731     46   27   4.7   3369   3   AC0099731     47   27   4.7   3369   3   AC0099731     48   49   17825   3   AC0099731     49   27   4.7   3369   3   AC0099731     40   20   20   20   20   20   20   20	15   28   4.9   410   8   AF467161   AF467161   Lasthee   AF467161   Lasthee   AF467161   AF467161   Lasthee   AF467161   AF467161   AF467161   Lasthee   AF467162   AF467162   Lasthee   AF467162	υ	14	. 29	5.1	1728		AC114323	ACCOSAGO HOMO SAPI
16   28   4.9   4.11   8   AF467129	16   28   4.9   411   8   AF467129   AF467129   AF467129   Lasther   18   4.9   411   8   AF467129   AF467129   AF467129   Lasther   18   4.9   411   8   AF467129   AF467129   AF467129   Lasther   18   4.9   411   8   AF467129   AF4672232   AF4672232   AF46722329   AF46722329   AF46722339   AF4670129   AF4772330   AF4777330		15	28	4	4		NC414343	ACIT4323 HOMO Sapi
17         28         4.9         411         8 AF467143         AF467143           18         28         4.9         411         8 AF467143         AF467148           20         28         4.9         1436         9 BC015515         BC015055           21         28         4.9         1436         9 BC015615         BC015055           22         28         4.9         1845         9 BC016875         BC015055           23         28         4.9         1865         9 BC016875         BC016675           24         28         4.9         1855         9 BC016875         BC016675           25         28         4.9         2115         10 BC007136         BC016675           25         28         4.9         2215         10 BC007136         BC016763           26         28         4.9         2328         AX345380         AX345380         AX345380           29         28         4.9         13919         AX345380         AX355480         AX355480           29         28         4.9         130652         2 AC016098         AC04625         AC04625           30         28         4.9         132000	17   28   4.9   411   8   AF467142   AF467142   Lasthen     18   28   4.9   411   8   AF467142   AF467142   Lasthen     19   28   4.9   411   8   AF467142   AF467156   Lasthen     20   28   4.9   411   8   AF467156   AF467156   Lasthen     21   28   4.9   1436   9   BCO10519   BCO10519   Homo scale     22   28   4.9   1855   9   BCO10519   BCO10519   Homo scale     23   28   4.9   1855   9   BCO10519   BCO10519   Homo scale     24   28   4.9   1855   9   BCO105136   BCO107136   Homo scale     25   28   4.9   1855   9   BCO105136   BCO107136   Homo scale     26   28   4.9   13919   BCO004625   AX345380   AX345380   AX345880   Sequence     29   28   4.9   13919   BCO004625   AX345380		16	28	4	•		101/0144 001/0144	AF46/161 Lasthenia
18         28         4.9         411         8 AF467148         AF467148           19         28         4.9         481         3 AY04834         AY044834           20         28         4.9         1635         9 BC0105055         BC010519           21         28         4.9         1645         9 BC010519         BC010519           22         28         4.9         1865         9 BC010519         BC010519           24         28         4.9         1865         9 BC010519         BC010519           25         28         4.9         1865         9 BC010519         BC010519           26         28         4.9         5536         6 AX34698         AX34638           27         28         4.9         5536         6 AX34698         AX34638           28         4.9         13919         6 AX34648         AX34638         AX34638           29         28         4.9         4249         AX36440         AX34638           30         28         4.9         130010         2 AC004625         AC004625           31         28         4.9         1300010         2 AC005252         AC016095	18         28         4.1         8 AF467156         AF46714B         AF4671AB         AF4671AB         AF4671AB         AF4671AB         AF4671AB         AF4671AB </td <td></td> <td>17</td> <td>2,0</td> <td></td> <td>• &lt;</td> <td></td> <td>671/05/404</td> <td>AF46/129 Lasthenia</td>		17	2,0		• <		671/05/404	AF46/129 Lasthenia
19         28         4.9         4811         9         AV4401150         AV44034           20         28         4.9         1436         9         BC115065         BC015065           21         28         4.9         1649         9         BC010519         BC015065           22         28         4.9         1849         9         BC010565         BC010519           24         28         4.9         1855         3         AB062683         AB062683           25         28         4.9         1855         3         AB062683         BC010519         BC010519           25         28         4.9         1855         3         AB062683         BC010569           25         28         4.9         1858         6         AX346988         AX346988           4.9         13919         6         AX346988         AX346988         AX346988           28         4.9         13919         6         AX345380         AX346988           29         28         4.9         130010         2         AC016625           31         28         4.9         130010         2         AC016625           3	19         28         4.1         8 AF467130         AF467156         Lasthen           20         28         4.9         1436         9 BC015053         BC015056         Homo st           21         28         4.9         1436         9 BC015053         BC015056         Homo st           22         28         4.9         1845         9 BC0160575         Homo st         BC010519         Homo st           23         28         4.9         1865         9 BC016675         Homo st         BC001519         Homo st           24         28         4.9         1865         9 BC016675         Homo st         BC0017136         Homo st           25         28         4.9         1865         9 BC016675         Homo st         BC0017136		2	a a c		* <		AF40/148	AF467148 Lasthenia
20 28 4.9 181 3 AYU44834 AYO44834 AYO44834 22 2.8 4.9 1635 9 BCO10519 BCO10	20 28 4.9 1436 9 BC010519 BC010519 Homo strength		9 6	9 0		* 0		AF40/156	AF467156 Lasthenia
21         28         4.9         1435         9         BC010505           22         28         4.9         1845         9         BC010519         BC010519           23         28         4.9         1865         3         BC012663         AC0001513           24         28         4.9         1865         3         BC012663         BC0105683           25         28         4.9         1865         3         BC012663         BC000156           26         28         4.9         1865         3         BC007136         BC007136           27         28         4.9         13919         6         AX346988         AX346988           AX346988         AX346988         AX346988         AX346988         AX346988           AX366480         AX346988         AX346988         AX346988           AX366480         AX346988         AX346988         AX346988           AX366480         AX346988         AX346988         AX346988           AX366480         AX346489         AX346988         AX346988           AX366480         AX346489         AX346489         AX346489           AX366480         AX366480         AX346698	22         28         4.9         1635         9         BCU15053         BCU15055         Homo as a BCU15015           22         28         4.9         1645         9         BC010619         BC010619         BC010619         Homo as a BC010619         BC010619         Homo as a BC010619         Homo as a BC010619         Homo as a BC0106263         BC0106675         Homo as a BC010667         Homo as a BC010667         Homo as a BC010667         Homo as a BC010136         Homo as a BC010625         Homo as a BC010625         Homo as a BC010625         Homo as a BC010625         Homo as a BC010662		20	9 0				AY044 B34	AY044834 Stomoxys
22 28 4.9 1849 9 BC008675 BC008675 BC010519 BC010562 BC01	22 2 8 4.9 1855 9 BCO10519 Homo as ACO10519 Homo as ACO10		3 5	9 0		d (		BC015065	Homo sa
24 4.9 1849 9 BC008675 BC008675 BC008675 22 4.9 1849 9 BC008675 BC008675 BC012562 22 28 4.9 1865 9 BC012563 BC012563 BC012562 28 4.9 1865 9 BC012563 BC012563 BC012562 28 4.9 5215 10 BC007136 BC012563 BC012562 28 4.9 5218 6 AX34588 AC004625 AC004625 AC003762 32 4.9 130010 2 AC025292 AC03762 AC16098 AC010769 AC01076	24		4 6	9 0		9 9		BC010519	fomo sa
24 28 4.9 1855 3 AB0022683 AB0022683 AB062683 AB062683 AB062683 AB062683 AB062683 AB062683 AB062683 AX34698 AX346988 AX346989731 AX34698731 AX346988 AX34698731 AX3469888 AX346988 AX3469888 AX3469888 AX3469888 AX346988 AX3469888 AX346988 AX346988 AX346988 AX34	2.5         2.6         4.9         185.0         3 AB062683         AB062683         Bombyx           2.5         2.8         4.9         186.5         9 BC012562         BC012562         BC012562         BC007136         BC007137         BC007137         BC007137         BC007137         BC00716		7 (	9 0	-	±0 €		BC008675	das omo!
25 28 4.9 1855 9 BC012562 BC012562 25 28 4.9 2115 10 BC010136 AX34580	25 28 4.9 1850 9 BC012562 BC012562 Homo et al. 1850 9 BC012563 Homo et al. 1850 9 BC012563 BC012663		3 6	9 0	-	9		AB062683	30mbyx m
25 28 4.9 5218 10 BC007136 BC0	25 28 4.9 2115 10 BC007136 BC007136 Mus mm		* u	9 0	-	9 6		BC012562	lomo s
27         28         4.9         5528         b AX345898         AX345988         AX345988           28         4.9         13919         6 AX356480         AX345380         AX345380           29         28         4.9         42499         8 AC004625         AC004625         AC004625           30         28         4.9         100652         2 AC16609         AC004625         AC004625           31         28         4.9         130010         2 AC025392         AC16609         AC16609           33         28         4.9         132000         2 AC160976         AC16676         AC16676           34         28         4.9         152472         3 AC100486         AC106769         AC106769           36         28         4.9         153624         3 AC104066         AC104066         AC104066           37         28         4.9         159658         9 AC104066         AC104066         AC104066           39         28         4.9         168145         3 AC104062         AC104066         AC104066           40         28         4.9         176827         9 AC021306         AC102306         AC104066           41         28	26         4.9         5928         b AX34698B         AX34698B         AX34598B         AX3459BB         AX3459BB         AX3459BB         AX3459BB         AX3459BB         AX3459BB         AX3459BB         AX3459BB         AX3456BB         AX3564BB         AX3664BB         AX3564BB         AX3664BB         AX3664BB         AX3664BB         AX366AB         AX36AB         A		יי א כ	9 0	-	7		BC007136	Mus mu
28	28 4.9 13919 6 AX345380 AX345380 AX356480 Sequent Colored Colo	י כ	9 6	9 0	•	ה ה		AX346988	Sequence
29 28 4.9 13919 6 AX356480 AX356480 30 28 4.9 7722 9 AC003625 AC094625 31 28 4.9 17722 9 AC016058 AC004625 32 28 4.9 100652 2 AC116098 AC016098 33 28 4.9 132000 2 AC025292 AC052529 34 28 4.9 132000 2 AC025292 AC016098 35 28 4.9 13288 2 AC010769 AC010769 36 28 4.9 155354 2 AC010769 AC010769 37 28 4.9 15958 9 AC104062 AC104062 38 28 4.9 15958 9 AC104062 AC104062 40 28 4.9 168145 9 AC105306 AC022306 41 28 4.9 176827 9 AC022306 AC022306 42 28 4.9 176827 9 AC022306 AC022306 43 28 4.9 209764 10 AL645468 AC65468 44 27 4.7 330 11 G41782 G41782 BC107697	28 4.9 42499 6 AA356480 AX356480 AX356480 Sequence 28 4.9 42499 8 ACO04625 ACO04625 Arabidde 23 ACO03762 ACO03771 ACO09771 ACO097	י כ	\ C	9 0	•	9		AX345380	equenc
30 28 4.9 42499 8 ACO04625 ACO04625 ACO04625 30 28 4.9 100652 2 ACO04625 ACO04625 ACO04625 31 28 4.9 100652 2 ACO05922 ACO0592 ACO16098 ACO16098 ACO16098 ACO16098 ACO16098 ACO16098 ACO16098 ACO16096 ACO16098 ACO16098 ACO16098 ACO16098 ACO16098 ACO16098 ACO16098 ACO16098 ACO16098 ACO1609971 ACC22306 ACO22306 ACO1609731	29         24         9         47949         8         AC004625         AC004625         Arabida           30         28         4.9         17022         2         AC106098         AC016098         AC016098         AC016098         AC016098         AC016098         AC016098         AC016099         AC016098         AC016099         AC16099         AC16	ט נ	2 C	87.0	•	139		AX356480	equenc
30 28 4.9 77722 9 AC093762 AC093762 AC093762 AC093762 AC093762 AC093762 AC093762 AC093762 AC093762 AC095292 AC090769 AC090776 AC090776 AC090776 AC090776 AC090776 AC090777 AC09077 AC0907 AC	30         28         4.9         1772 2 yr         9 AC093762 Homo services           31         28         4.9         100652 2 AC116098 Homo services           32         28         4.9         130010 2 AC025292 AC025292 Homo services           34         28         4.9         133808 2 AC010769 Homo services           35         28         4.9         13388 2 AC010769 Homo services           36         28         4.9         15247 2 AC010769 Homo services           36         28         4.9         15247 2 AC010769 Homo services           37         28         4.9         15958 9 AC104062 Homo services           38         28         4.9         15968 9 AC104062 Homo services           40         28         4.9         159171 Home services           40         28         4.9         170022 2 AC104062 Homo services           41         28         4.9         17092 2 AC021559 Homo services           42         28         4.9         17092 2 AC021559 Homo services           43         28         4.9         17092 2 AC021559 Homo services           41         28         4.9         17091 2 ALB08114 AC02306 Homo services           42         4.9         17091 2 ALB08114 AC02306 Homo	c	א נ	870	•	424		AC004625	rabid
31 28 4.9 100652 2 AC116098 AC116098 AC116098 ACC15099 ACC15099 ACC15092 3 2 4.9 132000 2 AC016076 AC116076 AC116076 AC116076 AC116076 AC116076 AC116076 AC116076 AC116076 AC116076 AC110769 AC110769 AC10769	24 4.9 100652 2 AC0156098 AC1166098 Homo services 2 AC025292 2 AC025292 2 AC02529 2 AC0216976 Dictyos 34 28 4.9 152472 9 AC000486 AC00486 Homo services 2 AC010769 Homo services 2 AC021369 Homo services 2 AC021371 Homo services 2 AC		ۍ د د	58	•	777		AC093762	Omo
3.2 28 4.9 130010 2 ACC155292 ACC05252 1	32         28         4.9 1320010         2 AC025592         AC025292         AC025292 Homo services           34         28         4.9 132000         2 AC116976         AC106769 Homo services           35         28         4.9 152472         9 AC010769         AC010769 Homo services           36         28         4.9 155354         2 AC107591         AC107591 Rettus           37         28         4.9 155354         2 AC107591         AC107591 Rettus           38         28         4.9 156815         9 AC104062         AC104062 Homo services           40         28         4.9 176827         AC021559         AC104062 Homo services           40         28         4.9 176827         AC021559         AC021559 Homo services           40         28         4.9 176827         AC021559         AC022306 Homo services           41         28         4.9 179191         2 ALB08114         ALB08114 Mus mus           42         28         4.9 179191         2 ALB08114         ALB08114 Mus mus           44         27         4.7         330         11 G41782         G41782 B308C6548           45         27         4.7         369         3 AP400199         AC00199731 Homo services		7 6	28	•	1006		AC116098	OHO
3 28 4.9 132000 2 AC116976 AC116976 AC116976 E	34 28 4.9 132800 2 AC116976 AC116976 DICTYOS 35 28 4.9 13388 2 AC010769 AC010769 Homo se 36 28 4.9 155354 2 AC107591 AC10769 Homo se 37 28 4.9 155354 2 AC107591 AC107591 Rattus 38 28 4.9 159658 9 AC104062 AC107602 Homo se 39 28 4.9 170022 2 AC0104062 AC107591 Rattus 40 28 4.9 170022 2 AC021306 AC021306 Homo se 41 28 4.9 17082 2 AC021306 AC021306 Homo se 42 28 4.9 209764 I AL6898114 AL689468 Mouse 43 28 4.9 216250 9 AC099731 AC089731 Homo se 44 27 4.7 330 11 G41782 G41782 B308C6/5		3.5	28	•	1300		AC025292	CHO
34 28 4.9 133888 2 ACO10769 ACO10769 3 35 28 4.9 152472 9 APP000486 ACO1076916	34         28         4.9 133888         2 ACO10769         ACO10769 Homo Seconds           35         28         4.9 153472         9 AP000486         AP0004511         AP0005159         AP0005159         AP0005159         AP0005159         AP0005159         AP0005159         AP0005159         AP0005159         AP0005169         AP0005169         AP0005169         AP0005169         AP0005169         AP0009731         AP00009731         AP00009731	ט	2	28	•	1320(		AC116976	i cr
35 28 4.9 153472 9 AP000486 AP000486 AP000486 F   36 28 4.9 15534 2 AC107591 AC107591 8   37 28 4.9 15658 9 AC104062 AC104062 AC104062 H   38 28 4.9 176022 2 AC021559 AC021559 H   40 28 4.9 176027 9 AC022306 AC022306 H   41 28 4.9 170191 2 ALB08114 ALB0814 ALB08114 ALB0814 ALB0814 ALB0814 ALB0814 ALB0814 ALB	35         28         4.9 1523472         9 AP0000486         AP0000486 Homo See           36         28         4.9 155354         2 AC107591         AC107591         RALLOS           37         28         4.9 158658         9 AC104062         AC104062         AC104062           38         28         4.9 168145         9 AL15977         AC1021559         AC1021559           40         28         4.9 17022         2 AC021559         AC021559         AC021559           41         28         4.9 176827         9 AC022306         AC022306         AC0021559           42         28         4.9 17919         2 ALB08114         ALB08114         ALB08114           43         28         4.9 210250         9 AC099731         AC099731         AC099731           44         27         4.7         330         11         G41782         BO0806545           45         27         4.7         369         3 AP400199         AC0099731         AC0090P4	U	34	28	•	1338		AC010769	
36 28 4.9 15354 2 AC107591 AC107591 8 AC107591 8 AC107591 8 AC107591 8 AC104662 AC1051559 AC105164 AC	36 28 4.9 155354 2 AC107591 AC107591 CALL STATES 37 28 4.9 155558 9 AC104062 AC104062 Homo se		35	28	•	15247		AP000486	
37 28 4.9 15658 9 AC104062 AC104062 AC104062 AC104062 AC104062 AC104062 AC104062 AC104062 AC105171 H ALIS9171 AC021559 AC021559 AC022306 AC0222306 AC02222306 AC02222306 AC02222306 AC02222306 AC02222306 AC02222206 AC0222206 AC0222200 AC022200 AC02220 AC02220 AC02220 AC02220 AC02220 AC02220 AC02220 AC02220 AC02	37         28         4.9 159658         9 AC104062         AC104062 Homo sa           38         28         4.9 1708145         9 AL159171         AL159171 Human D           39         28         4.9 170824         2 AC021559         AC021559 Homo sa           40         28         4.9 170827         2 AC022306         AC0221559 Homo sa           41         28         4.9 179191         2 ALB08114         AL808114 Mus mus           43         28         4.9 209764         10 AL645468         AL645468 Mouse           44         27         4.7 216250         3 AC099731         AC099731 Homo sa           44         27         4.7 330         11 G41782         G41782 B308C6/5           45         27         4.7 369         3 AF400199         AC099731		36	28	•	15535		AC107591	1
38 28 4.9 168145 9 ALI59171 ALI69171 AL	38 28 4.9 168145 9 AL159171 AL159171 AL159171 AL159171 AL159171 AL159171 AL159171 AL159171 AL159171 Human D S	υ	37	. 58	•	15965		AC104062	
39 28 4.9 170022 2 AC021559 AC022306 H 4 2 9 179191 2 ALB08114 ALB08114 ALB08114 ALB08114 ALB08114 ALB08114 ALB08114 AC099731 AC0	39 28 4.9 170022 2 AC021559 AC021559 HOMO SB 40 28 4.9 176827 9 AC022306 AC022306 HOMO SB 41 28 4.9 176827 9 AC022306 AC022306 HOMO SB 42 28 4.9 209764 II 0 AL64546B AC08114 Mus mus AL64546 BOOS ACOS ACOS ACOS ACOS ACOS ACOS ACOS A	υ	38	28	•	16814		AT.159171	
40 28 4.9 176827 9 AC022305 AC022306 AC0222306 AC0222306 AC0222306 AC0222306 AC0222306 AC022306 AC0222306 AC02222306 AC02222306 AC02222306 AC02222306 AC02222306 AC02222206 AC02222206 AC02222206 AC02222206 AC02222206 AC02222206 AC0222206 AC022206 AC0222206 AC0222206 AC0222206 AC0222206 AC0222206 AC0222206 AC0222206 AC0222206 AC0222206 AC022206 AC02	40 28 4.9 176827 9 AC022306 AC022306 Homo sa 4.2 28 4.9 179191 2 AL808114 AL808114 Mus mus 4.3 28 4.9 209764 10 AL645468 AC082316 AC089731 AC099731 AC099731 Homo sa 4.7 4.7 330 11 G41782 G41782 B308C65/8 45 27 4.7 369 3 AF400199 AC09199 AF400199 Spodopt		39	28	•	17002		AC02155	uman
41 28 4.9 170191 2 ALBORILLA ALCOZISOS ACOZISOS ACOZISOS ALBORILLA ALBORILLA 42 28 4.9 209764 10 ALGOSIGA ALGOS	41 28 4.9 179191 2 ALBOB114 ALBOB114 Mus mus 42 28 4.9 209764 10 AL645468 AL645468 AL645468 Musus 82 4.9 216250 9 AC099731 AC099731 Homo sa 44 27 4.7 330 11 G41782 AC099999 AC099999 Spodopt 45 27 4.7 369 3 AF400199 Spodopt	o	40	28		17683		20222006	0110
42 28 4.9 209764 10 AL645468 AL646468 43 28 4.9 216250 9 AC099731 AC009731 AC009730 AC00730 AC0073	42 28 4.9 209764 10 AL645468 AL645468 Mouse 43 28 4.9 216250 9 AC099731 AC099731 Homo sa 44 27 4.7 330 11 G41782 G41782 B308C6/S 45 27 4.7 369 3 AF400199 AF400199 Spodopt	U	41	28	•	17910		ACC44300	0 0 8
28 4.9 216250 9 AC099731 AC09782	28 4.9 216250 9 AC099731 AC099731 AC099731 AC099731 AC099731 AC099731 AC099731 AC099731 AC09731 AC009731 AC009731 AC00199 AC400199 Spodopt		4.2	000	•	7000		ALCOCALL4	an aus
27 4.7 330 1 441782 641782 8 27 4.7 330 3 AF400199	27 4.7 330 11 G41782 ACU99731 Homo sap 27 4.7 330 11 G41782 G41782 B308C6/SP 27 4.7 369 3 AF400199 AF400199 Spodopte			0	•	, ,	>	400	15468
27 4.7 359 3 AF400199	27 4.7 369 3 AF400199 AF400199 Spodopte.		2 4	0 6	•	170T7		29973	1731 Homo sap
2/ 4·/ 369 3 AF4 00199	2/ 4./ 369 3 AF400199 AF400199 Spodopte		* 4	7 0	•	2,0	7	641782	'82 B308C6/SP
S SSTOOM WE STOOM			0	/7	4.4	9	m	F40019	199 Spodopte

ALIGNMENTS

AP003416

173699 bp DNA linear PLN 17-MAY-2002
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
PAC clone:P0456E05.
AP0003416, GI:20804922 RESULT 1 AP003416/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0456E05.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

AUTHORS

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

RFLAATRPISVOGDLNLFPSLPYSCSLAAAGLVL" join(1857418678,1882118984,2075221058,2187022177, 2237722536) /gene="rep0456605.3" join(1857418678,1882118984,2075221058,2187022177, 2237722536) /gene="rep0456605.3" /note="rep0456605.3" /note="contains EST AU070785(R10238) similar to Arabidopsis thaliana chromosome 3, At3948360 unknown protein" /codon_start=1 /protein_id="BAB92604.1" /protein_id="RAB92604.1" /protein_id="RAB9260FEREIDERSABABABABABABABABABABABABABABABABABABAB	HICTEGCTEVGPVGRAPAAAPCPAYATACRGLQLLIRHFSRCHRTSCPRCQRAWQLLR LIHAALCODLPOGHCNTPLCMQFRREEERAARARARGDDDGWGLLVKRVRVARAMS SLGRRRQMSCSQC" complement(join(2355823638,2483724941)) /gene="P0456505.4" complement(join(2355823638,2483724941)) /gene="P0456505.4" /gene="P0456505.4" /note="contains BST Au162265(E30874) unknown protein" /codon_start=1 /protein.1d= BBB92605.1" /Abrotein.2d= BBB92605.1"	/translation="MYKVATYFAMTEGAFLEWQSMDRVHVWIALHQDEKKERWERERE IRRWQAREMAONESES" complement(join(26102. 26407,26766. 26901,2702827170, 2765627784,2815428402,2898829359)) /gene="p0456605.5" complement(join(26102. 26407,26766. 26901,2702827170, 2765627784,2815428402,2898829359)) /gene="p0456605.5" /note="hypothetical protein magnesium transporter-like protein" /codon_start=1 /protein_id="pab92606.1"	/db_xref="G1" 1208492/" /db_xref="G1" 1208492/" /db_xref="G1" MRP&BAGGGGGGGRRKAAAAAARREWLVVPASGQARVEEA /translation="MRP&BAGGGGGGGRRKAAAAAAASREWLVVPASGQARVEEA /translation="MRP&BAGGGGGGGGRRKAAAAAASREWLVVPBSVTJAAKUTJAAKULLENSK GRHAVMARTGLPARTLASSBOQABETDMBGESSAVTSPPALITSTTPMELEMYRKIS DPARASSTVOLDARTLASSBOQABETDMBGESSAVTSPPALITSTTPMELEMYRKIS NVGGMTISNSMPTLTARACONTRVLPFEFRALEVCLESACRSLEEETSTLEGGAVPA INDELTSKISTVENDERRASNEWRFWETTLGTTROTTFILDDENDARAEWTLTEKLTR OGLIGITARISTRERVDDTBDTNINILDDKONGLLOMGCWLSTATVVITAGVAVVGLFGM NTGISLANDFTNEERRASNEWRFWETTLGTTAGTTAVYTAMGWGRRSGLLO"   oln(36977 . 37082,37255 . 37479,37607 . 37701,37823 . 38015, 38424 . 38764,39169 . 39399,39493 . 39645) /gene="pto45605.6" /gene="pto45605.6" /gene="pto45605.6" /gene="pto45605.6" /gene="pto46605.6" /gene="pto45605.6"	/product="proline transport protein-like" /protein_id="BabB92607.1" /db_xref="G1:20804928" /db_xref="G1:20804928" /translation="MaASSLDAEAAAAGODKAGSGSYTTAATHAIDIDTDSWQOYGVI LVVGRYGAYLESNIAMAPUGWGGNGILACLFIGGASWYANWILAGLHVIDGORFIRY RUMGFVFGRKMYITWFIDFILLIGNMGTILLGGRALKALHARESSHSPARLOWF RDLMGFVFGRKMYITWFIDFILLEDFILLGHAATHAIDIDTOSORFIRY RATGEVYFARAFVPFISAMRWHATSAALTVAYDVALIVILIKDGKSNKOKDYWH IAATGEVYFARAFVPFISAMRWHATSGLAFEIQSTLKREVYSNRRRELLLGYTAGAAVYYG GTQARKVFGARGARAILVORTSGLAFEIQSTLKREVYSNRRRELLLGYTAGAAVYYG ISVAGYWAYGAAVSTLPDOLSGPSWATVILNAFPFWGDFVNLFGSFVLFFPIFFB ORLDEGENFSKYNLGRRLLARGLYFGBNARFVTALFFFWGDFVNLFGSFVLFFPLFMFPS MVVLKIKGKDEAGRWNRIWHWGIINASSVLSVVTTAAAVRLIVHNASYYHFFPLDM" complement(join(40277 40417, 40717 40773, 40875 41073, 41173 41300, 41399 41564, 41677 412841, 43717 44055)) /gene="P0456E05.7"
gene CDS	gene	gene	gene	aeue
Sasaki,T., Matsumoto,T. and Yamamoto,K.  Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC Lone:PQ456E05  Published Only in Database (2001)  2 (bases 1 to 173699)  2 (bases 2 to 173699)  2 (bases 2 to 173699)  2 (bases 3 to 173699)  3 (bases 2 to 173699)  3 (bases 3 to 173699)  3 (bases 4 to 173699)  3 (bases 4 to 173699)  3 (bases 4 to 173699)  4 (bases 4 to 173699)  5 (bases 4 to 173699)  5 (bases 4 to 173699)  6 (bases 4 to 173699)  7 (bases 4 to 1736999)  8 (bases 4 to 1736999)  8 (bases 4 to 17369999)  8 (bases 4 to 17369999)  9 (bases 4 to 173699999)  9 (bases 4 to 1736999999999999999999999999999999999999	NCBI NonRedundant Protein database, nr  (ttp://ncbi.nlm.ndv.yov/blast/db) and the cDNA sequence database at  RCP. Protein inm.ndh.gov/blast/db) and the cDNA sequence database at  RCP. Protein homologies of the coding regions were searched against  NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent  NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent  A gene with identity or significant homology to.a protein is  A gene with identity or significant homology to.a protein is  Significant bame, 'putative' and 'like protein'. A gene without  Significant homology to any protein but with EST homology (covering  Significant homology to any protein but with EST homology (covering  Significant homology to any protein but with EST homology (covering  Like protein, A gene predicted with a gene prediction program  'unknown' protein. A gene predicted with a gene prediction program	is classified as a 'hypothetical' protein.  The orientation of the sequence is from 17 to SP6 of the PAC clone.  The orientation of the sequence is from 17 to SP6 of the PAC clone.  This sequence of P0456E05 clone has an overlap with P0470A12 (DDBJ:  AP003436) at the position 130,058 to 173,699 of 3' end Detailed  information on overlap and assembly quality together with  annotation of this entry is available at  thtp://rgp.dna.affrc.go.jb/GenomeSeq.html.  Location/Qualifiers  1173699  /corganism="Cryza satiup" (japonica cultivar-group)"  /cultivar="Nipponbare" /db_xref="taxon:39947"	.10785) .10785) .tein"  "reacycvergorgnabwiarppaparae	13131. 13131. 1319. 13459. 1358/, 1360. 1370, 1370, 1370, 1370, 1300. 1313. 13

FEATURES

gene

gene

CDS

ന

```
**Louis Traylor only in Database (2001)

Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission

Submitted (21.MAR-2001) Takuji Sasaki, National Institute of Direct Submission

Submitted (21.MAR-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondal 2-1-2, Tsukuba, Ibaraki 305-6602, Japan (E-mali:tsasaki@ilas.affrc.go.jp, URL.http://rgp.dna.affrc.go.jp/, On Oct 17, 2001 this sequence version replaced gi:13430001.
Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, as well as Splicepredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0, ESTS represent
                                  Institute of Agricultural Science and Technology(NIAST), RDA, 249 Seodun-dong, Suwon 441-707, Korea (E-mail:jhhahn@rda.go.kr, Tel:82-31-290-0308)
Tel:82-31-290-0309, Fax:82-31-290-0308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APU03436 14 DNA 11 DNA 17-APR-2002 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0470A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                 * Working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as it is available and the accession number will be preserved.

* 53113: contig of 53113 bp in length

* 53214 172405 contig of 119191 bp in length

* 172405 172504: gap of unknown length

* 172405 172504: gap of unknown length

* 172405 172504: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA clone:P0470A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 174218
/organism="oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0470A12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 174218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="P0456E05"
49037 a 38377 c 37185 g 49417 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 2.5
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.7%; Score 44;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /variety="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP003436
AP003436.2 GI:16197551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.0
Matches 44; Conservative
                                                                                                                                                     NIAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
AP003436/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                 /ULTANALAL - V. I. J. UDOUGO STATE A PROGRAM STATE OF STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complement(join(40277. .40417,40717. .40773,40875. .41073,
41173. .41300,41399. .41504,41677. .41756,42145. .42242,
42324. .42437, 42523. .42663,42757. .42841,43717. .44055))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC091071 174218 bp DNA linear HTG 27-MAR-2001 Oryza sativa (japonica cultivar-group) chromosome 1 clone P0456E05, A*** SEQUENCING IN PROGRESS ***, 3 ordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 174218)
Lee,J.-S., Hahn,J.-H., Yoon,U.-H., Lee,M.-C., Yun,D.-W., Kim,H.-I.
                                                                                                                      /note="contains ESTS AU101665(R2414), D24709(R2594)
Similar to Arabidopsis thaliana chromosome 5, At5g14420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (Dases 1 to 174218)
Hahn, J.-H., Eun, M.Y. and Kim, H.-I.
Direct Submission
Submitted (27-MAR-2001) Rice Genome Sequencing Project, National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 173699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157564 ACTACCAGGAGGTGGACTACTGCTCGAGGAGGTGAGGTCGGTG 157521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 8; Length 1/3/
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa PAC P0456E05 genomic sequence
                                                                                                                                                                                                                                         /protein_id="BAB92608.1"
/db_xref="GI:20804929"
                                                                                                                                                                                    unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.7.,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC091071.1 GI:13450004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
cos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
AC091071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
```

ô đ

```
/couch_scatc="putative RNA helicase"
/product="putative RNA helicase"
/product="putative RNA helicase"
/product="putative RNA helicase"
/product="20161357"
/db_xref="G1:20161357"
/db_xref="31:20161357"
/db_xref="G1:20161357"
/db_xref="31:20161357"
/db_xref="31:2016135"
/db_x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41290. 41359,41646. 141710,4237. 40913. 141002,41120. 41176,421290. 41359,41646. 421710,42307. 42361,42603. 42730,428183. 42906,43104. 43173,43522. 43723,43820. 43909,43104. 44630,44713. 44799,46231. 146311,46310. 46836,46920. 47036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join 40309. .40472,40627. .40822,40913. .41002,41120. .41176,

join 41359,41646. .41710,42307. .42361,42603. .42730,

42818. .42906,43104. .43173,43622. .43723,43820. .43909,

43983. .44131,44519. .44630,44713. .44799,46231. .46311,

46380. .46604,46714. .46836,46920. .47036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAB90282.1"
/db_xref="c1:20161358"
/translation="MAAAGGLPASATLLLLVIAAVAVAPLASAVRPVSDAHRSAAAEL
/translation="MAAAGGLPASATLLLLVIAAVAVAPLASAVRPVSDAHRSAAAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="Bab90280.1"
/db_xref="G1:20161356"
/db_xref="G1:20161356"
/translation="MDSGGTASPAGVAGDGAGGRGSVFRGDDAPKLLAALKEWKEGLD
ivtgkvkaltrkvknoldtatooffterlachtertyferkrkoldtyferkakglsveghp
vyrslyfilflerinfildrkhryqicklthaalsgaagekevdsygsperge
FGRGGYOQQHVYKETFQEIDRSGSGRHHHNHNHGNDYLAVRETKVEEDFNTCTGEFR
ERROSFLLKSD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(34470. .34734,34836. .34921,35025. .35117,
35201. .35364,35440. .35601,35682. .35861,35978. .36414,
36513. .36568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(34470. 34734,34836. 34921,35925. 35117,35201. 35301. 35501,35682. 35861,35978. 36414,35201. 355681. 35681. 35681. 35681. 35681. 36414, 35513. 355681. 36414. 36414. 36414. 36418. 36414. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 36418. 3641
RHAARHAVRNEALGVVVVLRHVPSPVAATWTRRKOOCATGAALPRYEAHTIENTTIGE
GEEEHDVRQPPQGGLRTLRLHQQPRRYESTSCARIGGGSRAGEKHPTLNCQHQRHDRT
TDDQATVRNTTLKRKTTCMSVCHGRVQVWVQAPYQG"
complement(23929, .24237)
complement(23929, .24237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MAQYYSBVDHCAEEMNRPPHAGGEHYAVRRESYEEVDEMARAGR
GHHGNGGGGGHLGYSGSRHGDAHLGGHREEHLVHGDEHRHGHGGGRQYDSCTGQYYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(27239. .27499,30542. .30622,30720. .30899,3099enent(join(27239. .2165).)
30998-.31165).
/gene="P0470A12.5"
/note="contains EST AU070442(S15668)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(27239. .27499,30542. .30622,30720. .30899,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4, F7J7_90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /joce="contains ESTs
D15893(C1477),C72138(E1066),AU101125(E1066)
similar to Arabidopsis thaliana chromosome
unknown protein
                                                                                                                                                                                                                                                                                                                    complement(23929, .24237)
/gene="P0470A12.4"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB90279.1"
/db_xref="G1:20161355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0470A12.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36513. .36568))
/gene="P0470A12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30998. .31165))
/gene="P0470A12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and 'like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orlentation of the sequence is from SP6 to T7 of the PAC clone. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"MSKLAIIGRSSGLPRSNEGMRLLFSAVICVMLGYLFGISFPTVN
/translation-"MSKLAIIGRSSGLPRSNEGMRLLFSAVICVMLGYLFGISFPTVN
VTKLHFPSEIISYEBKDSGITTGTLLNHAMTSANSKRNNSESNSDEIPKIYVPTNP
VTKLHFPSEIISYEBKDSGITTGTLLNHAMTSANSFRNSESNSDEIPKIYVPTNP
KGABGLAGIVVPETDLTLARRIMGEPSEDLTSQPRVWYAKRFLHPDIVAPVDYIFIW
DEDLSVQHFNAPATNDWDEFEWSKRAIHVSVRRGTKWWYAKRELDPDIVAPVDYIFIW
WCTDPHLPPCAATVEIMATVFSRDAWRCVWHMIQNDLVHGWGLDFALRRCVBEPHEKI
GVYDSQWVIHQVIPSLGNQGTAENGRTPWBGVRAKCKEWGMFQKRLADAEKAYYLGK
GITPPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="marrrygggrseygggngeargrrrqprsggrseargarrrlprrg
SPASPPSGRREAGEEGSGGGGRAPVINVTTRRSRKPWRDSSGGRRDHAASRHDSIHT
RERTNWNGAIKLRPTFYGTREFRCCKPSLVVTPIWAGILGCHLCVLARLLCLROORWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement of the first state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mamarrgnggrovgaysygygyskrovnyhsossesytyvytkm
Demsyhenavokmsssfreekvyeooggaggdvovcrnggaaagavokhtyeekkeee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement(15118. .16344)
/gene="P0470A12.2"
complement(15118. .16344)
/gene="P0470A12.2"
/gene="contains EST AU069076(C51993)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB90277.1"
/db_xref="G1:20161353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAB90278.1"
/db_xref="G1:20161354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAB90276.1"
/db_xref="GI:20161352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="P0470A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
```

CDS

CDS

gene

FEATURES

ഗ

ô

Gaps

ö

Mon Jun 16 14:55:55 2003

```
REX INDERES 1 to 185133)

REX MUZDY, A. Addens.C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alisbrooks, S.L., Amaratunge, H.C., Ase, J.R., Aslet, M., Banka, T., Barbaria, J., Benron, J., Binage, K., Blankenburg, K., Bonnin, D., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Aslet, M., Banka, T., Barbaria, J., Benron, J., Binage, K., Blankenburg, K., Bonnin, D., Barbaria, J., Bernon, P., Burkett, C., Burrell, K.L., Byrd, N.C., Cales, Brown, R., Byrd, N.C., Carler, M.D., Dathorne, S.R., David, N.C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Dalaney, K.R., Delgado, O., Denn, A.L., Dinn, H. H. Delaney, K.R., Delgado, O., Denn, A.L., Dinn, Y., Dinn, H. H. Douthwatte, K., Darper, H., Dugan-Rocha, S., Durbin, K.J., Earnbart, C., Edgar, D., Edvards, C.C., Elhal, C., Escottc, M., Earlbart, C., Edgar, D., Edvards, C.C., Elhal, C., Escottc, M., Harris, K., Hart, M., Havlak, P., Hahe, S., Hamilton, K. Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Ganzen, P., Hawes, A., Harland, S., Kallsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratcvic, J., Kureshi, A., Canonson, R., Jolivet, S., Joudh, S., Karlsson, E., Kelly, S., Khan, U., Kling, L., Korvah, J., Kovar, C., Liu, J., Li, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Luna, R., Maj, J., Martin, R., Maj, J., Martin, R., Maj, J., Berry, G., Martin, R., Maj, J., Martin, R., Maj, J., Perry, J., Perrs, L., Rober, M., Neal, D., Newtson, J., Rober, M., Neil, C., Martin, R., Man, M., Mell, D., Newtson, J., Rober, R., Martin, R., Man, R., Man, R., Man, R., Man, M., Rober, M., Rojubokan, I., Rolle, M., Rula, S., Soott, G., Shen, H., Shooshtari, M., Rojab, A., Rojubokan, T., Rolle, M., Rojubokan, T., Rolle, M., Rojubokan, T., Rolle, M., Rolle, M., Stone, H., Scherer, S., Scott, G., Shen, H., Washing, S., Wardin, S., Wartin, R., Walle, M., Will, Walle, M., Walle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A linear HTG 23-JUL-2002
*** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
       1. .185481
/organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                     Length 185481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 others
                                                                                                                                                                                                                                                                                                                      7.7%; Score 44; DB 2; L6
100.0%; Pred. No. 2.5e-12;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus clone CH230-274116, ***, 77 unordered pleces.
                                                                                                                                                                                                                            41493 g 50653 t
                                                                          /variety="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                   /clone="P0470A12"
51439 a 41522 c 41493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC119716.4 GI:21902555
HTG; HTGS_PHASE1.
Rattus norvegicus.
Rattus norvegicus
                                                                                                                                                     /chromosome="1
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus.
                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
AC119716
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALL Unpublished

Interpretation of the part of the paper of the gape between the grounded by the submitted (29-MAR-2001) Rice Genome Sequencing Project, National Institute of Agricultural Science and Technology(NIAST), RDA, 249 Tel:80-131-290-0309; Rax:82-31-290-0309; Rax:82-31-200-0309; Rax:82-31-200-030
ADNITEHATIKALSOSTANDA RAMAN ANDITALLALYS VGGLISTIKOGHNIVULPD
KNOT KALEDSTRENDEN AND ANDITAL AND SEVOGLISTIKOGHNIVULPD
KNOT KALEDSTRENDEN POREKHUDAREK KGPITTSASVURGYT SEPANASCKLIN
FGENTIGLAR FFLGIGLPGSAKDE FWO DIEV FVEHJELDEN KYRESLTSKOOLK VETTV
FGSAAPPLIKUNGVIGSDSKVITTETRELOPDINNYH ZUDIALK ZUDOKY SILVE
FGSAAPPLIKUNG SKOTTTETRELOPDINNYH ZUDIALK ZUDOKY SILVE
VELSAAPHLOK LRISFOLST PLGAT FREHOVELKKH MDSK VENEHL FVURGSARQFK ZUL
PELGLVER FYTLGGRYDLELAVODAANENSE LRACHTELDDE PRAPERAR PROPEKTIVE
SER KFGPRKETSHIFRS PEKREF FREHOVELKEN FREHLEVURGSARQFK ZUL
PARAARERS SER FREH FREPERREPRELSFRANGILL LLD TUGFLIGLMRLGVULKNEPSL
SAKOKRA"
SAKOKRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(47978. .48061,48179. .48239,48314. .48378,48478. .48759,48837. .48911,49020. .49094,40242. .49298,49552. .49655,49763. .49964,50111. .50213,50317. .50378,50507. .50561,50738. .50841,50926. .51048,51175. .51219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG 29-MAR-2001 clone P0470A12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC091088.1 GI:13487944
HTG; HTGS_PHASE2.
Oryza sativa (japonica cultivar-group).
Gryza sativa (japonica cultivar-group).
Gryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sprmatcophyta; Manoliophyta; Liliopsida; Poales; Poacea;
Brhartoideae; Oryzeae; Oryza.
1 (bases 1 to 185481)
Lee,J.-S., Hahn,J.-H., Yoon,U.-H., Lee,M.-C., Yun,D.-W., Kim,H.-I.
                                                                                                                                                                                                                                                                                                                                                        complement(join(47978. .48061,48179. .48239,48314. .48378
48478. .48759,48837. .48911,49020. .49094,49342. .49298,
49552. .49625,49763. .49964,50111. .50213,50317. .50378,
50507. .50561,50738. .50841,50926. .51048,51175. .51219,
51967. .52059,52148. .52561))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7:7%; Score 44; DB 8; Length 185095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC091088 185481 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 1 *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 7.7%; COLL 1.0. 2.50
Best Local Similarity 100.0%; Pred. No. 2.50
Matches 44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
AC091088
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
```

ð q us-10-090-035-3.rge

COMMENT

```
bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                       bp in length
length
                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                  length
bp in length
                                                                                                              bp in length
length
                                                                                                                                                                                           1210 bp in length
                                                                                                                                                                                                                                  bp in length
in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ength
                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                          length
                                                                                                                                                                                                                                                      length
                                                       length
                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
of 2466
                                                                                                                                                                                                                                                                       of 1224 b
unknown l
of 1475 b
                                                                                                                                                                                                                                                                                                                                unknown l
of 2427 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                     unknown
of 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
of 1378
                                                                                                                                                      of 1408 lunknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 1318
                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                               1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                 of 1310
                                                                                                                                                                                                                                  of 1110
                                                                                                unknown
                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of
gap of unki
contig of
gap of unki
                                                                                                                                                                                                                                                                                                                                                                                                                               οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                            contig
gap of
                                                                                                                                                          contig
gap of
                                                                                                                                                                                               contig
gap of
                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
                                       contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                               contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qap of
                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87277:
89743:
89843:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41418
444192
446265
463655
463655
550456
550456
660366
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
66127
                        23379
224479
224672
226825
225825
227235
227235
227335
237335
237335
331263
31263
31263
31263
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31687
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 77 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                               Submitted (01-MAY-2002) Human Genome Sequencing Center, Department Stubmitted (01-MAY-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases I to 185133) Morley, K.C. Direct Submitsed (23-JUL-2002) Human Genome Sequencing Center, Department Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA On Jul 18, 2002 this sequence version replaced gi:20467917.
                                                                                                                                                                                                                                                                                                                    bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1001: contig of 1001 bp in length
1101: gap of unknown length
2138: contig of 1037 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 1394 bp in length gap of unknown length contig of 1039 bp in length contig of 1373 bp in length contig of 1373 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 1405 E
gap of unknown 1
contig of 1075 b
gap of unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
of 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19105:
19205:
20676:
20776:
22169:
    Unpublished
2 (bases 1 to 185133)
                                                                                                                                                                                                                                                                                                              Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13818
                                       Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8566
8666
9855
9955
111360
11460
12535
13719
13819
14941
15041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16429
17845
17845
17945
19106
19206
20677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1002
1102
2139
2239
    JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
```

g ò

```
Web site: http://www.isc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N. Ayele.K. Beckstrom-Sternberg.S.W., Benjamin,B.,
Blakesley,R.W., Bouffarlom-St. Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighl,P.,
Maduro,O.L., Masiello,C., Waskeri,B., Mastrian,S., McDowell,J., Pearson,R., Stantripop,S., Tomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="H2A histone family, member C"
/protein_did="AAH32756.1"
/db_xref="GI:199566"
/translation="MSCRGKQGCKARAKAKTRSSRAGLQFPVGRVHRLLRKGNYAERV
GAGAPYYLAAVLEYTFAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVT
13039 208 t
3139 208 t
                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 69 Row: p Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 15718718.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY102542
Arabidopsis thallana hypothetical protein (At2g23370/F26B6.2) mRNA, AY102542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thale cress.

Arabidopsis thaliana
Bukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wagnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 1275)
Xiao, Y., Ishmael, N., Kumar, N., Redman, J., Riedmuller, S.,
Utterback, T., Whitelaw, C.A., Fraser, C.M. and Town, C.D.
Cloning and sequencing of full length cobas for hypothetical genes from chromosome 2 of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xiao,Y., Ishmeel,N., Kumar,N., Redman,J., Riedmuller,S., Utterback,T., Whitelaw,C.A., Fraser,C.M. and Town,C.D. Direct Submission
Submitted (08-MAY-2002) Plant Genomics, The Institute for Research, 9712 Medical Center Drive, Rockville, MD 20850, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1138;
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="Locusio:3339"
/db_xref="taxon:9606"
/clone="MGC:44857 IMAGE:5581631"
/tlssue_type="Eye, retinoblastome"
/clone_lib="RHH_MGC_67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Leus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 5.1%; Score 29; DB Similarity 100.0%; Pred. No. 0.0 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CCCACGCGTCCGCCCACGCGTCCGCACAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 CCCACGCGTCCGCCACGCGTCCGCACAG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 g
                      Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY102542.1 GI:21805664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                 ö
                                                                                                                                                                                                                                                                                     PAT 06-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens, H2A histone family, member C, clone MGC:44857 EC032756 EC032756 GC:21595675 GC:21595675 MCC:455756 MCC:4595675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and Elashoff,M.R. Molecular toxicology modeling Patent: WO 0210453-A 508 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                   Length 185133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Locally ... . 569
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/note="EMBL/GenBank Accession No. AI007824"
- 98 c 117 g 222 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 569;
                                                                                          Indels
                                                                                                                                                                                                                                                                                  linear
91514: contig of 1671 bp in length
                                       Match
Local Similarity 100.0%; Pred. No. 2.2e-05;
es .31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 5.1%; Score 29; DB 6; Lo Best Local Similarity 100.0%; Pred. No. 0.00022; Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                51879 ACCCACGCGTCCGCCCACGCGTCCGCACAGC 51909
                                                                                                                                                                                                                                                                                DNA
                                                                                                                       1 ACCCACGCGTCCGCCCACGCGTCCGCACAGC 31
                                                                                                                                                                                                                                                                     AX400832 569 bp 1
Sequence 508 from Patent WO0210453.
AX400832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 GTAATACTAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene Logic, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     AX400832.1 GI:21337012
                                                                                                                                                                                                                                                                                                                                                                  Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                       Query Match
Best Local S
                                                                                                                                                                                                                           RESULT 6
AX400832/C
LOCUS
                                                                                                                                                                                                                                                                                  DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
BC032756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMARK
COMMENT
```

ò

ö

Gaps

ö

Genomic USA

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                 RESULT 10
BC012959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                         ă
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio alcohol dehydrogenase (ADH) mRNA, complete cds. AF295407.1 GI:15428577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
2. (Dases 1 to 1450)
Tanguay, R.L. and Vasiliou, V.
Direct Submission
Direct Submission
Submitted (15-AUG-2000) School of Pharmacy, University of Colorado Health Sciences Center, 4200 East Ninth Ave, Box C238, Denver, CO 80262, USA
                                                                                                                                                                                                                       KAOPPKHLMOLLNIETARGKSIVSPCAKOĞLLPLTIPLVKMSPGSSIALLRMPTAPSS
MEMPVVEVQKHCVWFLANNVDQFIHRILVEDDVSKPERCSOBIFNAAGEAGKKLYSKG
DAFSSSRLMDLDAYLLRKVGLEPBOLERSKVIRHIENGDHVSALVATEFYTKGNFPGFA
RPFAFNAKULLKLGRHLEAKDARGALKSSWWTLGCRYEEIAQIAEWGEEQIAOYKER
VTGEGKQRDIDRGKFWAQASLDEAAFLLNLASLEGTWDESLERVAQCYKEAGLNDIAK
                                                                                                                                            /evidence-not_experimental
/product-"hypothetical protein"
/protein_d="AAWT671.1"
/db_xref="G1:21805665"
/translation="WHRGAAVFGRRRELILLHGSRNFARSFCSSSSLSEHECFIKDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanguay, R.L. and Vasiliou, V. Identification and characterization of the zebrafish alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
 /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.1%; Score 29; DB 8; I 100.0%; Pred. No. 0.00023; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1242 GTAATACTAAAAAAAAAAAAAAAAAAAAA 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             546 GTAATACTAAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="At2g23370/F26B6.2"
232 c 308 g 348
                                                                                                                                                                                                                                                                                                                                                                                      gene-"At2g23370/F26B6.2"
                                                                                /gene="At2g23370/F26B6.2"
29. .1051
                                                                                                                     /gene-"At2g23370/F26B6.2"
                                                                                                                                                                                                                                                                                                                                         /gene="At2g23370/F26B6.2"
                                                     /note="ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1450
/organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           /note="alternative"
1251
                                                                                                                                                                                                                                                                                                                                                          'note="alternative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ADH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ADH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                              FVLYRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Danio rerio.
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
hes 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                       386
                                                                                                                                                                                                                                                                                                                                                                                                                         polyA_site
                                                                                                                                                                                                                                                                                                                                                                               polyA_site
                                                                                                                                                                                                                                                                                                                               polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
AF295407
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                gene
                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

```
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: j Golumn: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755673. I. 2879 action/Qualifiers consortium/Loransmark.mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus, staufen (RNA-binding protein) homolog 1 (Drosophila), clone MGC:13708 IMAGE:4188394, mRNA, complete cds. BC012959 BC012959.1 GI:15277959
                                                                             /translation="MATAGKUTKCRAAVAWEPRAPLAMAEBIEVAPPOGGEIRIKVIAT
/translation="MATAGKUTKCRAAVAWEPRAPLAMAEBIEVAPPOGGEIRIKVIAT
GLCHTDLYHLVDGDKRGFPVVLGHESAGVVESVGPGVTLDYRRGDKVIFLESQCGKKK
GLCHTDLYHLVGESSWARKTHDINAEPRESFETCRGGTILQFWGTSTFSETYTUNONAVA
IDENAFLINGESGATTGTGAAVAWTAGVTPGSVCAVFGLGAVGTAAVAGKTNAGAS
RIFAVDINEKKFEKAKVFGATDFLNPKAFNKPISEVLIEMTNGGGVDFSIECTGNTEV
MRSALESCAKGWGVSVVVGWTRNOEDRAFDILJTGKTWKGSLFGGFKCKDSVFKLVR
DYMSGKIMLDEFITHKNNLEVNDAINLAKTGGGIRTIMTVSK"

3 316 c 359 t 359 t
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 2879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Salivary gland, 10 week old female mouse"/clone_lib="NCI_CGAP_SG2"/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (20-MUG-2001) National Institutes of Health, Mammalian
Submitted (20-MUG-2001) Cancer Genomics Office, National Cancer
Gene Collection (MCG), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anuradha
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
Email: capabs remail.nth.gov
Email: capabs remail.nth.gov
Inssue Procurement: Jeffery E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anny Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurack
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="staufen (RNA-binding protein) homolog (Drosophila)"
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                 5.1%; Score 29; DB 5; Length 1450; 100.0%; Pred. No. 0.00023; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MGC:13708 IMAGE:4188394"
/product="alcohol dehydrogenase"
/protein_id="AAK97853.1"
/db_xref="G1:15428578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAH12959.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CCACGCGTCCGCCCACGCGTCCGCACAGC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCACGCGTCCGCCCACGCGTCCGCACAGC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                                                                                                                                                                                                                                                                ๙
                                                                                                                                                                                                                                                                                                                419
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
```

Gaps

ö

Dear, P., Kumpf, K.,

BASE COUNT ORIGIN

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 11 AK025519

ò 임 ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

```
Dictyostellum discoideum chromosome 2 map 109820-140341 strain AX4, AC115592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from Hay Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Blochemistry I (http://www.uni-koeln.de/dictyostelium/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MYRISVINDCINSIVNAERQGKROVLVRPSSKVIVKFLEVMMKK
RYIGEFEIVDDHRSGKIVIDLIGRINKCGVISPRFDVTLDEIEKWASYLLPSRQFGHI
VLTTSLGIMDHNEARTRHTGGKLLGFFY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MINIELISKEKKVIGYDENCILVGEIEKSTNKHLLIGTVDGKII
VYLNDEEIEVLETKGSSIQQLELLDTTKFGSIDVISGDSNGNLVIFSNHQILYRDTLN
GSITSIITHRLSIGDSLGLVTSIKPHQNAIMRYKIPSVNQTLNSLIDSDIIAINPNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(2504. .2668,2759. .3450,3569. .3911))
/note="ORE_ID:dd_01555"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 30523)
Gloeckner,G., Elchinger,L., Szaffranski,K., Pachebat,J., Dear, Lehmann,R., Baungart,C., Parra,G., April,J.F., Gulgo,R., Kumr, Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agency : Deutsche Forschungsgemeinschaft (DFG).

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence and Analysis of Chromosome 2 of Dictyostellum
        Length 3194;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Dictyostellum Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="40S ribosomal protein S15A"

    .30523
    /organism="Dictyostelium discoideum"

     DB 9; Le
0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAL92279.1"
/db_xref="GI:19569977"
                                                                                                                                        3165 GTAATACTAAAAAAAAAAAAAA 3193
Query Match
5.1%; Score 29; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 29; Conservative 0; Mismatches
                                                                                                           546 GTAATACTAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAL92278.1"
/db_xref="GI:19569976"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697. .971
/note-"ORF_ID:dd_01553"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"ORF_ID:dd_01554"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="2"
/map="109820-140341"
                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE2.
Dictyostellum discoldeum.
Dictyostellum discoldeum
                                                                                                                                                                                                                                                                                                                                                                                                                    AC115592.1 GI:19569975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 30523)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /psendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noegel, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumgart, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Funding
                                                                                                                                                                                                                                                                                                     LOCUS
DEFINITION
                                                                                                                                                                                                                                                 RESULT 12
AC115592/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                           ö
                                                                                                                                                            a
                                                                                                              LRRLPPLPAVERVKREVERTKKSOPTCKLOTADDYGGGNNPISRLAGIGGAKKEKEPEYM
LLTERGLPRRREFVMQVKVGHHTAEGYGTNKKVAKRNAAENMLEILGFKVPQAQPAKP
LLTERGLPRRREFVMQVKVGHHTAEGYGTNKKVAKRNAAENMLEILGFKVPQADPAKP
EVAGAVGTVFKREGGRKYTFFEPSPGDENGTSKNDEFRMPLLSGGTSPTAETILKSNISSGH
VPHGPRTRPSEQLYTLSRAAPNPAKTVTAMIARELLYGGTSSTAETILKSNISSGH
VPHGPRTRPSEQLYTLSRAQGFQVEXKDFPKNNKNEVYSLINGSSQPPLVSHGIGKDV
ESCHDMAALNILKLLSELDQGSTEMPRTGNGPVSACGRC"

735 c 699 g 647 t
                                  /translation="MXKPVDPHSRMQSTYSYGMRGGAYPPRYFYPFPVPPLLYQVELS
VGGQDFNGKGKMRPPVKHDAPARALRTLQSEPLPERLEVNGREAEEBNNKSELSQVF
EIALKRNLPVNFEVARESGPPHMKNFVTRVSYGEFVGEGEGKSKKISKKNAARAVLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugano, S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-ANG-2000) Sumio Sugano, Institute of Medical Science, Onlyversity of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 29-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKO25519
3194 bp mRNA linear PRI 29-SEP-2000
HOMO Sapiens CDNA: FLJ21866 fis, clone HEPO2379, highly similar to
AF001938 Homo sapiens staufen protein (STAU) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AK025519.1 GI:10438059 oligo capping; fis (full insert sequence). Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_llb:HEP clone:HEP02379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEDO human con a sequencing project supported by Ministry of International Trade and Industry of Japan; con full insert sequencing; Research Association for Blotechnology; cDNA library construction, 5 - 6 3 '- end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="highly similar to AF061938 Homo sapiens staufen
protein (STAU) mRNA"
1 787 c 732 g 781 t
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                              Length 2879;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                               Ouery Match 5.1%; Score 29; DB 10; PBest Local Similarity 100.0%; Pred. No. 0.00023; Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="HEP"
/note="cloning vector pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2821 GTAATACTAAAAAAAAAAAAAAAA 2849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 GTAATACTAAAAAAAAAAAAAAAAAA 574

    .3194
    /organism-"Homo sapiens"
/db_xref-"taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_line="HepG2"
/cell_type="hepatoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="HEP02379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 3194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1. .3194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       894
```

misc\_feature

BASE COUNT ORIGIN

source

FEATURES

CDS

```
complement(join(11012. 11317,11409. 11524,11604. 11766))
/note="ORF_ID:dd_01558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVTAIHDFLPGEQTYTELKGHRIQLNFDFDKVDTATYNGLFLPGGRCSEFLRLDDRVI
EIVKDFNTNKKPIAAVCHGAQVLTAANIVSGIKCTAYPACRPEVQQAGGIYQDIAVDD
VYDGHIYSGKAWPCHPKLLGFIKLLGTTITHN"
complement(jOin(1238). .16761,16921. .18037))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNSARSNNPILQGMGYEEDTPEEQQQQEITSNNDNSGNNNSNNNGASDKSYFTIYGN
INNDANQTLTGHTDLEHYDLESDSKRIXYQQQQQQQDQQQQQQQQQQQQQDOX
INNGYTINPHLTESQQLSSGYPLSLPSPYPHINPYTNNNSNSNNSYNNNN
GNDVYSENNNSNNNNNSNNKKKYKKKSKRNIFKKKQDKESDLNKSNTPIIIKDNDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKOLEQLLVNETKSIVLYACYLKEYNEPIETIQTCOKIOLLLAYFMFRAYNTWILMEL
LKKDLQIKLTSDYSEPYLNILFRCNQIDKTNTIIFYNTYTSGKSIIAEDIDKRLDDL
STKDLVDYSCHROKHSILGHESSSKWRKSTSNNILDHDNIYTIKOKETIDMLSDRNRWL
YTSELLEYAR IKFKOYIPILDSNKELCNIHILRTHDDIVSLINKLOSHRNNRDLFR
YYMIQLIQFGSRNSIKYLRSICDNVGEIDFVLKIMVEHFNIEFYSLGADIQDDSPSYH
ONDERNYRYDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKILEDSÖMDIKSADLEDLHLKYHPKELQTYITTSIDSIILYNNPKLIIMVLKILLEQY
INDSKPFTLTEIERSYFIGEYSEIGKHRDQEIIEEMIKMISNIPISSTSILGTREYKV
IRGMDLRMYSKYQKLLPMGHSIKTSFDSKENQRLDIFKNFGQHGVNLSTKSKSASLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETIDWLSDIETGGCSILNIRDTLHSKLKOMKLDFSTSELLEYARIKFKQVIPILDSNK
KLPSIHILRTHDDIVSLINRLNESNFIDNENLFKYYMIQLIOFGSRNSNKYQRSICDN
VGEIDLVLETMVEHENIEEVSQGAXIQVHDDENKYKIRTYQQIINLSKIKVNVNHFPNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSYLLQTFIKLLNFDGTKFLLDNSNGKKLLFNEKAFKDRFHNRIYISKYSYKGLIDFI
QYLIDKFLEGPLSFTNLLLILNFLYLKLIRVNNLTIDQIKTAYQLISNYIEINNSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MTRNILIITGDYTEDYETYAVKQMLELVGYNVHLVSPGKKSGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mSNYNGDYHYNNEQQQQNHHQQYRLTTDNSAILNGGVSYDLLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFLIDKFKDCQLSLSNLSLILNYLFLKLIRVNSLTIGQIKKAYQLISHYIEINRSKHN
SYYLKTLSPIIGSCITVGEDPTNGSKRNGPYFNYDIDTSVYTFEYIFKNNNPRINLF
FHYFEMELVEKKINQIKEPFLNFKLLKLIIKTFDLESFIKFDSLLQQHEFNLKRKNH
NYVNGEQEDANDSNFFNIKVQFRVNINK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NECKGEDKSIKEHIEDVKGELGCISTSIDSVLLYFEFYYCNYHVNSKSKSIPTSIQTQ
IDDIIQNNKPYYTIKQLEQLLYNETKSIVLANSTKEKNETIETIETKOOIQLLAMY
MIKTYNTNVLMFLIKKPLYLIKLTSNYCEPYLDILFGCNQIDKTNIIIFYNTYKSOKSI
TABDIDKKPLDDLISYKDLVDFGNKQLHSILGNESSSKWKEIASNLIDNDKIYTIKDK
SPVNCMCIGYFDSNLSTSSPSSNASSNSNSTSSSSASLSPQIALGCENGFIYLLVDFK
IYPYCQIGYPITKLNKMKYSDINNNDNDNNYNGNNNSNGDDDDDDDDDLDILICTGY
FNSIKMFYNKEVICDHSLDDWCHTLSIGQVENNGDKTIVIGKLDNTIEYLKPFKLIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mnneyneySeklewkvfkNiyLlnCifDNkCCYKSKKFKTITSI
DSMLKHKQYQILICKLKANENLNFKSTYRIIEKIYEIKDIELFKEINSLLLTNGYQED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYYYLKTLSPIIASCITVCEDPTGEYPTSGSKRERPFLNYDIDTSVYTFEYIFSNRTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDLNKFIDSTIMDIVKDSYNVGMFSKMLDNNNPRITLFLHYLEMELEKRKTNQIKEPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNYQIFKLIIKTFDIESFIKFDNLLQQNEFHIIRENHNVVNGEQENANDSRDGEQNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDHGEHENLTIKELFCNGEKPLLSSNMVEWLGEIIIHKDYSDYKDIINYLFKKYEHQL
                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mnnecneyseklewrifknkyllncifknkcchkskkfkTlasi
nsilkhkoyollvcklkanenlyfnntyrliekiyeikdielfkelnslllkgy@d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKIĻFDGDCDIKSADLFDLHLQYHPKELQTYITTSIDSIILYNNPKLIIVVLKILĒQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDSKPFTLTEIERNYFIGEYSEIGKHRDQEIIEEWIKMISNIPISPTSILGTREYKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Potential phospholipid-transporting ATPase IK"
/protein_id="AAL92283.1"
                                                                                                                                                          .5169,5377. .6077,6139. .6530,6628. .7348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="Putative intracellular protease/amidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"hypothetical protein"
/protein_id-"AAL92281.1"
/db_xref-"G1:19569979"
                                                                                                                                                                                                                                                                                                    /protein id="AAL92280.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAL92282.1"
/db_xref="G1:19569980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"ORF_ID:dd_01557"
                                                                                                                                                                                                 7577. .7592)
/note="ORF_ID:dd_01556"
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:19569978"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:19569981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTQLLIKICTH"
                                                                                                                                                             Join (4519.
```

CDS

CDS

```
/procedings Annual Annu
                                                                       CLAINNHUNNNNDEOTTSSYNTSTDKSQLLSMKTNOVTTSKYNVFFFFIPKYTFYOPSRLA
GLANNHUNNNNNDEOTTSSYNTSTDKSQLLSMKTNOVTTSKYNVFFFFIPKYTFYOPSRLA
GLANNHUNNNNNDEOTTSSYNTSTDKSQLLSMKTNOVTTSKYNVFFFFIPKYTFYOPSRLA
NLYTLAIVILCMESFSPVGPVSSLTPLLVVIAVTSKFBLAEDLKRHQDMETSINGRETS
IYRRPYSTISPTASKEDLKRRQSTRNGESLPADI ICLSSSRSDGSRAYLETANLDGETNLK
SKVGYFQSCHWEDTKVGDITYVKNGESLPADI ICLSSSRSDGSRAYLETANLDGETNLK
AKSSISKCOWI KGAKDLDDFSCKVDYEGPNDI YSFDGVLTILKGFERSNIGDSTVVP
TYNYVPYSTODLLLEGTKLRATDWYTGVYTYSGYDTTIKRNASKSAGKRSSVERGVNN
KLLILFLLOTI ICTICSIGHNRWHLEDDKDAKPWY IDYDPGOTEDFIVYSYVILYYTL
IPLEAMYVSHEMIRYGSNAHFINDSDLEWYDESTDTPAQARNT NINEELGOIQYLFSDKTG
ITJCHAYNGSKSHHRYRGGTNSGCSVIPKYQAASPDEESLILYCLAICWYLIERNKE
SGGSGGGGDASSSINPLGIPVQPEISIPILEDGOTEYTKKEENKE
IDDLAMNHDNSKSHHRYRGGTNSGCSVIPKYQAASPDEESLILTAARYGFILKSREDN
ITTISVHCRREFELLNVLERNYRREMSYTYKNORYGIKIYCKGADSVIFERRKKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIIAPSIALLPYIIVSLNSWLFNTDNLSLOKINLEKKGFIRMNDL"

join(19281. 20573, 20689. 20828, 20921. 21274, 21386. .22049)

/note="ORF_ID:dd_01551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHCVGILLOSTERHLSEPACSGIRTICAMSVRTIEHEETIAWNKIHQEASISLVKKAEKV
DAACELIEKDLLIGSTGIEDRLQDHVPETISALREAGIKWAVTGGDGFALSISTS
SAVINEMELILLINESNRQALMKRLLIT SNERRLHFNDMSGRMGSVKYLEKLEKVA
SKIRLEPEDAPLILLINESNRGALMKRLITI SNERRLHHFNDMSGRMGSVKYLEKLEKVA
TCESVVCCRCSPSQKAKVVNLVAERSFLFGDGAITMSIGDGANDVPHIQKAHVGVGIS
FREGMQAVALLASDFAIANFSMLRRLILUHGNRSYKRMTKLILYSFSKNIALSISQFWFG
FREGREGGMIYFPEFETLXNALFETSLYBFLGTFDOPTKEDDLLNRPLYRVCOSNSP
FSTWKFIWWVFIGMWOSAIIFFVMNTSTIEGGKTLGIMSIGTAAXIXLVVTVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFSSLETLYLENCHLSLKNSTLSSLSTIPULRLLNLNGNOWDRILPIDGYFKSLNEIS
LCNNFISNLFRIANLYHTSYPLLTRVOLFGNPVVDPRIFQPNLDSLISSIQVNKTIQF
ITTQPPFLLYSNINQKPQPQLQQQQQQQQQQQQQQTQQSKRLLPPHKSGSSPSINRSSP
IKQLEDLSSDAALFYNYQSSPSQHHQQQIQQQQQYYDLNDXQNYFSTNEGNVIIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QISFITRYWTRQTILAVSISVVSTFLFVMLYSVLGRYVEADATHIIFELYALPTFWLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAIATTTSITKKLTTGEKIKQYFKLKKLFPKSPFSSGHNNNYNNNDNNIINNNNNN
LKLFVSVVSLQDPSDNSLILLTASLVGSFDIERDESASSSSQAKASRCIFFYGSDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Putative NADP-dependent oxidoreductases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(22709. .22962,23136. .23832))
/note="ORF_ID:dd_01552"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 30523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB 2; Le
Pred. No. 0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAL92286.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAL92284.1"
/db_xref="G1:19569982"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 GTAATACTAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_1d="AAL92285.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNPSINELSLSDLTINDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.1%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
Matches 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
ISM Chloroplast Lasthenia gracilis
Chloroplast Lasthenia gracilis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusaterids II; Asterales; Asteraceae; Asteroideae;
Lebenieae; Lasthenia.

I (bassa 1 to 410)
RS Chan, R., Baldwin, B.G. and Ornduff, R.
Cryptic goldfields: A molecular phylogenetic re-investigation of
Lasthenia californica sensu lato)
AL Am. J. Bot. 89 (7), 1103-1112 (2002)
CE 2 (bassa 1 to 410)
CE 3 (bassa 1 to 410)
CE 3 (bassa 1 to 410)
CE 4 (bassa 1 to 410)
CE 5 (bassa 1 to 410)
CE 6 (bassa 1 to 410)
CE 7 (bassa 1 to 410)
CE 7 (bassa 1 to 410)
CE 8 (bassa 1 to 410)
CE 9 (bassa 1 to 410)
CE 1 (bassa 1 to 410)
CE 1 (bassa 1 to 410)
CE 2 (bassa 1 to 410)
CE 3 (bassa 1 to 410)
CE 4 (bassa 1 to 410)
CE 5 (bassa 1 to 410)
CE 6 (bassa 1 to 410)
CE 7 (bassa 1 to 410)
CE 7
DOE Joint Genome Institute and occurrent Submitseld Submitseld (3-APR-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 23, 2002 this sequence version replaced gi:19224972. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center www.jgi.doe.gov Einishing Completed at Stanford Human Genome Center www.spgc.stanford.edu Quality >-40 99.9% of Sequence; Estimated Total Number of Errors is 0.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLN 15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF467161
Lasthenia gracilis isolate calil53 tRNA-Lys (trnK) gene, intron; and maturase K (matK) gene, partial cds; chloroplast genes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /specimen_voucher="Neese and Painter 2552 (JEPS)" /db_xref="taxon:182806"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 172823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
5.1%; Score 29; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Lasthenia gracilis"
/organelle-"plastid:chloroplast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166787 GTAATACTAAAAAAAAAAAAAAAAAAAAAA 166759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 546 GTAATACTAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="5"
/clone="RP11-93N19"
56281 a 29916 c 30420 g 56206
                                                                                                                                                                                                                                                                                                                                      1. .172823
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /isolate="cali153'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="trnK"
/note="tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF467161
AF467161.1 GI:21759599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="matK"
/codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chloroplast products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="trnK"
<1. .175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="matK"
<1. .175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lasthenia gracilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF467161
                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
        AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF467161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                               PRI 01-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 112226)
DOE Joint Genome Institute.
DOE Joint Genome Institute.
DIECT SUBLASSION
Submitted (15.0V-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 112226)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 23-APR-2002
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112226)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (01-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jan 1, 2002 this sequence version replaced g1:16930902.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 172823)
DOE Joint Genome Institute.
Dorect Submission
Submitsed (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 172823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172823)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                        AC099486 112226 bp DNA linear PRI 01-JAN-
Homo sapiens chromosome 5 clone CrD-2011G10, complete sequence.
AC099486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC114323 172823 bp DNA linear PRI 23-API
Homo sapiens chromosome 5 clone RP11-93N19, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 112226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www.jgi.doc.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 5.1%; Score 29; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CTD-2011G10"
36508 a 19376 c 19390 g 36952 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .112226
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                 AC099486.2 GI:18030138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC114323
AC114323.2 GI:20270116
                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Unpublished
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                     DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                     KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                        RESULT 13
AC099486
LOCUS
                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC114323/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
```

à g

```
/transl_table=11
/product="maturase K"
/protein_id="AnAM77460.1"
/db_xref="GT:2175600"
/translation="RAFIKRFGSQLLEEFTTEEEQVFSLTFPRVSSISRRLSRKRIWY
LDIVCINDLANYE"

BASE COUNT 139 a 142 t

Query Match
Query Match
Query Match
Query Match
100.0%; Pred. No. 0.00075;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 TAATACTAAAAAAAAAAAAAAA 574

Db 221 TAATACTAAAAAAAAAAAAA 248

Search completed: June 16, 2003, 07:56:05
Job time: 1698.8 secs
```

Н

```
June 16, 2003, 06:35:31; Search time 39.9504 Seconds (without alignments) 4406.275 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 50, App]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                         US-10-090-035-3
574
1 acccacgcytccgcccacgc.....aaaaaaaaaaaaaaa 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3
Sequence 3
Sequence 6
Sequence 6
Sequence 1
Sequence 2
Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            882724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-280-116-50
US-08-998-416-981
US-08-998-416-981
US-09-98-416-984
US-09-280-116-85
US-09-280-116-85
US-09-380-116-85
US-09-372-422A-17
US-09-380-116-1
US-09-280-116-1
US-09-09-180A-2
US-08-74-41
US-09-180A-2
US-08-180A-2
US-08-180A-15-1
US-09-345-882-1
US-09-345-882-1
US-09-345-882-1
US-08-688-417-5
US-08-688-417-5
US-08-688-417-6
US-09-345-880-116-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-336-536-74
US-09-091-097-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                         OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ល់ល់ល់ល់ល់ល់ល់ល់ល់ល់ល់ល់ល់ល់ល់ល
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
```

Sequence 12, Appl Sequence 5, Appl Sequence 122, Appl Sequence 3, Appl Sequence 7, Appl Sequence 1, Appl Sequence 6, Appl Sequence 19, Appl Sequence 19, Appl Sequence 2, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 3, Ap	Human Protease Homologs	Length 212; ; Indels 0; Gaps 0;	YA GOSSYPII
749 4 US-09-257-583-12 810 4 US-09-072-993C-5 944 4 US-09-227-357-122 1132 3 US-08-894-731-3 1164 2 US-09-395-674B-7 1164 2 US-09-395-674B-7 1184 4 US-09-286-529-6 1376 4 US-09-286-529-6 1376 4 US-09-286-529-6 1376 4 US-09-943-184-44 1454 4 US-09-972-422A-19 1619 2 US-08-997-36A-2 1630 4 US-08-997-36A-2 181 4 US-08-997-36A-7 2191 4 US-09-284-465A-1 2191 4 US-09-298-731-25 2197 1 US-08-233-005-3 2197 1 US-08-233-005-3	SSULT 1  5-09-280-116-50  Sequence 50, Application US/09280116A  Patent No. 6331447  Patent No. 6331427  GENERAL INPORANTION: APPLICANT: RObison, Keith E.  TILLE OF INVENTION: NOLGEL Acid Molecules Encoding Human TILLE OF INVENTION: NOLGEL 3000/176965  CURRENT APPLICATION NUMBER: US/09/280,116A  CURRENT APPLICATION NUMBER: US/09/280,116A  CURRENT FILING DATE: 1999-03-26  NUMBER OF SQU 100 SS: 268  SOFTWARE: PatentIN Ver. 2.0  LENGTH: 212  TYPE: DNA  ORGANIZH: HOMO SAPIENS  FERATURE: OTHER INFORMATION: Zinc carboxypeptidases	5%; Score 26; DB 4; .0%; Pred. No. 0.028; 0; Mismatches 0 CACGGTCCGC 26	Application US/08998416 Application US/08998416 By Marion: Philippsen. Peter Pohlmann. Rainer Steiner, Sabine Mohr. Christine Wendland, Jurgen Knechtle, Philipp Rebischung, Corinne WURTION: GENOMIC DNA SEQUENCES OF ASHBYA WUENTION: AND USES THEREOF SECUENCES: 1152 SIN O. 6239264artis Corporation 3054 Cornwallis Road Seearch Triangle Park USA
22222222222222222222222222222222222222	SULF 109-280-116-50 Sequence 50, Application Patent No. 6331427 GERERAL INFORMATION: APPLICANT: RODISON, Kei TITLE OF INVENTION: NO. FILE REFERENCE: 5800.24 CURRENT APPLICATION NUMBER OF SEQ ID NOS: 2 SOFTWARE: PatentIN Ver. SEQ ID NO 50 LENGTH: 212 TYPE: DNA ORGANIEM: HOMO Saplens FEATURE: COHER INFORMATION: 21n	1tch 2al S 26 1	RESULT 2 US-08-998-416-981/C Sequence 981, Application US/08998 Patent No. 6239264 GENERAL INFORMATION: APPLICANT: Philippsen, Peter APPLICANT: Philippsen, Rainer APPLICANT: Mondrand, Jurgen APPLICANT: Wendland, Jurgen APPLICANT: Wendland, Jurgen APPLICANT: Wendland, Jurgen APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENOMIC DN, TITLE OF SEQUENCES: 1152 CORRESPONDENCE ADDRESS: 1052 STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolin COUNTRY: USA
	RESULT 1. US-09-280-1 ; Sequence ; Patent No ; GENERAL II ; APPLICAN ; TITE OF ; FILE OF ; CURRENT ; CURRE	Query Me Best Loc Best Loc Matches Qy	RESULT 2 US-08-998-416-99 Sequence 981, Sequence 981, GENERAL INFO, APPLICANT: APPLICANT

```
Score 26; DB 4; Length 717;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                            PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JUNESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 ATACTAAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CONKIIN, DARFELL C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, SI
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08950720A Patent No. 6046028
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. TIMOTHATION:
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 904:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                      , MOLECULE TYPE: DNA (genomic)
, ORIGINAL SOURCE:
, ORGANISM: PAG1563UP
, US-08-998-416-904
                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.5%; Scc
Best Local Similarity 100.0%; Pi
Matches 26; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SAWISIAK, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE, POCKET NUMBER: 97
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .08-950-720A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mohr, Christine
Wendland, Jurgen
Rnechtle, Philipp
Rebischung, Corinne
NVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKER NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFRAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.5%; Score 26; DB 4;
100.0%; Pred. No. 0.024;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 ATACTAAAAAAAAAAAAAAAAA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 ATACTAAAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GENOMIC DNA SEQUITITE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUCHRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 904, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
                                                                                                                                                                        FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             981:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Philippsen, Peter
Pohlmann, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1152
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24-DEC
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAG1604RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-08-998-416-904/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-998-416-981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT
```

g ŏ

Gaps

ö

```
Length 1210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1384;
                     Ouery Match 4.5%; Score 26; DB 4; Length 121
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                           Sequence 17, Application US/09372422A

Patent No. 6313375

GENERAL INFORMATION:
APPLICANT: Evancois Barrieu

TITLE OF INVENTION: Malze Aquaporins and Uses Thereof
FILE REFERENCE: 0919-08-11

CURRENT APPLICATION NUMBER: US/09/372,422A

CURRENT PILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: US 60/098,692

PRIOR APPLICATION NUMBER: US 60/098,692

NUMBER OF SEQ ID NOS: 49

SEQ ID NOS: 49

SEQ ID NO 17

LENGTH: 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MODIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,218A
FILING DATE: 01-OCT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08942218A
Patent No. 5935835
CENERL INFORMATION:
CENERL INFORMATION:
APPLICANT: McCarte-Roshak, Amy
APPLICANT: Marshall, Lisa
TITLE OF INVENTION: Human Myt-1 Kinase Clone
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
                                                                                                                                        5 ACCAGGGTCGGCCACGCGTCGC 30
                                                                                                              1 ACCCACGCGTCCGCCCACGCGTCCGC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACCCACGCGTCCGCCCACGCGTCCGC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ACCCAGGGTCGGCCCACGCGTCGC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....urkESSEE: Ratner & Prestla STREET: P.O. Box 980 CITY: Valley Forge STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,389
FILING DATE: 11-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (95)...(959)
US-09-372-422A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-942-218A-1/c
                                                                                                                                                                                                                                               US-09-372-422A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-280-116-85/c
Sequence 85, Application US/09280116A
Sequence 85, Application US/09280116A
Setent No. 6331427
GENERAL INFORMATION:
APPLICANT ROBISON, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SSOTMARE: Patentin Ver. 2.0
LENGTH: 1021
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09560639
Fatent No. 632334
GENERAL INFORMATION:
APPLICANT: Kingsbury, G.
APPLICANT: Leiby, K.
TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
CURRENT APPLICATION NUMBER: US/09/560,639
CURRENT APPLICATION NUMBER: 60/155,862
EARLIER APPLICATION NUMBER: 60/155,862
BARLIER FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PRAESED for Windows Version 3.0
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.5%; Score 26; DB 4; Length 1021;
100.0%; Pred. No. 0.022;
tive 0; Mismatches 0; Indels
                                                                                                                                        Ouery Match
4.5%; Score 26; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                               1 ACCCACGCGTCCGCCCACGCGTCCGC 26
                                                                                                                                                                                                                                                           42 ACCACGCGTCCGCCCACGCTCCGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 ACCCACGCGTCCGCCCACGCGTCCGC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCCACGCGTCCGCCCACGCGTCCGC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: aspartyl proteases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (1)..(1021)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-85
; FEATURE: Coding Sequence; NAME/KEY: Coding Sequence: LOCATION: 77...481
COTHER INFORMATION:
US-08-950-720A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (84)...(557)
US-09-560-639-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 12
LENGTH: 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-560-639-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ö

Gaps

```
250 ACCCACGCGTCCGCCCACGCGTCCGC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACCCACGCGTCCGCCCACGCGTCCGC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 ACCCACGCGTCCGCCCACGCGTCCGC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-724-394A-15/c
; Sequence 15, Application US/08724394A
; Patent No. 5872237
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09409180A Patent No. 6444802 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      TELEPHONE: (908) 654-5000
TELEFAX: (908) 654-7866
INFORMATION FOR SED ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2205 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEX: CDS
; LOCATION: (300)...(2414)
US-09-409-180A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-888-077A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 2864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-409-180A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1504
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1504;
                                                                                                                                                                                                                                                                                                 Score 26; DB 2; Length 1448;
Pred. No. 0.021;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: trypsin-like serine proteases US-09-280-116-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.5%; Score 26; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 26; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                     Query Match 4.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACCCACGCGTCCGCCCACGCGTCCGC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 ACCCACGCGTCCGCCCACGCGTCCGC 39
                                                                                                                                                                                                                                                                                                                                                                                     1 ACCCACGCGTCCGCCCACGCGTCCGC 26
                                                                                                                                                                                                                                                                                                                                                                                                             46 ACCCACGCGTCCGCCCACGCGTCCGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-888-077A-41
; Sequence 41, Application US/08888077A
; Patent No. 6020143
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09280116A Patent No. 6331427 GENERAL INFORMATION:
      REFERENCE/DOCKET NUMBER: ATG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CILL.
STATE: Nu
COUNTRY: USA
TP: 07090-1497
                                                                                                                                                                                                                                     ; MOLECULE TYPE: CDNA US-08-942-218A-1
                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     us-09-280-116-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
SOFTWARE: ASCII.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-JUL-1997
CIASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INTEMATION:
NAME: PALISI, THOMAS M
REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: White, David
APPLICANT: White, David
APPLICANT: White, David
APPLICANT: Slos-Santlago, Inmaculada
APPLICANT: 2110s-Santlago, Inmaculada
APPLICANT: 2110s-Santlago, A No. 6444802el Human Aminopeptidase
FILE REFERENCE: 5800-59
CURRENT APPLICATION NUMBER: US/09/409,180A
CURRENT FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
4.5%; Score 26; DB
Best Local Similarity 100.0%; Pred. No. 0.(
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1..2205
OTHER INFORMATION: /note= "mutTM1-TM2"
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                  COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CONTANEE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,618
FILING DATE: 19930406
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/07/257,696
FILING DATE: 140-027-1988
ATTORNEY,AGENT INFORMATION:
NAME: FOX, SAWIEL L
REGISTRATION NUMBER: 0654.0490001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3747 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
4.5%; Score 26; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.5%; Score 26; DB 3; Best Local Similarity 100.0%; Pred. No. 0.018; Matches 26; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Frederic de Sauvage
APPLICANT: Arnon Roshenthal
TITLE OF INVENTION: Fused
FILE REFERENCE: P1272
CURRENT PFLICATION NUMBER: US/09/031,563A
CURRENT FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3688 ATACTAAAAAAAAAAAAAAAAAAAAAA 3713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 ATACTAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09031563A Patent No. 6022708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-392-277-1; Sequence 1, Application US/09392277A; Sequence 1, Application US/09392277A; Patent No. 6451977; BENERAL INFORMATION:
        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: unknown N
; LOCATION: 4160, 4243, 4361
; OTHER INFORMATION: unknown
US-09-031-563-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
LENGTH: 4880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-031-563-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08044618
Patent No. 5449605
GENERAL INFORMATION:
APPLICANT: SMULSON, MARK
TITLE OF INVENTION: CANCER BY THE USED OF RESTRICTION TO
TITLE OF INVENTION: POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)
TITLE OF INVENTION: POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
APPLICAMT: Feder, Joun N.
APPLICAMT: Kronmal, Gregory S.
APPLICAMT: Lauer, Peter M.
APPLICAMT: Lauer, Peter M.
APPLICAMT: Lauer, Peter M.
APPLICAMT: Thomas, Winston
APPLICAMT: Wolff, Reger K.
TITLE OF INVENTION: Sequences and Antibodies Thereto
APPLICAMT: Wolff, Reger K.
APPLICAMT: Wolff, Reger K.
APPLICAMT: Wolff, Reger K.
APPLICAMT: Wolf, Winston
APPLICAMT: Wolf, Winston
APPLICAMT: Wolf, Winston
ATTER OF SEQUENCES 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TWO Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: GA
CONNTRE: USA
CONNTRE: LBM PC COMPALINE
APPLICATION NUMBER: US/08/724,394A
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/724,394A
CLASSIFICATION NUMBER: US/08/724,394A
CLASSIFICATION NUMBER: US/08/724,394A
CLASSIFICATION NUMBER: US/08/724,394A
TELEPAM: 415-576-0300
INFORMATION FOR SED ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TELEPAM: 415-576-0300
INFORMATION FOR SED ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: ODD.COX: not relevant
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.5%; Score 26; DB 2; Length 3416;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 ACCCACGCGTCCGCCCACGCGTCCGC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: 1.3416
.: OTHER INFORMATION: /note= "cDNA 44"
US-08-724-394A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-044-618-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: STATE: ZIP: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

Search completed: June 16, 2003, 08:47:04 Job time: 42.9504 secs

```
å
1
                                                                                   June 16, 2003, 03:58:29; Search time 188.731 Seconds (without alignments) 6849.143 Million cell updates/sec
                                                                                                                                            4370478
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               2185239 seqs, 1125999159 residues
                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                                                                                                                                                                      OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                           0
                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                           Word size :
                                                                                                                                                                                                                                              Searched:
                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                         Databas
```

N_Geneseq_101002:*  1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DaT:*  2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*  3: /SIDS2/gcdata/geneseq/geneseqn-embl/NA1981.DAT:*	* . / SIDS2/gcgdata/geneseq/geneseqn.embl./NA1983.DAT;* 5: /SIDS2/gcgdata/geneseq/geneseqn.embl./NA1984.DAT;* 6: /SIDS2/gcgdata/geneseq/geneseqn.embl./NA1985.DAT;* 7: /SIDS2/gcgdata/geneseq/geneseqn.embl./NA1985.DAT;* 8: /SIDS2/gcgdata/geneseq/geneseqn.embl.NA1987.DAT;* 9: /SIDS2/gcgdata/geneseq/geneseqn.embl.NA1987.DAT;* 9: /SIDS2/gcgdata/qeneseq/geneseqn.embl.NA1987.DAT;*	10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NR1989.DAT:* 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NR1989.DAT:* 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NR1991.DAT:* 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NR1992.DAT:* 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NR1993.DAT:* 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NR1993.DAT:*	NA1995. NA1996. NA1997. NA1999.	22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:* 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:* 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
 96				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Describtion		Dat secreted pro	Human gografied allie	Branch Jenney Orl	uman Illunune/naema	Himsa gossots	Human Secreted pro	Human Ovarian and	Himan polynacieoti	TOORTONIA TOO HOUSE OF T
SUMMARIES	Ę		2 AAF97898	4 ABK62601	2 AAF81796					2 AAI57944	2 AAK51691	
	DB	ij	2	24	22	22	22	20	24	22	22	
	Length		806	569	1926	296	401	532	1592	2674	4929	
đ	Query e Match Length DB T		5.4	5.1	5.1	4.9	6.4	4.9	4.9	6.4	4.9	
	Score		31	29	58	28	28	28	28	28	28	
	Result No.		п	°	m	4	S	9	7	œ	σ	
	•											

AAI58784         Human polynucleott           ABL34086         Human immune syste           ABL32478         Human immune syste           ABL92305         Chemically treated           AAI30125         Human SNP oligonuc           AAI3064         Human colon cancer           AAI88702         Human polynucleoti           AAI88703         Human polynucleoti           AAK68891         Human polynucleoti           AAK68892         Human colon cancer           AAK68891         Human colon cancer           AAK68891         Human colorectal c           AAK694         Probe #5382 for ge           AAK10412         Human bone marrow           AAK1031         Human bone marrow		(55196 Human colon cancer (55196 Human colon cancer (55590 Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Human colon cancer (51245 Human polynucleoti Human polynucleoti Human secreted pro Corn clone 7002148 Human polynucleoti Human secreted pro Corn clone 7002148 Human polynucleoti Human secreted pro Corn clone 7002148	ALIGNMENTS	protein cDNA, SEQ ID NO: 25.  d protein; immunomodulatory; antisclerotic; antiinflammatory; anti-HIV; cytostatic; cardiant; -anglogenic; ophthalmological; neuroprotectant; tonorulsant; antialzhelmers; antiparkinsonian; vulnerary; vaccine; gene therapy; cancer; nate data; infection; ss.  99US-0155709. BENOME SCI INC.
244422222222222222222222222222222222222	3555555555	20000000000000000000000000000000000000	908 BP .	cDNA, SEQ I ; immunomod ilammatory; ilc; ophthal int; antialz y; vaccine; y; vaccine; i; infection 6013.
4.9 4929 6.9 5928 6.9 139193 6.7 233 6.7 381 7.7 391 7.7 451 7.7 451 7.7 474 7.7 474 7.7 474			rd; cDNA; 1rst entry	ad protein cDNA ed protein; im ed protein; im 1. antinflam 1. anglogenic; ticonvulsant; ticonvulsant; ticonvulsant; ticonvulsant; ticonvulsant; 1. 1. 2000WO-US26013 99US-0155709 GENOME SCI IN
22222222222222222222222222222222222222	444444	4444444444	standa 01 (f	secreted prote secreted prote ological; anti-anglo pic; anticonvu crobial; vulne n coordinate daptens. 21658-A120011999; 99US-11999; 99US-1-1999; 94-KP
			.r. 1 7898 AAF97898 st AAF97898; 01-JUN-2001	uman; srmato srmato srcula, cottinic otein mo saj 20012; -MAR-; -SEP-; -SEP-; I. F
0000		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	F97	AXX XXX XXX XXX HU KW HU KW NO XXX YX

```
The present sequence encodes one of 32 novel human secreted polypeptides.

The nucleic acid molecules and polypeptides they encode may be used in the nucleic acid molecules and polypeptides they encode may be used in the prevention, diagnosis and treatment of diseases such as immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases of Schmitter syndrome, Chaga's cardiomyopathy and coronary (e.g. Schmitter syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. thurington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic secreted polypeptides. They may also be used as DNA probes in diagnostic secreted polypeptides may be used as antigens in the capture of antibodies and in assays to identify modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat sequence differentially expressed in response to a hepatotoxin #508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis.
                                       Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Castle AL, Elashoff MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 22; Length 908;
Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 908 BP; 242 A; 290 C; 197 G; 175 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.4%; Scor.
100.0%; Pred. No. v...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACCCACGCGTCCGCCCACGCGTCCGCACAGC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson KR,
                                                                                                              Claim 1; Page 730; 890pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK62601 standard; cDNA; 569 BP
                                                                                                                                                                                                                                                                                                                                                                                                                      their expression and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-244880P.
2001US-290029P.
2001US-290645P.
2001US-292336P.
2001US-295798P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-297457P.
2001US-298884P.
2001US-303459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2001; 2001WO-US23872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-222040P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.43
Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200210453-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2000;
02-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-2001;
13-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK62601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK62601/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

Gaps

ö

The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression in tissues or cells exposed to the global changes in gene expression in unexposed tissues or toxic toxin and comparing these to gene expression in unexposed tissues or calls. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the heaptcotxicity of a compound, comprising detecting the level of heaptcotxicity of a compound comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or compression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the method can also be used to identify an agent which modulates the coxic response and predict cellular pathways that a compound modulates to the method utilises a set of at least two probes (on a solid or support in kit form), where each of the probes comprises a sequence that support in kit form), where each of the probes comprises a sequence that system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a capical in the specification. The method is useful for elucidating quobal containing information used to present information used to relate a prediction or identifying the expression and for identifying to a known toxin. The genes may be used as tissues or cell exposed to a known toxin. The genes may be used as containing an expression information may be used as diagnostic markers in capical public markers in a gene expression in the special containing and order the appearance of the physiological state of tissue or cell expression information may be used as diagnostic markers or the propession or identification or identification as defined a gene expressed sequence tas expressed sequence tas equence tas gene expressed sequence predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in Sequence 569 BP; 132 A; 98 C; 117 G; 222 T; 0 other; Claim 1; Seq ID No 508; 239pp; English. unexposed tissues or cells -WPI; 2002-241625/29. 

Gaps ö 5.1%; Score 29; DB 24; Length 569; 100.0%; Pred. No. 0.026; rative 0; Mismatches 0; Indels Query Match 5.1% Best Local Similarity 100.0 Matches 29; Conservative ò

ö

AAF81796 standard; cDNA; 1926 BP 12-JUN-2001 (first entry) AAF81796; RESULT 3 g

dermatological; immunosuppressive; antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; vaccine; antialzheimer; antiparkinsonian; antimicrobial; vulnerary; gene therapy; immune disorder; hyperproliferative disorder; cardiovascular disease; cancer; anglogenic disorder; neurological disorder; infectious disease; wound healing; regeneration; chemotaxis; chromosome 20; ss. Human; secreted protein; diagnosis; immunomodulatory; antisclerotic; Human secreted protein gene 10 SEQ ID NO:20. 

Homo sapiens.

WO200112775-A2.

```
17-JAN-2001; 2001WO-US01354
                                                                                                                  02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-AUG-2000;
4-AUG-2000;
4-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 - AUG - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 - AUG - 2000
4 - AUG - 2000
4 - AUG - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-SEP-2
                                                                                                                                                                                                                                                                                                                                                                                                        AMEB1787 to AAFB1817 encode the human secreted proteins given in AAB74733 to AAB74772. Human secreted proteins can have activities based on the tissues and cells they are expressed in. Example of activities include: CC tissues and cells they are expressed in. Example of activities include: antiinflammatory; antisclerotic; dermatological; immunosuppressive; vascular; anti-anglogenic; ophthalmological; neuroprotectant; noctropic; vascular; anti-anglogenic; ophthalmological; neuroprotectant; noctropic; canticonvulsant; antialzelmers; antiparkinsonlan; antimicrobial; and vaccine. Human secreted proteins can be used in quene therapy and conversed with inappropriate polypeptide expression. For example, NAM1 associated with inappropriate polypeptide expression for example, NAM1 cand PEP1 may be used to treat disorders associated with decreased conversed with appropriate polypeptide expression for example, NAM1 cand affect the activity of proteins by expressing inactive proteins or that affect the activity of proteins by expressing inactive proteins or consupplement the patients own production of polypeptides. Disorders, hyperproliferative disorders (e.g. cancers), candiovascular diseases and/or conformation and inactive production of conformations and conformation and invantances in the exemplification of the necessity invantion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                              Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2122.
                                                                                                                                                                                         Wei P, Baker KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.1%; Score 29; DB 22; Length 1926; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 29; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                            Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1926 BP; 519 A; 429 C; 430 G; 548 T; 0 other;
                                                                                                                                                                             Rosen CA, NI J, Florence KA, Fiscella M, Wei i
Birse CE, Young PE, Komatsoulis GA, Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 446; 485pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK57062 standard; cDNA; 296 BP.
                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                        16-AUG-2000; 2000WO-US22325.
                                                                                                    99US-0149182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                   WPI; 2001-147550/15.
P-PSDB; AAB74742.
                                                                                                  17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157182-A2
                    22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK57062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK57062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
```

g ò

```
Ruben SM;
                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                        000US-0256719
                                                                                                                                                                                                                                Rosen CA, Barash SC,
                                                                                                                                                                                                                                       WPI; 2001-483426/52.
P-PSDB; AAM84281.
         02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
                                                                                                                                                                                                                   05-JAN-2001;
                                                                                                                                                                                     05-DEC-2000;
                                                                                                                                                                                  5-DEC-2000;
                                                                                                                                                                                         05-DEC-2000;
06-DEC-2000;
                                                                                                                                                                                               08-DEC-2000
                                          20-OCT-2000;
                                                                            NOV-2000;
                                                                                      08-NOV-2000
                                                                                         08-NOV-200
                                        20-OCT-2
```

2

```
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

C amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

C activity, and can be used in gene therapy and vaccine production. (I)

C proteins and polynucleotides may be used in the prevention, diagnosis and

C treatment of diseases associated with inappropriate (I) expression. For

example, they may be used to treat disorders associated with decreased

C expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (I) by expressing inactive proteins or to

c supplement the patients own production of (I). Additionally, (I)

C supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting

CC the nucleic acids into a host cell and culturing the cell to express the

protein. (I) proteins and polynucleotides may be used to prevent,

diagnose and treat immune/haematopoietic-derived cells: AAK64703

CC cancers and cancer metastases of haematopoietic-derived cells: AAK64703

CC cancers and cancer metastases of haematopoietic-derived cells: AAK64703

CC CARRORS from the present invention. AAK54912 to AAK64950 and AAM82169

C represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, cytokine, cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 7372; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                          Claim 1; SEQ ID NO 2122; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 296 BP; 110 A; 66 C; 57 G; 61 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 7372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . AAI87312 standard; cDNA; 401 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-514838/56.
P-PSDB; AA007381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI87312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI87312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

S

```
ö
         The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, memalopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; gene therapy; protein therapy; cancer; weight; tumour; chromosome mapping; forensic; haematological disease; allergy; inflammation; cell proliferation; viral infection; wound healing; modulation; appetite; behaviour; food additive; preservative; ss.
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                       4.9%; Score 28; DB 22; Length 401; 100.0%; Pred. No. 0.07;
                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                            Sequence 401 BP; 92 A; 110 C; 78 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein gene 14 clone HHEPT60.
                                                                                                                                                                                                                                                     100.0%; Pred. No. 0.0 vative 0; Mismatches
                                                                                                                                                                                                                                                                                             2 CCCACGCGTCCGCCCACGCGTCCGCACA 29
                                                                                                                                                                                                                                                                                                           1 CCACGCGTCCGCCCACGCGTCCGCACA 28
                                                                                                                                                                                                                                                                                                                                                                                       AAX22224 standard; DNA; 532 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            970S-0052873
970S-0052873
970S-0052874
970S-0053440
970S-0053441
970S-0053442
970S-0055683
970S-0055724
970S-0055726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US14613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0055952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97us-0056359
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9903990-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                  AAX22224;
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                           AAX22224
                                                                                                                                                                                                                                                                                                                                                                RESULT
×8888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                8
```

```
The invention relates to nucleic acid sequences (AAX22211 to AAX22283) encoding human secreted proteins (AAY0183 to AAY01454). The secreted proteins (AAY0183 to AAY01454). The secreted control gene sequences are deposited with the ATCC under deposit number ATCC 209188, 209139 or 209114. Host cells contraining vectors comprising the nucleic acid sequences are used for the recombinant expression of useful for preventing, treating or amelorating medical conditions are 9.9 protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by the sequences, or its fragments are useful for chromosome identification conditions the amount of the new polypeptides. The nucleic acid sequences, or its fragments are useful for chromosome identification therapy; for (forensic) identification of individuals; as molecular contexpy; for (forensic) identification of individuals; as molecular weight markers; to identify related sequences or specific mRNM; in the repetutioally to inhibit or activate particular polypeptides are therapeutically to inhibit or activate particular polypeptides and useful as immunoassay reagents (including for in vivo inaging) and wide range of disorders may be treated with the polynucleotide and contexperite infermitation, cancer or other forms of cell proliferation, viral contexperite, behaviour etc. and as food additive or preservative. The condulate differentiation of embryonic stem cells, to modulate wight, appetite, behaviour etc. and as food additive or preservative. The present sequence represents a gene encoding a human secreted protein axxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; acadiovascoular disorder; respiratory disorder; neurological disorder; gastrolntestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antilnflammatory; gynaecological; reproductive; chromosome 3q21-25;
                                                                                                                                                                     New nucleic acids encoding secreted human proteins - potentially useful for treating and diagnosing diseases and identifying specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
4.9%; Score 28; DB 20; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 28; Conservative 0; Mismatches 0; Indels
Duan R, Feng P, Ferrie AM, Florence KA, Fouad J;
Greene JM, Hu J, N1 J, Rosen CA, Ruben SM, Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 532 BP; 113 A; 146 C; 126 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ovarian antigen HSPSI74 cDNA, SEQ ID NO:187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACCCACGCGTCCGCCCACGCGTCCGCAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 ACCCAGGGTCGGCCCAGGGTCCGCAC 78
                                                                                                                                                                                                                                                                  Claim 4; Page 176; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ54307 standard; cDNA; 1592 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-2002 (first entry)
                                                                                               WPI; 1999-132234/11.
P-PSDB; AAY01396.
                                                                                                                                                                                                                        binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ54307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ54307
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
```

ö

Homo sapiens

WO200200677-A1.

03-JAN-2002

Birse CE,

```
The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system incompating and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinhinhian activity, chemokinetic activity, haemostatic and thrombolytic activity, cencer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed
                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 22; Length 2674;
Pred. No. 0.049;
; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2674 BP; 906 A; 529 C; 580 G; 659 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Asundi V, Chen R, Ma Y,
Wang J, Wang Z, Wehrman T, Xu C, Xue AJ,
Zhao QA, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.0%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACCCACGCGTCCGCCCACGCGTCCGCAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 147; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 ACCCACGCGTCCGCCCACGCGTCCGCAC
Human polynucleotide SEQ ID NO 147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000; 2000US-0662191
19-OCT-2000; 2000US-0693036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
P-PSDB; AAM38788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .N.S disorders
                                                                                                                                                                                                                                                                                                  WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia; ss
                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK51691
           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also cnompasses polypeptides 90% identical and polynucleotides 95% identical cc to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides and polypeptides in diagnosing, crecombinant vectors and host cells comprising human ovarian antigen of ovarian antigen polynucleotides and polypeptides in diagnosing, creating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and clasorders (e.g., infertility, disorders of pregnancy, anovulation, disorders, infertilored, ovarian cysts, and dysmenorrhoea), endocrine clasorders, infections (e.g., chlamydia, HTV, toxoplasmosis, and toxic shock syndrome, inflammatory conditions (e.g., mastitis, cophoritis and vaginitis), immune disorders (e.g., congenital and acquired toxoplasmosis, and toxic compoundeficiencies, autoimmune cophoritis, systemic lupus erythematosus), immunodeficiencies, autoimmune cophoritis, systemic lupus erythematosus, immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus, complantate ovarian disorders, neurological disorders, gastrointestinal disorders and urinary system disorders, ovarian antigen polypeptides and modulate ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used as food additives or to prepare antibodies (consequence represents cDNA encoding a human ovarian antigen of the functions of individuals and in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9%; Score 28; DB 24; Length 1592;
ilarity 100.0%; Pred. No. 0.054;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1592 BP; 458 A; 322 C; 338 G; 474 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACCCACGCGTCCGCCCACGCGTCCGCAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCACGCGTCCGCCCACGCGTCCGCAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 187; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI57944 standard; cDNA; 2674 BP
                                                                                                                                                         07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                              07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                      Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-147878/19
                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABP41230
```

ä

Wang

Ren F, Wa

ö

Gaps

ö

BP.

AAK51691 standard; cDNA; 4929

AAK51691;

(first entry)

22-ocr-2001

AAI57944;

2XXXX

RESULT 8 AA157944

셤 ð

Query Match

Matches

7

us-10-090-035-3.rng

nootropic; immunosuppressant; cytostatic;

leukaemia; ss Homo sapiens.

Human polynucleotide SEQ ID NO 987.

22-OCT-2001 (first entry)

```
peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries .
                                                                                                                                                                                                                                                                                                                              19-OCT-2000; 2000US-0693036
29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442253/47.
P-PSDB; AAM39628.
                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                           WO200153312-A1.
                                                                                                                                                                                                                                                                           09-JUL-2000;
                                                                                                                                                                                                                                                                                                     03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                    21-JAN-2000;
                                                                                                                                                                                                                                                                 25-APR-2000;
                                                                                                                                                                                                     26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                       Wang J, 1
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
             The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and etreatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                           Human: cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                           Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: Records for SEO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.9%; Score 28; DB 22; Length 4929;
100.0%; Pred. No. 0.044;
ive 0: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4929 BP; 1676 A; 904 C; 981 G; 1368 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1115-1120; 6221pp; English.
                                   Human polynucleotide SEQ ID NO 236.
                                                                                                                                                                                                                                                  20-JUN-2000; 2000US-0598075;
19-JUL-2000; 2000US-0620325;
01-SEP-2000; 2000US-0664936;
15-SEP-2000; 2000US-0663561;
20-OCT-2000; 2000US-0663325;
30-NOV-2000; 2000US-0728422;
                                                                                                                                                                                                                            2000US-0496914.
                                                                                                                                                                                                 05-FEB-2001; 2001WO-US04098
           06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-476283/51.
P-PSDB; AAM78558.
                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                   WO200157190-A2.
                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                          03-FEB-2000;
                                                                                                                                                                                                                                        27 - APR-2000;
                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                               Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

Ren F, Wang D; Zhang J;

Qian XB, Yang Y,

Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;

2000US-0620312. 2000US-0653450. 2000US-0662191.

2000US-0552317. 2000US-0598042.

2000US-0488725

26-DEC-2000; 2000WO-US34263

```
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAAM3642-AAM42213) with nootropic, the encoded polypeptides (AAAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypuclectides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat disease of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system classed neuropathies and central nervous system disease, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;. Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
4.9%; Score 28; DB 22; Length 4929;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 28; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4929 BP; 1678 A; 902 C; 982 G; 1367 T; 0 other;
Claim 1; SEQ ID NO 987; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACCCACGCGTCCGCCCACGCGTCCGCAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCACGCGTCCGCCCACGCGTCCGCAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
ABL34086/c
ID ABL34086 standard; DNA; 5928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

ö

Gaps

ö

100.08; Preq. ...

Conservative

Local Similarity nes 28; Conserva

Matches

ð g

AAI58784 standard; cDNA; 4929 BP.

AAI58784;

RESULT 10
AAI58784
ID AAI58
XX
AC AAI58

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, prof. epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                      comprising fragment of chemically modified gene, useful and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirineumatic; antiarthritic; antidiabetic; antipsoriatic; antilnflammatory; cancer; eye disease; arteriosclerosis; anaeute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5928 BP; 1649 A; 110 C; 1223 G; 2946 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2059; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO: 451.
                                                     Human 1mmune system associated gene SEQ ID NO: 2059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24;
0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9%; Score 28;
                                                                                                                                                                                                                                                                                                                   Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL32478 standard; DNA; 6593
                                                                                                                                                                                                                                                               30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                           02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 28; Conservative
                                     (first entry)
                                                                                                                                                                                                                                                                                                                    Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                   cytosine methylation
                                                                                                                                                                                                                                                                                                                                        WPI; 2002-130909/17.
                                                                                                                                                                                                  WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                              Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                     26-MAR-2002
                                                                                                                                                                                                                       03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL32478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                          gene; ds.
                 ABL34086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                Omo
       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA repair; cytosine methylation; PMS2L1; PMS2L12; PMS2L2; PMS2L3; PMS2, L4; PMS2L5; PMS2L6; MGMT; MSH2; NUDT1; TDG; INPPL1; RFC4; DDIT1L; FANCB; XRCC8; ataxia telangiectasia; aging; Bloom's syndrome; Cockayne syndrome; Nijmegen breakage syndrome; Werner syndrome; immunodeficiency; trichthiodystrophy; Fanconi's anaemia; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemically treated DNA repair gene fragment complementary to#57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24; Length 6593; 0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6593 BP; 1732 A; 121 C; 1448 G; 3292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 451; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 TAATACTAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9%; Score 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL92305 standard; DNA; 13919 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2001; 2001WO-EP03972.
                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                  02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200181622-A2.
                                                                                                                                                                                                                       WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-2002
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                              03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL92305;
                                                                                                        gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
ABL92305/c
```

```
variants of proteins related to amylases, amyloid proteins, angiopoietin, approsis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, Kinases, Colony stimulating factors, complement related proteins, cytochromes, kinesels, cytochromes, kinesterases. The present sequence is proteins, cytochromes, kinesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by the mm may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer continued the continued of the protein of pathogenic
                                                                                                                                                                                                                                                                                                                                                         Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to oligonucleotides encoding polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.7%; Score 27; DB 22; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer antigen encoding cDNA SEQ ID NO:120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51 BP; 11 A; 1 C; 3 G; 36 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 0.7 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM, Barash SC, Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 AATACTAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATACTAAAAAAAAAAAAAAAAAA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2342; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH33064 standard; cDNA; 233
                                          28-DEC-2000; 2000WO-US35498.
                                                                                             28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 27; Conservative
                                                                                                                                                                                                                                               Leach M;
                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                      WPI; 2001-465210/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200122920-A2.
                                                                                                                                                                                                                                            Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH33064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH33064
               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acids containing a sequence of at least 18 nucleotides of chemically treated DNA of genes associated with DNA repair, and theat complements. The invention also relates to nucleic acids comprising at least 18 base pairs of the chemically pretreated DNA of genes associated with DNA repair selected from PMSZLI, PMSZLIZ, PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; anglopoletin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; colony stimulating factor; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                  New nucleic acid derived from genes associated with DNA repair, useful for diagnosis, e.g. of ataxia telanglectasia, by determination of cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ir, and their complements.
The sequence data for this patent is not represented in the ification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 24; Length 13919;
Pred. No. 0.036;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13919 BP; 3717 A; 296 C; 3349 G; 6557 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 114; 25pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.9%; Score 100.0%; Pred. No. 0.0sr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 TAATACTAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                        Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human SNP oligonucleotide #3333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL30125 standard; DNA; 51 BP
                        2000DE-1019173
2000DE-1032529
                                                                                 01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Conservative
                                                                                                                                                                                                  Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Patent Office.
                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                           WPI; 2002-034446/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 28; Conserve
                           37-APR-2000;
06-APR-2000;
```

24-JAN-2002

AAL30125;

RESULT 14 AAL30125/c

g ð

Homo sapiens

05-JUL-2001

ö

Gaps

ö

0; Indels

```
WPI; 2001-235357/24.
P-PSDB; AAG73633.
```

cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene cancer antigens have cytostatic activity and can be used in gene diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing lanctive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inscrting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAH37199 represent sequences used in the exemplification of the Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -M.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922. AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon Claim 1; Page 2294; 9803pp; English 

Sequence 233 BP; 116 A; 37 C; 40 G; 40 T; 0 other;

ö Score 27; DB 22; Length 233; Pred. No. 0.19; 0; Indels 4.7%; Scor. 100.0%; Pred. No. v... 0; Mismatches 1 ACCCACGCGTCCGCCCACGCGTCCGCA 27 27; Conservative Query Match Best Local Similarity Matches 27; Conserva q ò

Gaps

Search completed: June 16, 2003, 06:54:05 Job time: 192.231 secs

OM nucleic

Run on:

```
Sequence 18, Appl Sequence 674, Appl Sequence 774, Appl Sequence 7993, Appl Sequence 2551, Appl Sequence 2551, Appl Sequence 255, Appl Sequence 16114, Appl Sequence 69, Appl Sequence 1651, Appl Sequence 72, Appl Sequence 72, Appl Sequence 72, Appl Sequence 1355, Appl Sequence 66, Appl Sequence 1355, Appl Sequence 662, Appl Sequence 662, Appl Sequence 642, Appl Sequence 27, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GCCGCTGCCCACACACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACCCACGCGTCCGCCCACGCGTCCGCACAGCAATCCACACAAGCACTTCGACGTCACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,28
PRIOR FILING DATE: 02/28/2001
FRIOR FILING DATE: 02/28/2001
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
9 US-10-105-891-28
9 US-10-098-841-148
9 US-10-098-841-148
9 US-10-918-995-1793-
9 US-09-918-995-7993
9 US-10-00-035-2561
9 US-09-925-299-265
10 US-09-918-995-265
9 US-09-918-995-265
9 US-09-918-995-265
10 US-09-918-995-265
10 US-09-918-995-265
10 US-09-918-995-265
10 US-09-918-995-1661
10 US-09-918-995-1661
10 US-09-918-995-1665
10 US-09-918-995-1665
10 US-09-918-96-66
10 US-09-918-95-1665
10 US-09-918-91-580-66
9 US-09-918-91-580-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.0%; Score 574; DB 9; L
Best Local Similarity 100.0%; Pred. No. 2.5e-278;
Matches 574; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              US-09-813-153-72
US-10-198-846-11355
US-10-239-676-56
US-09-764-891-6380
US-09-764-891-6380
US-09-764-872-642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10090035
Patent No. US20020170089A1
    10445
16892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (96)...(374)
US-10-090-035-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
28
22
22
22
22
24
25
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-3
200
222
222
222
222
223
233
233
233
241
241
                                                                                                 O
                                                                                                                                                                                                                                                                                                                                         O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 13, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 25, Appl
Sequence 1655, A
Sequence 1655, A
Sequence 1655, A
Sequence 1655, A
Sequence 26, Appl
                                                                                                              June 16, 2003, 07:57:31; Search time 127.198 Seconds (Without alignments) 6534.570 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-1
US-10-090-035-1
US-10-090-035-1
US-10-090-035-17
US-10-090-035-13
US-10-090-035-13
US-10-090-035-13
US-10-090-035-23
US-10-090-035-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-918-995-17655

US-09-917-800A-508

US-09-918-995-16259

US-09-918-995-6561

US-09-776-724A-24
                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-800-729-25
                                                                                                                                                                                                                                                                                                                                     1029858 seqs, 724030393 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                             OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.00000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.
                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                             Scoring table:
```

Word size :

Searched:

Sequence:

Database :

ö

0; Gaps

9

TCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACAGGTCTCACGCGCGGCG 240

181

ô

US-10-125-237-28

113 113 114 117 118 υv

Result No.

a

420

480

```
GGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCC
                  GTGCCTTATGTATGTCTGTTGATTGATTGTTCAGGGTCATCGTACTTGGCTATCGTA
244 CCAACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGACCA
                                                                                                                                                                                                                                                Sequence 1, Application US/10090035
; Sequence 1, Application US/10090035
; Patent No. US20020170089A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Proteins and Uses Thereof
; FILE REFERENCE: 35718/24290
; CURRENT FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2028/24091
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
: LENGTH: 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 313; DB 9; I
Pred. No. 2.3e-147;
0; Mismatches 3;
                                                                                                                                                                                54.5%;
nilarity 99.4%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (88) ... (367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-1
                                                                                                                                                                                                                                       RESULT 3
US-10-090-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 463,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                      421
                         301
                                            304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                               ď
                                                                                                                                                                                      ð
                                                                                                                                                                                                         g
                                         g
                                                                                                      ò
                                                                                                                         g
                                                                                                                                               δ
                        ò
                                                                 δ
                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CCAACCACCACCACCATGGTCACCAGGCGCCCACGGCTTCGTGGTGCGCGAGACCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                      360
                                                                                                        GTGCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTATCGTA 480
                                                                                                                                                           421 GIGCCTTATGTATGTCTGTGGTTGATGTTGTGAGGGTCATCGTACTTGGCTATCGTA 480
                                                                                                                                                                                         540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACCCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACTTCGACGTCACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGCTGCGCACAGACACAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTGCACGCACTCCTGTACGAATTACGACAATAAAGCTCGTGACCTGAATAAAACT
                                                                                                                                                                                                  181 TCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10090035;
Sequence 5, Application US/10090035;
Patent No. US20020170089A1
GENERAL INFORMATION:
TAPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
CURRENT APPLICATION UNDER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 574; DB 9; L
Pred. No. 2.5e-278;
                                                                                                                                                                                                                                541 TCTTCGTAATACTAAAAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.0%;
Matches 574; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (99)...(377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-5
                                                                                                                                                                                                                                                                                      RESULT 2
US-10-090-035-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                  241
                                                    241
                                                                       301
                                                                                            301
                                                                                                                361
                                                                                                                                  361
                                                                                                                                                      421
                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                 q
                                                                                                                                                   ò
                                                                                                                                                                      g
                                                                                                                                                                                              õ
                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                      q
                                                                                      a
                                                                                                                ò
                                                    요
                                                                         à
                                  ò
```

ö

Gaps ö 149 142 209 202 269 262 329

```
303
                                                                                                                                                                                                                                                                                                                                                                                     363
                                                                                                                                                                                                                                                                                                                                          424 CCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTATCGTACGT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489
                                                                                                                                                                                                                                                         244 ACCACCACCACCATGGTCACCACGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
                                                                                                                                                                                                                                                                                                                       484 GCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 CACAGACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGG
                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/10090035
Fatent No. US20020170089A1
GENERAL INFORMATION:
TILLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
CURRENT FILING DATE: 2002-02-28
FRICE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: 05/10/090,035
FRICE REPLICATION NUMBER: 60/272,227
FRICE SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 524
                                                                                                                                                                                                Length 580;
                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                           31.0%; Score 178; DB 9;
99.1%; Pred. No. 1.3e-79;
tive 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

24.2%; Score 139; DB 9;
Best Local Similarity 99.5%; Pred. No. 4.7e-60;
Matches 189; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544 TCGTAATACTAAAAAAAAAAAAAAAAAAAA 574
            NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (57)...(338)
NAME/KEY: misc_feature
LOCATION: (1)...(524)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                        Query Match
Best Local Similarity 99.1;
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Triticum aestivum
                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (99)...(380)
US-10-090-035-7
                                                                                         ORGANISM: Zea mays
                                          SEQ ID NO 7
LENGTH: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                       å
                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                å
450 TIGITCAGGGICAICGIACIIGGCIAICGIACGIGCACGCACICAGCICCIGIACGAAII 509
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 GCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 GIGGCCCCGGCCTTCGCCCGCCACGGCGGCGCGTCCAGGAGCACGTCGTCAAGGAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 GTGGCCCGGCCGGCTTCGGCCGCCACGGCGGCGTCCAGCAGCACGCAGCAGGAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGACATCAACACC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AAGTICGAGGAGGICGACACGGICICACGCGCCGGCGCCAACCACCACCACCACCAIGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                      US-10-090-035-9

Sequence 9, Application US/10090035

Sequence 9, Application US/10090035

Sequence 9, Application US/10090035

GENERAL INFORMATION:
TILE OF INVENTION: Nucleic Acids Encoding Defense Inducible TILE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/742990

CURRENT FILING DATE: 202-02-28

PRIOR RAPLICATION NUMBER: US/10/090,035

PRIOR RILING DATE: 02/28/2001

WUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                            510 ACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAATACTAA 555
                                                                                                               Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10090035
Patent No. US20020170089A1
GENERAL INC. US20020170089A1
GENERAL INC. US20020170089A1
TILE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE REFERENCE: 35718/243990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 194; DB 9;
Pred. No. 1.2e-87;
0; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.8%;
al Similarity 99.3%;
294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (53);...(331)
US-10-090-035-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 294; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-10-090-035-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
윱
                              à
                                                            g
                                                                                            ð
                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

ð

ò g

g ç

ģ g ò g

Gaps

ö

```
Sequence 21, Application US/10090035; Patent No. US20020170089a1; General INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof; TITLE OF INVENTION: Proteins and Uses Thereof; CURRENT APPLICATION NUMBER: US/10/090,035; CURRENT FILING DATE: 2002-02-28; PRIOR APPLICATION NUMBER: 60/272,227; PRIOR PAPLICATION NUMBER: 60/272,227; PRIOR FILING DATE: 02/28/2001; NUMBER OF SEQ ID NOS: 25; SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REPERENCE: 35718/242990 CURRENT APPLICATION NUMBER: US/10/090,035 CURRENT FILING DATE: 2002-02-28 PRIOR APPLICATION NUMBER: 60/272,227 PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.7%; Score 44; DB 9; Le Best Local Similarity 100.0%; Pred. No. 2.2e-12; Matches 44; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/10090035 Patent No. US20020170089A1
                                                                                                                                                                            ; LOCATION: (1)...(348); OTHER INFORMATION: n = A,T,C or G
US-10-090-035-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (61)...(333)
NAME/KEY: misc_feature
LOCATION: (1)...(591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
                                                                                                             NAME/KEY: CDS
LOCATION: (52)...(348)
NAME/KEY: misc_feature
                                              TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(591); OTHER INFORMATION: n US-10-090-035-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-10-090-035-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-15
SEC ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                      | FALEIL NO. USZUGACULSTORAL
| GENERAL INFORMATION:
| APPLICANT: Lalgudi, Raghunath V. |
| APPLICANT: Lalgudi, Raghunath V. |
| APPLICANT: Kamigaki, Laura Y. (Ito)
| APPLICANT: Ramigaki, Laura Y. (Ito)
| APPLICANT: Sherman. Bradley K. |
| TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING |
| FILE REFERENCE: PL-0012-1 CON |
| CURRENT APPLICATION NUMBER: 09/298,329 |
| PRIOR PILING DATE: 1999-04-21 |
| PRIOR FILING DATE: 1999-04-21 |
| PRIOR FILING DATE: 1999-05-05 |
| NUMBER OF SEQ ID NOS: 6332 |
| SOFTWARE: PERL PROGRAM |
| SEQ ID NO 2788 |
| LENGTH: 237 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 CACAGACACCAAGCGICGGCACCAAIGGCITACIACCAGGAGGIGGACTACIGCICGG 129
                                                                           4 CACAGACACACCAAGGGTCGGCACCAATGGCTTACTACCAGGAGGGGGACTACTGCTCGG 93
  31 CACAGACACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | NAME/KEY: misc_feature
| OTHER INFORMATION: Incyte ID No. US20020013958A1 700161180H1
| OTHER INFORMATION: Incyte ID No. US20020013958A1 700161180H1
| NAME/KEY: unsure
| LOCATION: 1. 125-146, 202
| OTHER INFORMATION: a, t, c, g, or other
| US-09-923-876-2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILMS DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.9%; Score 91; DB 10; Length 23
100.0%; Pred. No. 6.2e-36;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 AGGAGGTGAGGTCGGTGGCCCGGCCGGCTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 AGGAGGTGAGGTCGGTGGCCCCGGCCTT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2788, Application US/09923876 Patent No. US20020013958A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match. 15.9%
Best Local Similarity 100.C
Matches 91; Conservative
                                                                                                                                                                                                                                             250 ACCACCACCA 259
                                                                                                                                                                                                                                                                                         211 ACCACCACCA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-10-060-035-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                    ð
                                                                                                                                                                                               셤
                                                                                                                                                                                                                                           δ
                                                                                                   g
                                                            ò
```

Gaps

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICAMT: Hyseq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20111-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1201-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SEQ ID NO 17655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 908;
                                                                                                                                                           Length 584;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPLICATION TO THE AL.

TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEC ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                   Ouery Match
5.9%; Score 34; DB 9; L
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                   107 CCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
7e-06;
                                                                                                                                                                                                                                                           19 ACCCACGCGTCCGCCCACGCGTCCGCACAGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACCCACGCGTCCGCCCACGCGTCCGCACAGC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.4%; Score 31; DB Best Local Similarity 100.0%; Pred. No. 7e-Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (7)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (891)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) LOCATION: (896)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-918-995-17655/c
; Sequence 17655, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/09800729
Patent No. US20020068319A1
                         CCATION: (46)...(321)

NAME/KEY: misc_feature
LOCATION: (1)...(584)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                            .09-800-729-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-10-090-035-19
Sequence 19, Application US/10090035
TITLE OF UNVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 05/272,227
PRIOR APPLICATION NUMBER: 05/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
LENGER: 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/10090035
Fatent No. US20020170089A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 35718/341290
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 0S/10/090,035
FILE REFERENCE: 35718/341290
FRIOR FILING DATE: 2002-02-28
FRIOR FILING DATE: 2002-02-28
FRIOR FILING DATE: 2028/2001
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 23.
LENGTH: 584
                                                                                                                                                           Ouery Match 5.9%; Score 34; DB 9; Length 436; Best Local Similarity 100.0%; Pred. No. 2.3e-07; Matches 34; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.9%; Score 34; DB 9; L
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                         107 CCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 CCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: CDS
LCCATION: (54)...(326)
US-10-090-035-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Triticum aestivum FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-090-035-23
LENGTH: 436
                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AI007824
US-09-917-800A-508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.1%; Score 29; DB 10; Length 569; 100.0%; Pred. No. 7.4e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                               Length 538;
                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PITILE OF INVENTION: MOLECULAR TOXICOLOGY MODELING
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR PILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR PILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-05-05
PRIOR PILING DATE: 2001-05-05
PRIOR PILING DATE: 2001-05-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
                                                                                                                                                                                                                                    Query Match 5.1%; Score 29; DB 9; L
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 ACCCACGCGTCCGCCCACGCGTCCGCACA 181
                                                                                                                                                                                                                                                                                                                                          1 ACCCACGCGTCCGCCCACGCGTCCGCACA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-917-800A-508/c
; Sequence 508, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
                                                                                                     NAME/KEY: misc_feature

| LOCATION: (1)...(538)

| OTHER INFORMATION: n = A,T,C or G

US-09-918-995-17655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.1%
Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Logic, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 508
LENGTH: 569
LENGTH: 538
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                           엄
```

Search completed: June 16, 2003, 10:24:26 Job time: 129.198 secs

Q

RNOSEQ6C0

Title: Perfect score:

Run on:

Seguence:

Scoring table:

Word size :

Searched:

Database :

```
BG619318 RNOSEGGED
BG619318 RNOSEGGED
BG619383 RNOSEGGED
BG619383 RNOSEGGED
BG619390 RNOSEGGED
BG619390 RNOSEGGED
BG619390 RST12-H1
AA9798139 PACO00000
AT87315 945002EGG
BE025302 945002EGG
A1964534 496013D01
A7875545 603016F02
BE025303 945007EGG
A185545 603016F02
BES19299 945007B05
BES19299 945007B05
BES19299 945007B05
BM53085 F41710.V
BM53085 F41710.V
BM154114 F483611.V
BM154114 F483611.V
BM154119 AGENCOURT
BC22049 AGENCOURT
BC22049 AGENCOURT
BC22049 AGENCOURT
BC22049 AGENCOURT
BC389253 BJ389253
AW781844 S182454
BC77697 NXSI_073_
BG609663 323594 MA
AL70362 DKF2668K
AL26246 GG880404.V
BG109125 602281318
AV7557705 AV755678
AV757705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 bp mRNA linear EST 16-MAY-2000 (SK) Zee mays CDNA, mRNA sequence.
AW787732 AW787732.1 GI:7844510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 500)
Walbot,V.
Walbot,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Conteact: Walbot v
Conteact: Walbot v
Department of Biological Sciences
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 8221
Fax: 650 725 8221
Email: Walbot@stanford.edu
Plate: 945002 row: E column: 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                      AA979839
BM501439
AW787315
BE025302
AI964534
AW787314
AR855425
AI964458
                                                                                                                                                                                                      BE129644
AR789056
BE025303
BE025303
BE025303
BM288875
BM85464
BM530659
BM154314
BM1645
                                                                                                                                                                                                                                                                                                                                                                                                                                      BG609663
AL703622
AI226246
BF726297
AW985721
BG109125
AV755678
AV757705
                                 338.6
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
37.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
337.7
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays.
Zea mays
 LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
AW787732
 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW787732 945002E06
AW28876 707009E07
BE129897 945032C12
AW331212 707049E04
AY104409 Zea mays
BQ619167 RNOSEQ4E0
                                                                               June 16, 2003, 05:14:00 ; Search time 1370.39 Seconds (without alignments) 7989.092 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                          32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                          16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW787732
AW288876
BE129897
AW331212
AX104409
BQ619167
                                                                                                                                                                                                   OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_gss_mam: *
em_gss_mus: *
em_gss_other: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_est5:*
em_estfun:*
em_estcm:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_gas_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_gss_vrt:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_gss_pro:*
                                                                                                                                                                                                                                                                                                                                                                                                                     em_estba:*
em_esthum:*
em_estin:*
em_estov:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_gss_pln:*
                                                                                                                                            US-10-090-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_gss_inv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_gss_fun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_htc:*
gb_est3:*
gb_est4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ap_gas:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500
524
465
523
553
648
                                                                                                                                                                                                                                                                                                                                                                                                       EST: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.6
41.3
39.6
38.6
                                                                                                                                                                                                                                                                       0
```

/organism="Zea mays"

source

Score

Result

94304,

```
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                      307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
                                                                                                                                                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                              263
                                                                                                                                                                                                                                                                                                                                                                                                                 247
                                                                                                                                                                                                                                                                                                                                                                                                                                    323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
BE129897
                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA linear EST 16-JAN-2000
tissues from Walbot lab (SK) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 524)
Walbot,V.
                                    Atlasue_type="fassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/dev_stage="fully-grown"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="Organ: leasel, kernal, silk, husk, root, leaf;
/note="Organ: leasel, kernal, silk, husk, root; leaf;
/note="Organ: leasel, kernal, silk, husk, differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 fer additional sequencing."
a 159 c 156 g 88 t
                                                                                                                                                                            ö
                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                        448
                                                                                                                                                                                                                                      202
                                                                                                                                                                                                                                                                            262
                                                                                                                                                                                                                                                                                                208
                                                                                                                                                                                                                                                                                                                                      268
                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                   443 TIGIGCAGGGICATCGIACTIGGCIATCGIACGIGCACGCACICAGCICCTGIACGAATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGAGGTCGACACGGTATCACGCGCCGGCGCCAACCACCACCACCACCATGGTCACCAC
                                                                                                                                                                                                                                                                                      /cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (5K)"
                                   silk, husk, root, leaf"
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA libraries sequenced at Stanford
                                                                                                                                                                            ;
0
                                                                                                                                                         Length 500;
                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                          Score 308; DB Pred. No. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 707009E07.x4 707 - Mixed adult t
mays CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize ESTs from various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:6695663
                                                                                                                                                           tch 45.6%;
al Similarity 99.3%;
45%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW288876.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University
                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449
                                                                                                                                                                                                                                           143
                                                                                                                                                                                                                                                                                  203
                                                                                                                                                                                                     83
                                                                                                                                                                                                                       29
                                                                                                                                                             Query Match
Best Local $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
AW288876
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                  å
                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                       셤
```

```
21-JUN-2000
same as 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
Sea mays :
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: tassel, kernel, silk, husk, root, leaf; /note="Organ: tassel, kernel, solk library from fully vector: pGAD10; Site_1: ECORI; cDNA library from fully differentiated malze tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk, plant, root, leaf). Unidirectionally cloned."
                                                                                                                                                                                                                                                                                                                                                                      (SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 TIGIGCAGGGICATCGIACTIGGCIATCGIACGIGCACGCACTCAGCICCIGIACGAAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGHTHIN THE THE THEORY OF THE TRANSPORT OF THE TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGACATCAACACCTGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465 bp mRNA linear EST 94502012.X1 945 - Mixed adult tissues from Walbot lab, EST 2ca mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 305; DB 10; Length 524;
Pred. No. 0;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                          07
Stanford University
BS5 California Ave, Palo Alto, CA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotestanford.edu
Plate: 707009 row: E column: 07
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:8577260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match . 45.1%;
Best Local Similarity 99.3%;
Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE129897.1
```

```
Spermatophyta; Magnollophyta; Embryophyta; Tracheophyta; clade; Panicoldeae; Magnollophyta; Liliopaida; Poalea; Poaceae; PACC (1 (pases 1 to 523) Andropogoneae; Zea. Walhor v
                                                                                                                                                                                                                                                                                                                                 1. 523
/organism="Zea mays"
/cultivar="#x33"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
/note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
differentlated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGGCCACGGCTTCGTGGTGCGGGACCAGGGTCGAGGAGACATCAACACCTGCACC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGAGGTGAGGTCGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 CCGGCCGGCTTCGGCCGCCGCGCGCGTCCAGCACCACGTCGTCAAGGAGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adult tissues from Walbot lab (SK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 523;
                                                                                                                                                       Walbt, V.
Maize ESTs from various cDNA libraries sequenced
University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                             Unpublished (1999)
Contact: Walbot V
Department of Balological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, US.
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707049 row: E column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 268; DB; Pred. No. 0; 0; Mismatches
                                                                              Zea mays.
Zea mays
Eukaryota; Viridiplantae;
           707049E04.x1 707 - Mixed amays cDNA, mRNA sequence. AW331212 AW331212.1 GI:6827569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.6%;
1 Similarity 99.2%;
46%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389
                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
            DEFINITION
                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                             JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                 /note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: ECORI; cDNA library from fully
Vector in the site_1: ECORI; cDNA library from fully
fisher ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 CCGGCCGGCTTCGGCCGCCGCCGCGGCGCGCCAGCACGTCGTCGTAAGGAGAAGTTC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGAGGICGACACGGIAICACGCGGCGCGCCAACCACCACCACCATGGICACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGGCCACGGCTTCGTGCTGCGGGAGACCAGGGTCGAGGAGGACATCAACACCTGCACC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab, state as 707 (St)"
/tissue_type="tasse1, kernal, silk, husk, root, leaf" /dev_stage="fully-grown"
/lab_nost="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGAGGTCCACGAGGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                              at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     41.3%; Score 279; DB 10; Length 465; Conservative 0; Mismatches 3; Indels
                                    Maize ESTs from various cDNA libraries sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                       Contact: Walbot v
Contact: Walbot v
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbottestenford.edu
Plate: 945032 row: C column: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ďq
                                                                                                                                                                                                1. .465
/organism="Zea mays"
/cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523
            1 (bases 1 to 465)
Walbot, V.
                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGACAATAAGC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGACAATAAGC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 429; Conserv
                                                  University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW331212
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383
                                                                                                                                                                                                source
         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                            JOURNAL
                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
AW331212
LOCUS
                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
sequence.
BQ619167
BQ619167.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
                                                                                                                     Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
BQ619315
LOCUS
DEFINITION
        RESULT 6
BQ619167
LOCUS
DEFINITION
                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466
                                                                                     HTC 25-MAY-2002
                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="MaizeDB:637271"
/db_xref="MaizeDB:637271"
/db_xref="Axon:4577"
/clone="PC0124784"
/clone="the sequence is part of a project of EST
/note="this sequence is part of a project of EST
/note="this sequence is part of a project of EST
/note="this sequence is part of a project of EST
/note="this sequence is part of a project of EST
/note="this sequence is part of a project of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
yeargo addressing of BACs in conjunction with the Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTTATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATTGCTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                   1 (bases 1 to 553)
Analoey.C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
                                                                                                                                                                                                                                                                                                                              σŧ
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 261; DB 11; Length 553; Pred. No. 0; Mismatches 1; Indels
                                                                                      linear
                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 t
                                                                                    AY104409
Zea mays PC0124784 mRNA sequence.
AY104409
                                                                                                                                                                                                                                                                                                                                                                   1. .553
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping Project
                                                                                                                            AY104409.1 GI:21207487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.7%;
Matches 311; Conservative
                                                                                                                                                                                                                                                                     Overgo Probes
Unpublished (2002)
2 (bases 1 to 553)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTAATACTAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays.
                                                                                                                                                                                                                                                                                                          Coe, E.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537
                                                                                          LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                  JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                 AUTHORS
                                                                    RESULT 5
AY104409
                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                              음
         ð
```

ă,

```
Bukaryotay: viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryotayotay; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

El (Masses It o 648)

Wang H. and Bohnert, H.J. Genomics of plant stress tolerance
Unpublished (2002)

Unpublished (2002)

University of Illinois
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217265473
Email: bohnertlab@life.uluc.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQ619315 SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6C06_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536
EST 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292
                                                                                                                                                                                                                                                                                                                                                                                                           Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ619167 648 bp mRNA linear EST 27-JUN-1
RNOSEQ4E05_SK.abl Salt stressed Zea mays roots CDNA library Zea
mays CDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                    mays roots cDNA library'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.6%; Score 261; DE Best Local Similarity 99.7%; Pred. No. 0; Matches 311; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 537 TCGTAATACTAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 TCGTAATACTAA 544
                                                                                                                                                                                                                                                                                                                 1. .648
```

Ŋ

```
E 1 (bases 1 to 648)

S Wang, H. and Bohnert, H.J.

Genomics of plant stress tolerance

Contact: Mark Fredericksen

Contact: Mark Fredericksen

Contact: Mark Fredericksen

Contact: Mark Fredericksen

Contact: Department of Plant Biology

University of Illinois

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217265473

Email: bohnertlab@life.uiuc.edu.

Location/Qualifiers

L. 648

/organism="zea mays"

/organism="zea mays"

/organism="zea mays"

/organism="zea mays"

/organism="zea mays"

/clone="RNOSEOSDO1_SK.abl"

/clone="RNOSEOSDO1_SK.abl"

/flssue_type="Roots of the stressed zea mays roots cDNA library"

/dev_stage="zeage="zeage"

/dev_stage="zeage"

/dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 ACCACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGGGAGCAGGG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 TCGAGGAGGACATCAACATCCACCGCGAGGTCCACGAGGCGCAGGAGAGCTTCCTCG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGGCTAACTGAGCCGCCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panárcoideae; Andropogoneae; Zea.
1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Wang, H. and Bohnert, Eress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
                                                                                                                                                                                                                                                                                                                                                                                                                               Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ619337 648 bp mRNA linear EST 27-JUN-7
RNOSEOGEI2_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.6%; Score 261; DB 14; Length 6
99.7%; Pred. No. 0;
tive 0; Mismatches 1; Indels
                    Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
BQ619337
BQ619337.1 GI:21621331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 311; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   537 TCGTAATACTAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 TCGTAATACTAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mM NaC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                    REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
BQ619337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Wang, H. and Bohnert, H.J.
Connact: Mark Fredricksen
Unpublished (2002)
Contact: Mark Fredricksen
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGGGCTAACTGAGCCGCCGGCGGCGCATCCACGCCCGTTCGTGCTTGCCTGCGTG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
/clone="RNOSEQ6C06_SK.abl"
/clone="Lib="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ619318 648 bp mRNA linear EST 27-JUN-2
RNOSEQ6DOL_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ6DOL_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 ACCACCACCACCATGGTCACCACGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

38.6%; Score 261; DB 14; Length 648;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 311; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 t
                                                                                                                                                                                                                                                                                                                                                              bohnertlab@life.uluc.edu.
Locatlon/Qualifiers
1. .648
/organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 g
                        GI:21621309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:21621312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537 TCGTAATACTAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 TCGTAATACTAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mM NaCl
BQ619315
BQ619315.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
BQ619318
BQ619318.1
                                                               Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357
                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
BQ619318
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  品
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
```

ö

```
EST.
                                                                                                                                                                                                                                                                                        357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
BQ619390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                            å
                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ619383 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ7B02_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ7B02_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     417 CCTTATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGT 476
                                                                                                                                                                                                                                                                                                                                                                                  GCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT 536
                                                                                                                                                                                                                                                                                                                                 TCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGGCGCAGGGAGAGCTTCCTCG 356
                                                                                                                                                                                                                                                                                                                                                          352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
/organism="Zea mays"
/db xref="taxon:4557"
/db xref="taxon:4557"
/clone="Nh"Sadf612_x abl"
/clone="Nh"Sadf stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dov_stage="Z weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
mM NaCl"
                                                                                                                                                                                                                                                                              237 ACCACCACCACCACCATGGTCACCACGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
                                                                                                                                                                                                                                                                                         193 TCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCG
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                         Length 648;
                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61801, USA
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
                                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                        100 t
                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 648)
Wang, H. and Bohhert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61
Tel: 21/2655473
Email: bohnertlab@llfe.uluc.edu
                                                                                                                                                                                                                            Score 261; I
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bohnertlab@life.uiuc.edu.
Location/Qualifiers
1. .648
/organism="Zea mays"
                                                                                                                                                                                        193 c . 183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:21621377
                                                                                                                                                                                                                            Query Match 38.6%;
Best Local Similarity 99.7%;
Matches 311; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 TCGTAATACTAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
BQ619383
BQ619383.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477
                                                                                                                                                                                                                                                                                                                                        297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
BQ619383
                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                           δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
```

į,

```
SM Zea mays

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta: Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 648)

Wang, H. and Bohnert, H.J.

Genomics of plant stress tolerance
Genomics of plant stress tolerance
Unpublished (2002)

Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172656473

Fals: Abhorthalife ulinc.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                      416
                                                                                                                                                                                                                                                                                                                                                                                                                                                            412
                                                                                                                                                                                                                                                                    237 ACCACCACCACCATGGTCACCACGGCGACGGCTTCGTGGTGCGCGAGACCAGGG 296
                                                                                                                                                                                                                                                                                                                                            356
                                                                                                                                                                                                                                                                                                        292
                                                                                                                                                                                                                                                                                                                                                                                352
/db_xref="taxon:4577"
/clone="RNOSE07B02_SK.abl"
/clone_lib="salt stressed Zea mays roots cDNA library"
/tissue="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bolnertlab@life.uluc.edu.
Location/Qualifiers
1. 648
/organism="zea mays"
/db_xref="taxon.4577"
/clone="RNOSEQ7809_SX.abl"
/clone="Tope="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_zfage="2 weeks old"
/not="vector: pBluescript SK+; Stressed 24 hours at 1:
mM Nacl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ619390 RNOSEQ7B09_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ7B09_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 TCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGGCAGGGAGAGCTTCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                            Length 648;
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                    ï
                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                Score 261; DB; Pred. No. 0; 0; Mismatches
                                                                                                                                          100
                                                                                                                                          183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:21621384
                                                                                                                                                                                                Query Match 38.6%;
Best Local Similarity 99.7%;
Matches 311; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 TCGTAATACTAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11111111111
533 TCGTAATACTAA 544
                                                                                                                                              193 c
                                                                                                                        mM NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ619390
BQ619390.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sedneuce
```

a

ð

qq

ç 8 õ g ò g ò a

ò

```
Query Match
37.9%;
Best Local Similarity 99.7%;
Matches 306; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:3157217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 537 TCGTAAT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 TCGTAAT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
AA979839
AA979839.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
AA979839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                  ö
                                                                                                                                                                                 296
                                                                                                                                                                                                                               292
                                                                                                                                                                                                                                                                                356
                                                                                                                                                                                                                                                                                                                                                          BG840383
MEST12-H11.T7-1 ISUM4-TN Zea mays CDNA clone MEST12-H11 5', mRNA
                                                                                                                                                                                                                                                                                          417 CCTTATGTATGTCTGTGGTTGACTGGTTGTGGAGGGTCATCGTACTTGGCTATCGTACGT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 550)

Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)

On May 25, 2001 this sequence version replaced gi:14206705.
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pT713PAC; Site_1: EcoRI; Site_2: NotI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dr selected mRNA by priming
                                                                                                                                                                                             237 ACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
                                                                                                                                                                                                                                                              297 TCGAGGAGGACATCAACACCTGCACCGGGGAGGTCCACGAGGGGGGGAGAGAGTTCCTCG
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
                                                                                                                                ö
                                                                                  Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 515-2v4-2c.

Fmail: schnable@iastate.euu
PCR PRimers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T7-1 (AA TAC GCT CAC TAA AG)
BACKWARD: T7-1 (AA TAC GCT CAC TAA AG)
BACKWARD: T7-1 (AA TAC GAC TCA TAG)

LES

1. 550

| Corganism="Esca mays" |
| Cult.ya="basa mays" |
| Clone="texton: 4577" |
| Clone="texton: 4577" |
| Clone="texton: 4577" |
| Clone="texton: 550#4-TN" |
| Clone="texton: p7713PAC; Site_1: ECORI;
| Clone="texton: p7713PAC; Site_1: ECORI;
| Clone="vector: p7714PAC;
| Clone="vector: 
                                                                                                                             Indels
                                                                               DB 14;
                                                                       Score 261; DB
Pred. No. 0;
0; Mismatches
       100
       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:14242676
                                                                  Query Match
Best Local Similarity 99.7%;
Matches 311; Conservative
     U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
BG840383
BG840383.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays.
Zea mays
172
                                                                                                                                                                                                                  233
BASE COUNT
ORIGIN .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
BG840383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Pancooldeae; Andropogoneae; Zea.

1 (bases 1 to 546)

Expressed Squence Tags from B73 Maize Seedlings

L Unpublished (1997)

Contact: Schnable, PS

Schnable laboratory

Iowa State University

G405 Agronomy, Ames, IA 50011, USA

Tel: (515)-294-2299

Email: schnable@lastate.edu
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA979839 546 bp mRNA linear EST 26-MAY-1998
MEST2-B7 TW1412.Seq ISUM2 2ea mays cDNA clone MEST2-B7 5', mRNA
                                                                                                                                                                                                                                                                       237 ACCACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGGGAGACCAGGG 296
                                                                                                                                                                                                                                                                                         297 TCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGGTTCCTCG 356
                                                                                                                                                                                                                                                                                                                                                                       345
                                                                                                                                                                                                                                                                                                                                                                                            476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536
                                                                                                                                                                                                                                                                                                                                                  417 CCTTATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 GCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACTGAATAAAACTTCT
                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                 Length 550;
                                                                                                                                                                                                                                          indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGC-3')
Plate: MST2 row: B column: 7
Seq primer: tw1412 (5'-GAAGATACCCCACCAACC-3').
Location/Qualifiers
                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                   DB 12;
                                                                                                                                                                                                               Score 256; DB 1;
Pred. No. 0;
0; Mismatches
```

ö

Gaps

142 138 258 322

262

```
AW787315 436 bp mRNA linear EST 16-MAY-2000 945002E06.X2 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade, Panicoideae; Andropogoneae; Zea.

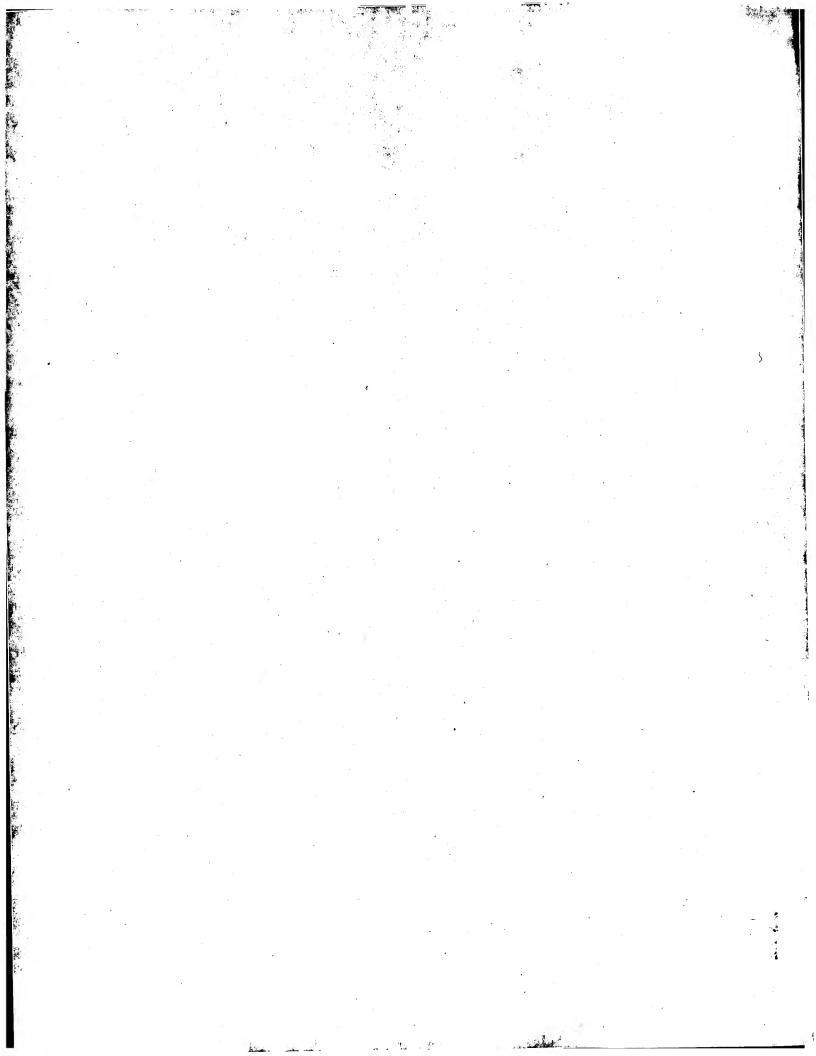
1 (bases 1 to 436)
Walbot,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA Tel: 515 270 5934
Fax: 515 254 2619
Email: rudolf.jung@pioneer.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                        GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCC
                                                                                                                                                                                                                                                                                                          Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                        /organism="Zea mays"
/db_xref="taxon:4577"
/clone_lib="Pioneer AF-1 array"
/note="Vector: pSportl; Site_1: Sall; Site_2: Not!"
150 c 133 g 53 t
                                                                                                                                                                                                                          Length 417
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA 94304, USA
                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University
Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ayev, Palo Alto, CA 94
Tel: 650 723 227
Fax: 650 725 8221
Email: Walbotestanford.edu
Plate: 945002 row: E column: 06.
                                                                                                                                                                                                                        ; Score 237; DB
; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW787315.1 GI:7844112
                                                                                                                                                                                                                            tch 35.1%;
al Similarity 99.4%;
337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays.
Zea mays
                                                                                                                                                                               ø
                                                                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST.
                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
AW787315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                              FEATURES
                                                                                                                                                                                                                                                                                                    ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                              /tissue_tipe="above ground tissues"
/tissue_tipe="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="%LilmFR Blue"
/lab_host="%LilmFR Blue"
/note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
/note="Grgan: green seedlings; Vector: paD-GAL4; Site_1:
/note="Gran Black green of green contacted as gloon-resulting why print was prepared from note of green green and strand synthesis, After the addition of EcoRI adaptors, the ds-connas were directionally cloned into the resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybrizAP lambda vector (Stratagene) and excised as pAD-GAL4 phagemids."
30 a 168 c 159 g the HybrizAP lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM501439 14-FEB-2002 A17 bp mRNA linear EST 14-FEB-2002 PACO000000000593 Pioneer AF-1 array Zea mays CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    477 GCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTTATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   끆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize opaque endosperm mutations create extensive changes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patterns of gene expression
Unpublished (2002)
Contact: Jung R
Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                    Score 255; DB 9; Length 546;
Pred. No. 0;
0; Mismatches 1; Indels
                                                                   /db_xref="taxon:4577"
                        l. .546
/organism="Zea mays"
                                                                                                   /clone_lib="ISUM2"
                                                                                     /clone="MEST2-B7'
                                                   /cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM501439
BM501439.1 GI:18661517
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.7%;
Best Local Similarity 99.7%;
Matches 305; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517 TCGTAA 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537 TCGTAA 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
                        source
                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
BM501439
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
```

셤 ò g ò 셤 ö 셤 õ g

ð 셤

```
/note-*Organ: tassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: EcoRI; cDNA library from fully differentiated malze tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
                                                                                                                                                                                               ô
                                                                                                                                                                                                           287
                                                                                                                                                                                                                                                                                                                                                                                                                                                              467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 ATCGTACGTGCACCCCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAAT 527
/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)."
/tissue_type="fassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                       CCGGCGCCAACCACCACCACCATGGTCACCACGGCGGCCACGGGTTCGTGGTGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTGCGTGCCTTATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCT
                                                                                                                                                                                              Gaps
                                                                                                                                                                                             ö
                                                                                                                                                              Query Match
34.3%; Score 232; DB 10; Length 436;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 432; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAACTTCTTCGTAAT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAACTTCTTCGTAAT 543
                                                                                                                             82
                                                                                                                                                                                                                                                           168
                                                                                                                                                                                                                                                                                                         228
                                                                                                                                                                                                                                                                                                                                                                                                                                                 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

Search completed: June 16, 2003, 08:38:41 Job time : 1384.39 secs



```
GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_pzn model

Run on: June 16, 2003, 10:02:07; Search time 1293.5 Seconds

(without alignments)
1164.422 Million cell updates/sec

Title: US-10-090-035-4
Sequence: 1 MAYYOEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
Scoring table: BLOSUM62
Xgapop 10:0, Xgapext 0.5
Ygapop 10:0, Xgapext 0.5
Ygapop 0:0, Ygapext 7:0
Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	score gre and 1s de	greater tr derived b	than or e by analy	equal Lysis c	to the score of the r of the total score dis	esult being printed, tribution.
		æ			SUMMARIES	
	Ö		Length	DB	. <b>QI</b>	Ξ.
-			1.5			
10	ים נ	3	177	1 -	2000	439 PAC00000
	'n	· ~	000	3 -	2,0	
4	2	•	1000	2	, -	732 945002E0
5	S	•	524	35	287	212 /07049E0
	499		466	ò	34	10 / 10 / 10 / 10 / 10 / 10 / 10 / 10 /
. 0	499		481	ο ο	53	50 4 95013
	499		539	σ		25 603010
σ,	499	•	546	σ		AS MEGHO-
10	499		550	12	2	383 MEGTI
11	499	_	553	Ξ	4	409 209
12	499		648	14	₫	167 RNOS
13	499		648	14	2	315 RNOS
44.	499	٠.	648	14	2	318 RNOS
5 T	499	٠.	648	14	2	337 RNOS
91	4.9		648	14	Ē	383 RNOS
77	499	٠.	648	14	ĕ	390 RNOS
10 C	4	٠.	326	10	ĕ	303 9450
J (	4	٠.	443	01	è	644 9450
2 5	4.	٠.	552	2	ĕ.	302 9450
22	4 4	<u>.</u>	476	25	Č,	299 9450
3.6	7		4 4 4 6	25	m d	314 9450
. 24	7	•	4 4 4	3 5	57	008 9450
25	423	•	0 0	? ?	າ່ເ	315 9450
26	423	•	46.5	10	9 6	672 PII_
. 27	423		485	32		738 PII_
28	423	•	513	14	ĭ	123 P11_
29	423.5	83.0	516	10	BE364814	BE364814 DT1 16 CO
30	423.	•	519	10	6	016 401
31	423	٠	522	ដ	8	15M 696
32	423	•	537	10	2	400 WS1
 	423	٠	541	2	5	136 WS1
2,0	417	•	348	10	2	507 WS1
30	410.	٠	209	7	8	394 WHE3
0 0	ת ה	٠	401	0	9	356 7070
, r	368	٠	274	10	83	375 7070
e c	367.	٠	311	15	2	120 1000
7 7	9 6	60.4	453	01	20	322 WS1
2.4	96	60.4	554	2	5	15 WS1
1 (	2 6	400	260	01	407	79 WS1
7 6	2 6	9.00	200	2;	57791	17 WS1_
7 *	2 6		000	2:	4638	183 WS1_4
* 4	2 6	9.5	2/5	2:	67971	13 WS1
?	S S	4.00	2/0	20	2501	14 WS1_7

BM501439 417 bp mRNA linear EST 14-FEB-2002	Zea mays	crack, ranicologae; Andropogoneae; Zea.
PAC000000000593 Pioneer AF-1 array Zea mays cDNA, mRNA sequence.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	1 (bases 1 to 417)
BM501439	Sperimatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC	Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and Jung. R.
NON NON	ORGANISM Zea mays  Eukaryota; Viridiplantae; S Spermatophyta; Magnollophyt	REFERENCE 1 (bases 1 to 417) AUTHORS Hunter, B.G., Beatty, M., Singletary, G., F. Jung.R.

ALIGNMENTS

```
walbot@stanford.edu
945032 row: C column: 12.
Location/Qualifiers
                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walbot, V
    Email:
Plate:
                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
COMMENT
                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
AW787732
                            FEATURES
                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE129897 465 bp mRNA linear EST 21-JUN-2000 945032C12.X1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
BE129897.1 GI:8577260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 465)
                                                                                                                                                                                                                                                                                                                                                                                                                  Maize opaque endosperm mutations create extensive changes in patterns of gene expression (2002)
Unpublished (2002)
Contact: Jung R
Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
7300 NW 62nd Avv., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                          Unpublished (1999)
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                               417
93
0
0
0
                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                           Email: rudolf.jung@ploneer.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          US-10-090-035-4 (1-93) x BM501439 (1-417)
                                                                                                                                                                                                                                5.6e-47
510.00
100.00%
100.00%
                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
                                                                                                                                                                                       81
                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
BE129897
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                               JOURNAL
COMMENT
                                                                                                                          FEATURES
              TITLE
                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                          ά
```

```
/organism="Zea mays"
/cultivar="%23"
/cultivar="%23"
/cultivar="%23"
/cultivar="%23"
/cultivar=10=7945 - Mixed adult tissues from Walbot lab,
/clone_lib=7945 - Mixed adult tissues from Walbot lab,
/clone_lib=7945 - Mixed adult tissues from Walbot lab,
/clone_lib=7945 - Mixed adult tissues root, leaf"
/dev_stage="full0B"
/dev_stage="full0B"
/dev_stage="full0B"
/dev_stage="full0B"
/dev_stage="full0B"
/dev_stage="full0B"
/dev_stage="full0B"
/derentiated maize tissues from an active Mutator plant.
fissue ratio is 4:2:1:1:1:1 (tassel, kenel, silk, husk,
rissue ratio is 4:2:1:1:1:1 (tassel, kenel, silk, husk,
rissue ratio is 4:2:1:1:1:1 (tassel, kenel, silk, husk,
ristue ratio is 4:2:1:1:1:1 (tassel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW787732 500 bp mRNA linear EST 16-MAY-2000 945002E06.X3 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) 2ca mays cDNA, mRNA sequence.

AW787732 GI:7844510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 ValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHisGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465
92
0
1
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto. CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-090-035-4 (1-93) x BE129897 (1-465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize ESTs from various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.26e-46
505.00
98.92%
98.92%
```

```
tissues from Walbot lab (SK
                                                                                                                                                                 /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DHIOB"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGADIO; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissues from Walbot lab (SK) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 524)
Walbot,V.
Walbot,V.
Walse ESTs from various cDNA libraries sequenced at Stanford University
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                             523
00 100
00 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524 bp
707009E07.x4 707 - Mixed adult t
mays cDNA, mRNA sequence.
AW288876.1 GI:6695663
                                                                                                                                                                                                                                                                                                                                                                                       US-10-090-035-4 (1-93) x AW331212 (1-523)
                                                                                                                                                                                                                                                                                                         2.58e-46
505.00
98.92%
98.92%
99.02%
                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                               ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                 source
                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
AW288876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                          /db_xref="taxon.4577"
/clone_llb="945 - Mixed adult tissues from Walbot lab, same as 707 (St)"
/tlsue_type="taxon.4577"
/tlsue_type="taxon.4577"
/dev_stage="fully-grown"
/lab_nost="bling"
/note="Organ: tassel, kernal, silk, husk, root, leaf;
/note="Organ: tassel, kernal, silk, husk, root, leaf;
/vector: pGAD10; Site_1: ECORI; CDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA linear EST 31-JAN-2000
tissues from Walbot lab (SK) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                   CDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945002 row: E column: 06.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Walbot V
Department of Blological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW331212 523 bp
707049E04.x1 707 - Mixed adult t
mays cDNA, mRNA sequence.
AW331212 GI:6827569
                                                                       /organism="Zea mays"/cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-4 (1-93) x AW787732 (1-500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malze ESTs from various
                                                                                                                                                                                                                                                                                 2.45e-46
505.00
98.92%
98.92%
99.02%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 523)
Walbot, V.
                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays.
                                                                                                                                                                                                                                    97
                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST.
                                                             Source
                                                                                                                                                                                                                                                                                  ..
02
.
                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
DEFINITION
                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KESULT 4
AW331212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

214

80

9

20

Ą

```
A1964458 496 - Stressed shoot cDNA library from Wang/Bohnert lab zea mays cDNA, mRNA sequence.
A1964458 A2964458 A195757171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays.

Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

Spermatophyta; Magnoliophyta; Liliopsida;

Sea.

1 (bases 1 to 481)

Walbot,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GlypheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGluGlu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="gea mays"
/outivar="B73"
/cultivar="B73"
/clone_lib="496" - stressed shoot cDNA library from
/clone_lib="496" - stressed shoot cDNA library from
/knsy_Bohnert_lab"
/tissue_type="seedling"
/dev_stage="seedling"
/dev_stage="salt stress"
/lab_host="E.coli XL Gold"
/note="crgan: shoot; Vector: pBluescriptII SK(+) XR;
/more_lorgan: shoot; Vector: BBluescriptII SK(+) XR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466
93
0
1
Contact: Walbot V
Department of Biological Sciences
Stanford University
Stanford University
Fas: 650 723 227
Fax: 650 728 8221
Fax: 650 728 8221
Fax: 640 728 8221
Fax: 640 728 8221
Fax: 650 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-090-035-4 (1-93) x AI964534 (1-466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.2e-46
499.50
98.948
97.948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
AI964458/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
COMMENT
                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. No. .
                                                                                                                                                                                                                  FEATURES
           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1964534 496 - stressed shoot cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence.
A1964534
A1964534.1 GI:5757247
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="bHi0B"
/note="corgan: tassel, kernel, silk, husk, root, leaf;
/note="corgan: tassel, kernel, silk, husk, root, leaf;
/note="corgan: tassel, kernel, root, leaf;
/octor: pGADIO, Site_1: ECORI: cDNA library from fully
/differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
plant. root, leaf). Unidirectionally cloned.

1 others
                                                                                                                                                                                                                                                                                                                                (SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 524
/cultivar="w23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walbot,V.
Malze ESTs from various cDNA libraries sequenced at University Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524
0
0
0
                                                    Stanford University
855 California Ave, Palo Alto, CA 94304, USA
7261: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707009 row: E column: 07.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                           Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-4 (1-93) x AW288876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.58e-46
505.00
98.92%
98.92%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
AI964534/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment
                                                                                                                                                                                                                  FEATURES
```

g

셤

ò

ð 셤 q ð g οy

ò

us-10-090-035-4.rst

```
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays
                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
AA979839
LOCUS
DEFINITION
                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
COMMENT
                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI855425
603016F02.x1 603 - stressed root cDNA library from Wang/Bohnert lab
Zea mays cDNA, mRNA sequence.
AI855425
AI855425.1 GI:5499558
                                                                                                                                                                                                                                                                                                                                                     60 GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 539) Walbot, V.
                                                                              1. .481
/organism="Zea mays"
/outlivar="873"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="496 - stressed shoot cDNA library from Wang/Bohnert lab"
/tissue_type="seedling"
/dev_stage="salt stress"
/lab_host="E.col1 XL Gold"
/note="Organ: shoot; Vector: pBluescriptII SK(+) XR; Wang/Bohnert!
/a 148 c 154 g 97 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481
0
0
1
                 CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Stanford University
855 California Ave, Palo Alto, CA 94
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 496010 row: H column: 04.
                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                             US-10-090-035-4 (1-93) x AI964458 (1-481)
                                                                                                                                                                                                                                               9.53e-46
499.50
98.94%
98.94%
97.94%
                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
A1855425/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
COMMENT
                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                     ç
                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                   윱
                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
```

```
PRATEGORY TO THE TABLE STATE OF THE TABLE STATE STA
```

```
41 Valaspībivalserargalaglyalaasn---Hishishishishishishishishishishishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001) on May 25, 2001 this sequence version replaced gi:14206705. Contact: Patrick S. Schnable Schnable Laboratory
                                                                                                                           Town State University

Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, 18-15:15-294-0975
Fax: 515-294-299
Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T7-1 (AA TAC GAC TCA CTA TAG).
LOCATIOn/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             550
93
0
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="12004-TN"
/tissue_type="Seedling and silk"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                               /cultivar="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-090-035-4 (1-93) x BG840383 (1-550)
                                                                                                                                                                                                                                                                                                                                             /organism="2ea mays"
                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MEST12-H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.11e-45
499.50
98.94%
98.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN.
                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
AY104409
              AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                  /clone_in="missize"/
/clone_in="missize"/
/clone_in="missize"/
/dev_stage="Tsow="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="xii.wFR Blue"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG840383 550 bp mRNA linear EST 29-MAY-2001
MEST12-H11.T7-1 ISUM4-TN Zea mays cDNA clone MEST12-H11 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 GGCCACGGCTTCGTGGTGCGCGGAGACCAGGGTCGAGGAGGAGAACATCAACACCTGCACCGGC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                        PCR PRIMERS
FORWARD: T7-YJ (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
BALE: MEST2 row: B column: 7
Seq primer: tw/412 (5'-GAAGATACCCCACCAAACC-3').
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546
00
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                 /db_xref-"taxon:4577"
/clone="MEST2-B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-090-035-4 (1-93) x AA979839 (1-546)
                                                                                                                                                              /organism="Zea mays"
                                                                                                                                                                              /cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:14242676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1e-45
499.50
98.94%
98.94%
97.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
BG840383
BG840383.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
BG840383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

~

```
sequence.
BQ619167
BQ619167.1
                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ619315
BQ619315.1
EST.
                                                          Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                  . No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
BQ619315
                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
      HTC 25-MAY-2002
                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panticoideae; Andropogoneae; Zea.

( Dases 1 to 553)

Hainey, C. F., Dolan, M., Miao, G. H., Vogel, J. M., Whitsitt, M.S., Arthur, L.M., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"this sequence is part of a project of EST assemblies resulting from the application of public contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Ins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ619167 648 bp mRNA linear EST 27-JUN-2
RNOSEQ4E05_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                     /clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
                                                                                                                                                                                                       Direct Submission
Submitted (22-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553
00
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
    mRNA
                                                                                                                                                                                                                                                         1. .553
/organism="zea mays"
/db_xref="maizeab.637271"
/db_xref="taxon:4577"
/clone="PCO124784"
Zea mays PCO124784 mRNA sequence. AX104409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-4 (1-93) x AY104409 (1-553)
                                                                                                                                                                                                                                                                                                                                                                                                                162 g
                                 AY104409.1 GI:21207487
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.11e-45
499.50
98.94%
98.94%
97.94%
                                                                                                                                                                         Unpublished (2002)
2 (bases 1 to 553)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                          Zea mays.
                                                                    Zea mays
                                                                                                                                                                                                 Coe, E.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
       DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ619167
LOCUS
DEFINITION
                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                          AUTHORS
                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
:SM Zea mays

Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cladd; Panicoideae; Andropogoneae; Zea.

S Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2126554473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .648
/organism="zea mays"
/db_xref="taxon:4577"
/dlone="RNSE405_SK.abl"
/clone="RNSE405_SK.abl"
/clone=lib="Salt stressed Zea mays roots cDNA library"
/dev_stage="Roots"
/note="vector: pBluescript SK+; Stressed 24 hours at 150
mM Nacl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ619315
RNOSEDGCO6_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEDGCO6_SK.abl similar to No homology, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      648
00011
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                     Email: bohnertlab@life.uluc.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-090-035-4 (1-93) x BQ619167 (1-648)
                                                                                                                                                                                                                                                                                                                                                                              183 g
GI:21621161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:21621309
                                                                                                                                                                                                                                                                                                                                                                                                                                    1.33e-45
499.50
98.94%
98.94%
                                                                                                                                                                                                                                                                                                                                                                                193 c
```

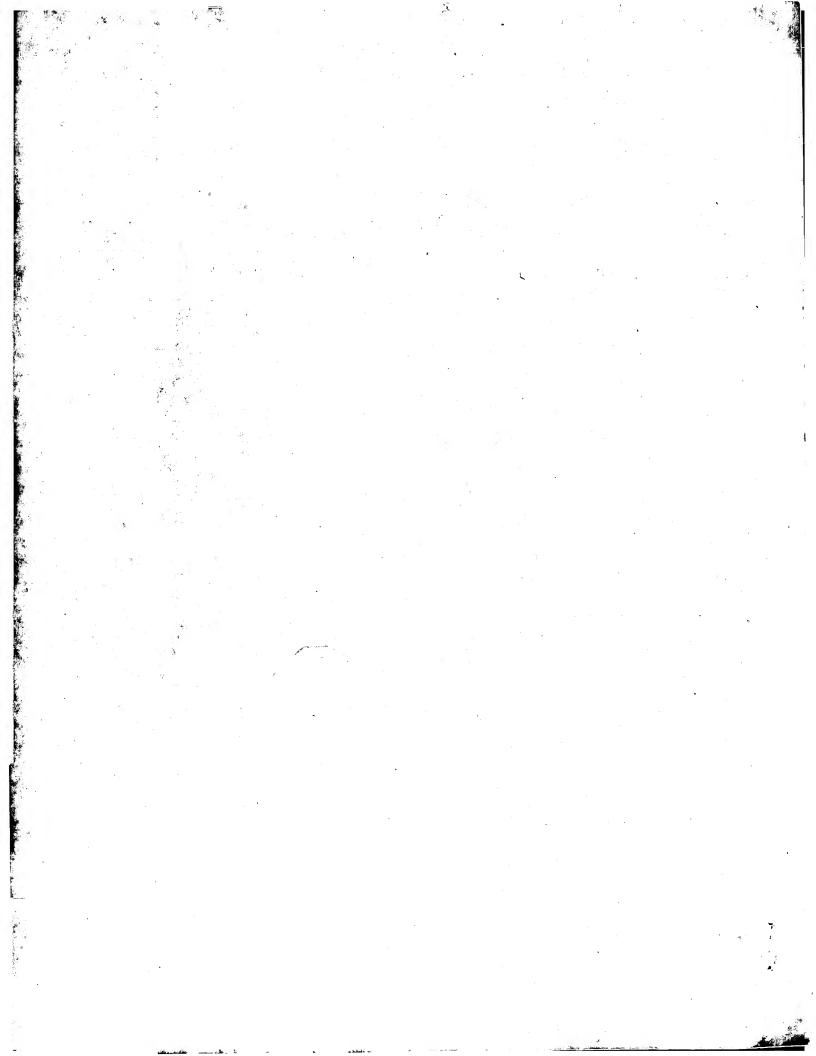
The state of the land

```
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
BQ619337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
JOURNAL
                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ619318 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6D01_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6D01_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; 2ea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; 2ea.
                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RNOSE06060_SK.abl"
/clone_lib="Salt stressed Zea mays roots cDNA library"
/tissue_Lype="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyPheGlyArgHisGlyGlyValGlnGlnHisValValLysGluLysPheGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluvalHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648
93
0
1
1
                                                                              | Leases | 1 to 648 |
| Wang, H. and Bohnert, H.J.
| Genomics of plant stress tolerance
| Unpublished (2002) |
| Contact: Mark Fredricksen |
| Contact: Mark Fredricksen |
| Department of Plant Biology |
| University of Illinois |
| 1201 W Gregory Dr., Urbana, IL 61801, USA |
| Tel: 217265547 |
| Email: bohnertlab@life.uluc.edu. |
| Location/Qualifiers |
| Corganism="Zea mays" |
| Corganism="Ze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-090-035-4 (1-93) x.BQ619315 (1-648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:21621312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.33e-45
499.50
98.948
98.948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mM NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
BQ619318
BQ619318.1 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
BQ619318
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
```

```
BQ619337 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6E12_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endangles, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 648)
Mang, H. and Bohnert, H.J. Genomics of plant stress tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                    at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mays roots cDNA library"
                                                                                                                                                                                                 Stressed 24 hours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648
93
0
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W. Gregory Dr., Urbana, IL 61801, USA 2172655473
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217265573
Email: bohnertlab@life.uiuc.edu.
                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                     /note="Vector: pBluescript SK+;
mm Nac1"
                                                                                                         1..648
/organisme"Zea mays"
/db_xref="taxon:4577"
/clone="RNOSEQ6D01_SK.abl"
/clone_lib="Salt stressed Zea ma
/tissue_type="Roots"
/dev_stage="2 weeks old"
                                                                                                                                                                                                                                  . 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W Gregory Dr., Urbana,
Tel: 2172655473
                                                                                                                                                                                                                                                                                                                                                                                 US-10-090-035-4 (1-93) x BQ619318 (1-648)
                                                                                                                                                                                                                                183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:21621331
                                                                                                                                                                                                                                                                                       1.33e-45
499.50
98.948
98.948
                                                                                                                                                                                                                                   193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ619337.1
                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ619337
```

```
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
1. '648
/ organism="Zea mays"
/ db_xref="taxon:4577"
/ clone="RNOSEQ6E12_SK.abl"
/ clone=lib="salt stressed Zea mays roots cDNA library"
/ tissue_type="Roots"
/ dev_astage="2 weeks old"
/ note="Vector: pBluescript SK+; Stressed 24 hours at 150
mM NaCl"
                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                     100 t
                                                                                                                                                                                                    US-10-090-035-4 (1-93) x BQ619337 (1-648)
                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: June 16, 2003, 12:16:36 Job time : 1296.5 secs
                                                                                                    183 g
                                                                                                                                       1.33e-45
499.50
98.94%
98.94%
                                                                                                   193 c
                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                   172
                                                                                                                             Alignment Scores:
                     source
                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                      Pred. No.:
          FEATURES
                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                    ö
```



```
ALIGNMENTS
                                                                               | BQ619337
| BQ619380
| BG840383
| AM785732
| AW787314
| BE129897
| BE129897
| BE129897
| BE129897
| BE129897
| BE129694
| AW78314
| AW784314
| AW784314
| BE2590123
| BE2590123
| BES590123
| BES590123
| BES590123
| BES590123
| BES990123
| BES9901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW924579
W21677
                                                                  500.6
500.6
500.6
6494.6
6494.6
6465.8
6461.8
6461.8
6411.2
626.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417
411.4
411.4
421.6
326.6
324.8
308.2
308.2
307.2
307.2
201.4
272.2
251.4
272.2
251.4
272.2
251.4
272.2
251.4
272.2
251.4
272.2
251.4
272.2
251.4
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
272.2
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
AY104409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                °,
                                                                                                                                                                                                       June 16, 2003, 01:23:01; Search time 1222.39 Seconds (Without alignments) 7604.943 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 acceaegegteegeceaege......aaaaaaaaaaaaaaaa 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
                                                                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est2:*
gb_ntc:*
gb_est3:*
gb_est4:*
gb_est5:*
em_est5:*
em_est6m:*
gp_gss:*
em_gss_lnn:*
                                                                                                                                                                                                                                                                                                                                                                              US-10-090-035-3
574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          em_esthum:*
em_esthum:*
em_estin:*
em_estov:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
```

Database :

Sequence:

Run on:

Searched:

BO619315 RNOSEOGCO BO619318 RNOSEOGED BO619318 RNOSEOGDED BO619318 RNOSEOGNED BO619318 RNOSEOGNED BO619310 RNOSEOGNED BO619310 RNOSEOGNED AW787732 945002E06 AW787314 945002E06 BE129897 945002E06 BE129897 945002E06 BE129897 945002E06 BE129897 945002E06 BE129844 945002E06 BE255008 945002E06 BE255008 945002E06 BE255008 945002E06 BE255008 945002E06 BE256013 PRI 14 BE AW745416 WSI 14 BO AW745416 WSI 14 BE BESS913 PIL 16 CO AW680016 WSI 14 BE BESS913 PIL 16 CO AW670969 WSI 14 BE BESS9138 PIL 16 ED BESS9507 WSI 16 ED BESS9507 WSI 10 ED BESSSO FIL 16 ED BESSS

z z	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	# A E O		<pre>vullitted (27-APR-2002) Maize Mapping Project, University of     Missouri, Columbia, MO 65211, USA     Location/Qualifiers     1553     /organism="zea mays"     /db_xref="maizeDB:637271"     /clone="PCO124784"</pre>
DEFINITION ACCESSION VERSION KEYWORDS SOUNCE ORGANISM	REFERENCE	AUTHORS	JOURNAL REFERENCE AUTHORS TITLE	FEATURES SOURCE
		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Describtion	AY104409 Zea mays BE025302 945028B09 AA979839 MEST2-B7 AW288876 707009E07 AW331212 707049E04 BQ619167 RNOSEQ4E0
em_gss_hum:* em_gss_luv:* em_gss_luv:* em_gss_vrt:* em_gss_vrt:* em_gss_mem:*	em_gss_other:* em_gss_pro:* em_gss_rod:*	mber of results predictor or equal to the score on alysis of the total sc	SUMMARIES Query Match Length DB ID	553 11 AX104409 552 10 BE025302 546 9 AA979839 524 10 AW328876 523 10 AW331212 648 14 BQ619167
	25: em_9 26: em_9 27: em_9	Pred. No. is the nu score greater than and is derived by a	t Ouery Score Match Len	1 521.2 90.8 2 518 90.2 3 509.6 88.8 4 507.2 88.4 5 500.8 87.2 6 500.6 87.2

Š. Result

```
AA979839 S46 bp mRNA linear EST 26-MAY-1998
MEST2-B7.TW1412.Seq ISUM2 Zea mays CDNA clone MEST2-B7 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: tassel, kernal, silk, husk, root, leaf; /note="Organ: tassel, site_1: EcoRI; cDNA library from fully differentlated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIGCTIGCCTGCGTGCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 CGACGTCACACGGGCGCTGCGCACAGACACCAAGCGTCGGCACCAATGGCTTACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AGGAGGTGGACTACTGGTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCCGGCTTCGGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HILLI | HILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACGCGCCGGCCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGG
                                                                                                                                                                                                                                             /db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot.lab,
same as 707 (SK)"
                                                                                                                                                                                                                                                                                                                  silk, husk, root, leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 518; DB 10;
Pred. No. 5.1e-68;
0; Mismatches 5;
                                                                             94304,
                                                                                                                                                                                                                                                                                                                  /tissue_type="tassel, kernal,
/dev_stage="fully-grown"
/lab_host="DH10B"
                 Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave. Palo Alto, CA 94
Tel: 650 723 227
Fax: 650 725 8221
Email: Walbot @stanford.edu
Plate: 945028 row: B column: 09.
                                                                                                                                                                                                                         /organism="Zea mays"
/cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; illarity 99.0%; Conservative 0
    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 521; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
AA979839
LOCUS
DEFINITION
                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
      JOURNAL
COMMENT
                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552 bp mRNA linear EST 07-JUN-2 adult tissues from Walbot lab, same as sequence.
                                               "Jose" this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Malze Mapping Project" 90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGCTTCCTCGCCAGGGCTAACTGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 GIGGCCCCGGCCGGCTTCGGCCGCCGCCGCGGCGTCCAGCAGCACGTCGTCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCACCACGGCGACCGCCTTCGTGGTGCGGGAGACCAGGGTCGAAGAGGACATCAAC
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
                                                                                                                                                                                                                                  Score 521.2; DB 11; Length 553;
Pred. No. 1.7e-68;
0; Mismatches 8; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE025302
945028B09.Yl 945 - Mixed
(SK) Zea mays cDNA, mRNA
BE025302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE025302.1 GI:8318737
                                                                                                                                                                                                                                          sch 90.8%;
al Similarity 98.0%;
539; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561 AAAAAAAA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAAAAA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
BE025302
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
```

셤

QQ à ద à

g ŏ g · Š g ò 셤

å

δ

ö

108

9

168 120 180 288

m

392 365 452

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Strantophyta; Balvaryota; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panlcodeae; Apdropogoneae; Zea.

1 (bases 1 to 524)

Walbot, V.
Malze ESTs from various cDNA libraries sequenced at Stanford University
University
University
Department of Biological Sciences
Stanford University
Stanford University
Basc California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 723 2227
Fax: 650 728 8221
Email: walbot estanford.edu
Plate: 707009 row: E column: 07.
                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA linear EST 16-JAN-2000 tissues from Walbot lab (SK) 2ea
                                                                                         /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="bullo"
/note="organ: tassel, kernel, silk, husk, root, leaf;
/note="organ: tassel, kernel, silk, husk, root, leaf;
/octor: pGADIO; Site_1: EcoRI; cDNA library from fully
differentiated malze tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."

a 170 c 157 g 89 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 CCGCACAGCAATCCACACAAGCACTTCGACGTCACGGGGGGGCTGCGCACAGACACACA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 GAGGICCACGAGCGCAGGGAGGTICCICGCCAGGGCIAACIGAGCCGCCGGCGGGCG
                        /db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 507.2; DB 10; Length 524;
Pred. No. 2.1e-66;
0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          524 bp
707009E07.x4 707 - Mixed adult t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .524
/organism-"Zea mays"
/cultivar-"W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

Best Local Similarity 99.0%;
Matches 520; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW288876.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays
                                                                                                                                                                                                                                                                                    573 A 573
                                                                                                                                                                                                                                                                                                                      A 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
                                                                                                                                                                                                                                                                                                                  546
                                                                       393
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
AW288876
                               ద
                                                                       ò
                                                                                                 g
                                                                                                                                          ò
                                                                                                                                                                      a
                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon.4577"
/clone="MEST2-B7"
/clone="MEST2-B7"
/clone="Lib="150M2"
/tlssue_type="above ground tissues"
/tlssue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="kli-MrR Blue"
/note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
ECORI; Site_2: xhoi; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dr selected mRNA by prining with an xhoi oligo-dr primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors; the resulting molecules were directionally cloned into the ECORI and Xhoi sites of the HybrizAP lambda vector
(Stratagene) and excised as RP thoras I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTTCGGCCGCCACGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 CACACAAGCACTTCGACGTCACACGGGCGCTGCGCACAGAACACCAAGCGTCGGCACCA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACCGGC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGACATCAACACACCTGCACCGGC 305
                                                                                  Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Pancoldene; Andropogoneae; Zea.

1 (bases 1 to 546)

S Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings
Contact: Schnable, PS
Schnable laboratory
Iowa State University
G405 Agronomy, Ames, IA 50011, USA
Tel: (515)-294-0975
Fax: (515)-294-0975
Email: schnable@lastate.edu
PCR PRIMETS
FORWARD: TAJA12 (5'-GAAGATACCCCACCAAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACCCACTATAGGGC-3')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 88.8%; Score 509.6; DB 9; Length 546; al Similarity 97.6%; Pred. No. 9e.67; 528; Conservative 0; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                         Plate: MEST2 row: B column: 7
Seq primer: tw1412 (5'-GAAGATACCCCACCAACC-3').
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .546
/organism="Zea mays"
/cultivar="B73"
                          GI:3157217
   AA979839
AA979839.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 528; Conserv
                                                        Zea mays.
                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273
                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

(SK

us-10-090-035-3\_1.rst

```
BQ619167 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ4E05_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                         482
                                                                      ö
                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                        422
                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 AACCACCACCACCACGATGGTCACCACGGCGACGGCTTCGTGGTGGGGGGCACCAGG 302
                                                                                                                                                                                                                                                                                                      362
                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                     423 GCCTTAIGTATGICIGIGGTIGACIGGIIGITCAGGGICAICGIACTIGGCIAICGIACG
                                                                                               63 CGCIGCGCACAGACACCAAGCGICGGCACCAAIGGCITACIACCAGGAGGIGGACIAC
                                                                                                              Gaps
                                                                      ö
                                               523;
Unidirectionally cloned.
                                                 Length
                                            Score 500.8; DB 10; Length
Pred. No. 1.9e-65;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
1. cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 TTCGTAATACTAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/db_xref="taxon:4577"
 t, root, leaf).
158 c 149 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ619167
BQ619167.1 GI:21621161
                                                   87.2%;
98.6%;
                                                                            Conservative
    husk,
                                                                 1 Similarity
505; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays.
                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
                125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482
                                                                                                                                                                                                          183
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                     Best Local
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
BQ619167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                       р
                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                 ద
                                                                                                                                                                                                                                   Ωp
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                용
                                                                                                                                                         δ
                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                       p mRNA linear EST 31-JAN-2000
tissues from Walbot lab (SK) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="2ea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
/note="Organ: tassel, kernel, silk, husk, root, leaf;
dector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                              202
                                                                                179
                                                                                                          262
                                                                                                                                  239
                                                                                                                                                            322
                                                                                                                                                                           140 TCACCACGCCGCCCACGCCTTCGTGGTGCGCGGAGACCAGGGTCGAAGAGGACATCAACAC 299
                                                                                                                                                                                                               382
                                                                                                                                                                                                                           443 IGACIGGIICITCAGGGICATCGIACIIGGCIAICGIACGIGCACGCACGCACICAGCICCIGI 502
         142
                                                                      TCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGGGTCGAAGAGGACATCAACAC
                                                                                                                                                                                                             CTGCACCGGCGAGGTCCACGAGGGAGGGTTCCTCGCCAGGGCTAACTGAGCCGC
                     GGTGGCCCCGGCCTTCGGCCGCCGCGCGCGCGCGTCCAGCACGTCGTCAAGGA
        AGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                   ACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Walbot V
Department of Biological Sciences
Stanfornia Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707049 row: E column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize ESTs from various cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                           523 bp
707049E04.xl 707 - Mixed adult t
mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW331212.1 GI:6827569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1, .523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                          503
                                                                                                                                                                                                                                                                                                                                                                                                 480
                                                                                                                                                                                                                                              300
                                      9
                                                                143
                                                                                        120
                                                                                                                 203
                                                                                                                                         180
                                                                                                                                                                   263
                                                                                                                                                                                                                     323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
AW331212
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
```

ð a

g δ 셤 ò g õ a

g å

셤 ŏ

쉱 ò

```
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
BQ619318
BQ619318.1
                                                                                                                                                                                                                                                                                                                                                                                                  AAA 574
                                                                                                                                                                                                                                                                                                                                                                                                               AAA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST.
Zea mays.
                                                                                                                                                                               95
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                             452
                                             source
                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
BQ619318
                                                                                                                                                                 셤
                                                                                                                                                     à
                                                                                                                                                                               ò
                                                                                                                                                                                           g
                                                                                                                                                                                                          ö
                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                           ;
;
                                                                                                             BQ619315
RNOSEQ6C06_SK.abl Salt stressed Zea mays roots cDNa library Zea mays cDNA clone RNOSEQ6C06_SK.abl similar to No homology, mRNA sequence.
                                                                                                                                                                   CGGCTTCGGCCGCCACGGCGGCGGCGTCCAGCAGCACGTCGAAGGAAAGTTCGAGGA 214
                                                                                                                                                451
                                                                                                                                                                                                                                                                                             500
                                                                                                                                                                                                                                                          511
                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
                                                                                        94
                                                                                                     80
                                                                                    CACACAAGCACTTCGACGTCACACGGG-CGCTGCGCACAGAAACACACAAGCGTCGGCACC
                                                                                           Gaps
                                                                           .,
4
                                                             DB 14; Length 648;
                                                                           Indels
                                                          87.2%; Score 500.6; DB 14;
llarity 97.6%; Pred. No. 1.8e-65;
Conservative 0; Mismatches 9;
                                         100 t
                                        183 g
                                                                                                                                                                                                                                                                                                                                                                                                                  GI:21621309
                                        193 c
                                 mM NaCl"
                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          BQĞ19315
BQ619315.1
                                                                                                                                                                                                                                                                                                                                         572 AAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                Lea mays.
                                                                       530;
                                                                                     36
                                                                                                                                         155
                                                                                                                                                                                                                                                  392
                                                           Query Match
                                                                                                                                                                                                                                                                                                                                               561
                                                                 Local
                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
BQ619315
LOCUS
DEFINITION
                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                               Q
                                                                                    à
                                                                                                              ð
                                                                                                                        8
                                                                                                                                     õ
                                                                                                                                                    요
                                                                                                                                                                   ò
                                                                                                                                                                              g
                                                                                                                                                                                                       g
                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                    g
                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                            8
```

```
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Locatlon/Qualifiers
1. 648
//organism="Zea mays"
//db_xref="taxon:4577"
//clone="RNOSEQGCO6_SK.abl"
//clone="RNOSEQGCO6_SK.abl"
//clone="lib="Salt stressed Zea mays roots cDNA library"
//clone="lib="Salt stressed Zea mays roots cDNA library"
//dev_stage="2 weeks old"
//ore="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ619318 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6D01_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6D01_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                214
                                                                                                                                                                                                                                                                                                                                                                                                     154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                        332 CGAGGTCCACGAGCGCAGGGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGGCCCGCCGGCGGCCCAGGGTAACTGAGCTCACGAGGCCCGGCGGCCCAGGGCAGGGCCCAGGGCAGGGAGCTTCCTCGCCAGGGCTAACTGAGCCGCGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 CACACAAGCACTTCGACGTCACACGGG-CGCTGCGCACAGACACACCAAGCGTCGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                 AATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 GGTCGACACGGTCTCACGCGCCGCCCA---ACCACCACCACCACCATGGTCACCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTCAGGGTCATCGTACTTGGCTATCGTACGTGCACTCAGCTCCTGTACGAATTAC
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                              183 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:21621312
                                                                                                                                                                                                                                193 c
                                                                                                                                                                                                                                                                                         Local Similarity ,... hes 530; Conservative
                                                                                                                                                                                                                mM NaCl"
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
  Examples and seek and seeks of the seeks of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GITCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATTAC 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGGICCACGAGGCAGGGAGGTICCICGCCAGGGCIAACIGAGCCGCCGGCGGCC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCCACGGCTTCGTGGTGCGGGGGCCAGGGTCGAAGAGGACATCAACACCTGCACCGG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGGCCCCGGC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCTTCGGCCGCCGCGGCGGCGTCCAGCACCACGTCGTCAAGGAGATTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 CGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGAGGAGTATCAACACCTGCACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 500.6; DB 14; Length
Pred. No. 1.8e-65;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sch 87.2%; al Similarity 97.6%; 530; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                            NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572 AAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORGANISM
                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . ŏ
```

σ

RESULT

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 AATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214
                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                       Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/db.zref="taxon:457"
/db.zref="taxon:457"
/clone="RobSE6E1_SK.ab1"
/clone=lib="Salt stressed Zea mays roots cDNA library"
/tissue_rype="Roots"
/dev_stage="2 weeks old"
/note="vector: pBluescript SK+; Stressed 24 hours at 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCCACGGCTTCGTGCTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 CGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGAGAATCAACACTGCACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGGTCCACGAGGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 GITCAGGGICAICGIACTIGGCIATCGIACGIGCACGCACTCAGCICCIGIACGAATIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCTTCGGCCGCCACGGCGGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGA
                  RNOSEQGEL2_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQGEL2_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 500.6; DB 14;
Pred. No. 1.8e-65;
0; Mismatches 9;
                                                                                                                                                                                                                                                            61801, USA
         mRNA
                                                                                                                                                                  Wang, H. and Bohnert, H.J.
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  100
        648 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                  183 9
                                                                           GI:21621331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 87.2%;
sal Similarity 97.6%;
530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   193 c
                                                                                                                                                                                                                                                                                                                                                                                                                       mM NaCl"
                                                                                                                                                                                                                                                                                                                  1. .648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 530; Conserv
                                                                BQ619337
BQ619337.1
                                                                                                      Zea mays.
Zea mays
                                                   sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                      172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141
                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
            LOCUS
DEFINITION
                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                     FEATURES
BQ619337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

GGCATCCACGCCGTTCGTGCTTGCCTGCGTGCTTATGTATG	44; 512 501 572 572 561		CREANLSM Zea mays  CREATUSM Zea mays  CLEATYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnollophyta; Liliopsida; Poales; Parcheophyta; Clade; Panicodeae; Andropogoneae; Zea.  CLAGE; Panicodeae; Andropogoneae; Zea.  (Dases I to 648)  TITLE  TITLE  Genomics of plant stress tolerance  JOURNAL  COMMENT  CONTACT: Mark Fredricksen  COMMENT  CONTACT: Mark Fredricksen  Department of Plant Blology  University of Illinois  1201 M. Gregory Dr., Urbana, IL 61801, USA	Tel: 217255473  FEATURES  Location/Qualifiers  Source  //organism="2.ge mays" //organism="2.ge mays" //ord yref="textor.id"		Query Match Query Match Best Local Similarity 97.0%; Pred. No. 1.8e-65; Matches 530; Conservative 0; Mismatches 9; Indels 4; Gaps 2; Qy 36 CACAAGCATTCAACGTCAACGGTCAACGCAAGACAACAAAGGTTCGCGTCGCCCACAACACAAAGGTTCGCCCCACACAAA	Db   21 CAGAGAGACATCGAGGCCGCTGCACACACACACACCACCCCCCCC
	RESULT 10 BQ619383 LOCUS BQ619383 LOCUS BQ619383 EQCUS BG619383 FINITION RNOSEQ7802_SK.abl Salt stressed Zea mays roots cDNA library Zea mays CDNA clone RNOSEQ7802_SK.abl similar to No homology, mRNA ACCESSION BQ619383 VERSION BQ619383. GI:21621377 KEYWORDS	Σ	University of Illinois 1201 W. Gregory Dr., Urbana, IL 61801, USA 1201 M. Gregory Dr., Urbana, IL 61801, USA Tel: 2172655473 Email: bohnertlab@life.uiuc.edu. Location/Qualifiers 1. 648	/note="Vector: pBluescript SK+; Stressed :nm Nacl" INT 172 a 193 c 183 g 100 t	Query match Best Local Matches 53 36 21	U	QY         215 GGTCGACACGGTCTCACGCGCCCCAACCACCACCACCACCACCACGG 271           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

```
86.2%;
ilarity 97.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 539)
                                                                                  al Similarity
524; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
                                          Ø
                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                   452
                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
AI855425/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                        8
                                                                                                                                                                 ò
                                                                                                                                                                                     ద
                                                                                                                                                                                                          ò
                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST12-H11.T7-1 ISUM4-TN 2ea mays CDNA clone MEST12-H11 5', mRNA sequence.
BG840383
BG840383.2 GI:14242676
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (basea: 1 to 550)
1 (basea: 1 to 550)
2 (ui.F., Cui.F., Guo.L., Ashlock, D.A, Wen.T.J. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14206705.
Schnable Laboratory.
                                                                                                                                                                          331
                                           391
                                                                380
                                                                                       451
                                                                                                             440
                                                                                                                                             Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
                                                                                       CGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGG
          CGAGGTCCACGAGGCAGGGAGGTTCCTCGCCAGGGCTAACTGAGCCGCCCGGCGGCC
                                                       GITCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR PRIMERS
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T7-1 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TCA CTA TAG).
1. .550
1. .550
//organism-"Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4577"
/clone="MET12-H11"
/clone=lb="ISDM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                           AAA 574
                                                                                                                                                                                                                                                AAA 563
                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                                 561
                                                332
                                                                    321
                                                                                          392
                                                                                                               381
                                                                                                                                      452
                                                                                                                                                           441
                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                 RESULT 12
BG840383
LOCUS
                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

à g

qq

임 ŏ g ά g ò g

ò

```
AI855425 539 bp mRNA linear EST 15-JUL-1999 603016F02.x1 603 - stressed root cDNA library from Wang/Bohnert lab
resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT/T13PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)." I others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373
                                                                                                                                                                                                                                                                                                                                               193
                                                                                                                                                                                                                                                                                                                                                                              271
                                                                                                                                                                                                                                                                                                                                                                                                            253
                                                                                                                                                                                                                                                                                                                                                                                                                                           331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133
                                                                                                                                                                                                                                                                                                                 214
                                                                                                                                                                                                                                                      154
                                                                                                                                                                                                           14 CCCACAAGCACTTCGACGTCGCACGCGCGCTGCACACAGAGCACACCAAGCGTCGGCACC 73
                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GITCAGGGICATCGIACITGGCTATCGIACGIGCACGCACTCAGCICCTGIACGAATIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                          155 CGGCTTCGGCCGCCGCCGCGGCGCGCCACCACGTCGTCAAGGAAGTTCGAGGA
                                                                                                                                                                                                                                                                                                                                36 CACACAAGCACTICGACGICACACGG-GCGCIGCGCACAGAACACAAGCGICGGCACC
                                                                                                                                                                                                                                                                                                                                                                                GGTCGACACGGTCTCACGCGCGCGCGCA---ACCACCACCACCACCATGGTCACCACGG
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walbbt,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                            4;
                                                                                                                             Length 550;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 223
Fax: 650 725 8221
                                                                                                                                DB 12;
                                                                                                                               Score 494.6; DB 12;
Pred. No. 1.5e-64;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpulshed (1999)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays cDNA, mRNA sequence.
AI855425
AI855425.1 GI:5499558
```

9

```
/note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio 18 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                           1. .500

/organism="zea mays"
/organism="zea mays"
/organism="sea"
/db.xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)*
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="bH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 CTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGGCGGCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 CCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 CAACCACCACCACCATGGTCACCACGGGGGCCACGGCTTCGTGGTGCGGGAGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 CGCCAGGGCTAACTGAGCCGCCGGCGGCGGCATCCACGCCCGTTCGTGCTTGCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 GTGCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCCTTATGTATGTCTGTGGTTGACTGGTTCAGGGTCATCGTACTTGGCTATCGTAC
              at Stanford
                                                                                                                                                                                                                                                                                                                                                                              Score 485.8; DB 10; Length 500;
Pred. No. 3.2e-63;
0; Mismatches 2; Indela 0;
Maize ESTs ...
University
Unpublished (1999)
Contact: Walbor,
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbor@stanford.edu
Plate: 945002 row: E column: 06.
Location/Qualifiers
'.500
              pednenced
                                                                                                                                                                                                                                                                                                                                                                              84.6%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.6
Matches 487; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481
                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
AW787314
                                                                                                                                            FEATURES
          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                     / ..539
/ Organism="Zea mays"
/ Coultivar="E33" mays"
/ Clone_lib="603 - stressed root cDNA library from Wang/Bohnert lab"
/ tissue_type="seedling"
/ tasue_type="seedling"
/ dev_stage="seell stress"
/ tab_host="E. coli XL Gold"
/ note="Organ: root; Vector: pBluescriptII SK(+) XR;
Seedling stressed root cDNA library from Wang/Bohnert lab"
157 c 172 g 119 t library from Wang/Bohnert lab"
                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                                                                                                                                                                        213
                                                                                                                                                                                                                                                                                                                                                                                                              270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 GCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays.

Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 500)
Walbot, V.
                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                        154 CCGGCTTCGGCCGCCACGCGGCGCGCGCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                       AGGTCGACACGGTCTCACGCGCGCGCCA---ACCACCACCACCACCATGGTCACCACG
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                Length 539;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                          Query Match 86.1%; Score 494.4; DB 9; Best Local Similarity 97.2%; Pred. No. 1.6e-64; Matches 525; Conservative 0; Mismatches 11;
            603016 row: F column: 02
Location/Qualiflers
1. 539
     walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW787732.1 GI:7844510
                                                                                                                                                                        16
  Email:
Plate:
                                                                                                                                                                                                                                                                                                                                                                                                          214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391
                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
AW787732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                           FEATURES
                                                                                                                                                                                                                                                                                 윱
                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
```

ö

Gaps

ő

120

241

301 240 361 300 421 360

420 481

```
/note="Organ: tassel, kernal, silk, husk, root, leaf; vector: pGAD10; Site_1: ECORI: CDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
AW787314 10.000 4496 bp mRNA linear EST 16-MAY-2000 945002E06.X1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.

WAW787314 GI:7844111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCCT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 GGAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCGCCGCGGCGGCGCGTCCAGCA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GGAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGCGGCGGCGGCGGCGTCCAGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 ACCACCACCACCATGGTCACCACGCCGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lea may yota juridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade; Pantcoideae; Andropogoneae; Zea. (Dases 1 to 496)
Walbot,V.
Walbot,V.
Walbot,V.
University
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 CGCACAGACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .496
/organism="Zea mays"
/cultivar="W2"
/db.xref="Ltaxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                              Contact: Walbot V
Department of Biological Sciences
Stanfornia Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 728 821
Email: walbotéstanford.edu
Plate: 949002 row: E column: 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 465.6; DB 10
Pred. No. 3.2e-60;
0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                              Zea mays.
                                                                                                                               Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Loca
Matches
                         DEFINITION
                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                  JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
```

091659 arabidopsis
020691 caenorhabdi
094669 mes musculu
042448 medicago sa
09vx61 drosophila
095124 medicago sa
09vx61 drosophila
094139 oryza sativ
08115 homo saplen
094139 oryza sativ
081754 fagus sylva
094460 drosophila
084696 drosophila
094411 drosophila
09441 drosophila
09441 drosophila
09441 drosophila
09441 drosophila
09445 drosophila
09445 drosophila
09545 emericella
095594 drosophila

10 Q9LF59 5 Q20691 11 Q920691 5 Q9VC84 10 Q9ZH24 10 Q9ZH24 10 Q9ZH24 10 Q9ZH29 10 Q9ZH29 10 Q9ZH29 10 Q9ZH29 10 Q9ZH29 10 Q9ZH29 5 Q9UAFO 5 Q9UAFO 5 Q9UAFO 5 Q9UAFO 5 Q9UAFO 5 Q9UAFO 5 Q9VZH 7 Q9VZH

```
RESULT 1
                                          June 6, 2003, 12:47:53 ; Search time 50 Seconds (without alignments) 383.248 Million cell updates/sec
                                                                          US-10-090-035-4
510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                  671580 seqs, 206047115 residues
                          OM protein - protein search, using sw model
                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                         sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                  SP_invertebrate: *
                                                                                                                                                                                                                                                                                                                                                sp_rv1rus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                         sp_organelle: *
                                                                                                                                                                                                                                                                                                                  sp_rodent:*
                                                                                                                                                                                                                                                                           sp_mammal: *
                                                                                                                                                                                                                                                                                                           SP_plant: *
                                                                                                                                                                                                                           SPTREMBL_21:*
                                                                         Title:
Perfect score:
                                                                                                          Scoring table:
                                                                                                                                                                                                                       Database :
                                                                                           Sequence:
                                                                                                                                  Searched:
                                            Run on:
```

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description			O9sm40 sporobolus			Q9sw63 arabidopsis	024643 arabidopsis	Q9p543 neurospora	Q8s0b4 oryza sativ	Q9uay0 caenorhabd1	Q9y219 homo sapien	0944q7 arabidopsis	O9fz33 arabidopsis	Q9w3d2 drosophila	Q9vvm5 drosophila	090wv0 petromyzon	. Caenorhabd1
SUMMARIES		a :	Q8S0B1	O9SM40	OBSUBS	30000	000000	004640	024643	OBCODA	2000	01000	094407	00500	00000	SOUTH THE PERSON OF THE PERSON	040000	9NES7	
		DB :	10	10	10	2	2	2	2 ~	, <u>-</u>		, 4			C	מו	13	2	
	Query	Length	229	95	102	196	196	250	1245	408	471	793	441	473	1561	168	381	735	
dP	Query	March	53.7	34.7	27.6	18.1	18.1	18.1	17.5	17.0	17.0	16.9	16.5	16.5	16.5	16.3	16.2	16.2	
	or CO		274	177	141	92.5	92.5	92.5	89	86.5	86.5	98	84	84	84	83	82.5	82.5	
	Result No.		(	7	٠.	4	S	9	7	æ	6	10	11	12	13	14	12	16	

RESULT 2 Q9SM40

```
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                  Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Hayashizaki Y., Bowst L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Iam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Ngwai J., Iam B., Lee J.M., Lin J., Liu S.X., Muach H.L., Sakurai T., Nguyen M., Onodera C.S., Palm C.J., Pham P. K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Torlumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R
        AT4936900/C7A10.460.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Beyan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Mayer K.F.X.,
Schueller C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.1%; Score 92.5; DB 10; Length 1 33.8%; Pred. No. 0.013; Live 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Z99707; CAB16766.1;
EMBL; AL161590; CAB80356.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schueller C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                  "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY057683; AAL15314.1;
InterPro; IPR001471; FF_ERF.
ProDom; PF000474; AP2-domain; 1.
ProDom; PF000423; TF_AP2; 1.
SEQUENCE 196 AA; 21392 MW; E423D5570745C9CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-KAY-2000 (TFEMBLrel. 13, Created)
01-KAY-2000 (TFEMBLrel. 13, Last sequence update)
01-JUN-2002 (TFEMBLrel. 21, Last annotation update)
TINY-11ke protein.
C7A10.460 OR A74G36900.
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; 080337; 2GCC.
Interpro; IPR001471; TF_ERF.
Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMIT.
ProDom; PD001423; TF_AP2; 1.
SMART; SM00380; AP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::|: |::
159 INDDLMECSSK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 VEEDINTCTGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SW63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09SW63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09SW63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :
ف
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAYYQE-VDYCSEEVRSVAPAGFGRH-GGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 YYQEVDYCSEEVRSVAPAGFGRHGGGVQOHVVKEKFEEVDTVSRAGANHHHHHGHHGGH
                                                                                                                     Putative glycine-rich protein.
Sporobolus stapfianus (Ressurection grass).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eperatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Chloridoideae; Eragrostideae; Sporobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Neale A.D., Blomstedt C.K., Bronson P., Le T.N., Guthridge K.,

Byans J., Gaff D.F., Hamill J.D.;

Evans J., Gaff D.F., Hamill J.D.;

"The isolation of lowly-transcribed genes which are induced during dessication of the resurrection grass Sporobolus stapfianus.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ242802; CAB61838.1;

"TREALMANDAL PROPERTY."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Subaki T., Matsumotonse(GA3) genomic DNA, chromosome 1, PAC
clone:P0470A12.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003436; BAB90279.1; --
SEQUENCE 102 AA; 11214 MW; 6FF1266B1CDE7768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.6%; Score 141; DB 10; Length 102;
45.8%; Pred. No. 2e-08;
iive 8; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                       8802; CAB61838.1; -.
95 AA; 10668 MW; D756DCE2B68DD85B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0470A12.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0932A6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                      OLYAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 177; DB 10;
Pred. No. 1.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 AA
                                  95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 G--GHG---FVVRETRVE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0932A6
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8S0B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0932A6
ID 099
AC 099
DT 01
```

g

g à

à

g

5

Gaps

11;

us-10-090-035-4.rspt

ς.

Holland

```
Eukaryota; Fung1; Ascomycota; Pez1zomycot1na; Sordarlomycetes;
Sordarialis; Sordarlaceae; Neurospora.
NCBI_TAXID=5141;
                                                                                     [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE U., Algn V., Hoheisel J., Brandt P., Fartmann B., I
Nyaketura G., Mewes H.W., Mannhaupt G.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                               Score 89; DB 3; Length 1245;
Pred. No. 0.29;
     Related to multifunctional cyclin-dependent kinase PHO85
B24H17.10.
                                                                                                                                                                                                                                                                                                                                       ANK repeat; Cyclin; Kīnase; Repeat.
SEQUENCE 1245 AA; 137798 MW; 16BD0F6A04596A9F CRC64;
                                                                                                                                                                        German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL356BJS; CAB92623.1;
HSSP; P42773; IIHB.
                                                                                                                                                                                                                                                                                                            PROSITE; PS50088; ANK_REPERT; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         45 SRAGANHHHHHGHHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                               17.5%;
72.2%;
                                                                                                                                                                                                                    InterPro: IPR002110; ANK. InterPro: IPR004129; GDPD. InterPro: IPR004331; SPX. Pfam; PF00023; ank; 6. Pfam; PF03009; GDPD; 1. Pfam; PF03009; SPX; 1.
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                 SMART; SM00248; ANK; 3
                                      Neurospora crassa.
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8S0B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
Q8S0B4
             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                          5.
                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

WEDLINE-97338147; PubMed-9192694;

A OKAMINO J.K., Caster B., Villarroel R., van Montagu M., Jofuku K.D.;

A OKAMINO J.K., Caster B., Villarroel R., van Montagu M., Jofuku K.D.;

The AP2 domain of APETALA2 defines a large new family of DNA binding

The AP2 domain of APETALA2

The AP2 domain of APETALA2

The AP2 domain of APETALA2

The AP3 domain of AP3 defines

EMBL; A700259; CAA05630.1; -.

DR EMBL; A7003103; AAA49776.1; -.

DR HESP: 08037; 2GCC.

DR FINTS; PR0037; 2GCC.

DR FINTS; PR00367; ETHRSPELEMNT.

DR PRINTS; PR00380; AP2; 1.
                                                                      21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHGH-HGGHGFVVRET--R 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R 69
                         18.1%; Score 92.5; DB 10; Length 196;
33.8%; Pred. No. 0.013;
Live 12; Mismatches 24; Indels 11; Gaps
                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 21, Last annotation update)
11NY-11ke protein (Fragment).
12NY-11ke protein (Fragment).
12NATADIOPSIS thaliana (Mouse-ear cress).
12NATADIOPSIS thaliana (Mouse-ear cress).
12NATADIOPSIS (Tracheophyta: Magnoliophyta: eudicotyledons; core eudicots: Rosidae; NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.1%; Score 92.5; DB 10; Length 259; 33.8%; Pred. No. 0.018; Live 12; Mismatches 24; Indels 11
 21362 MW; 0023D5571345C6A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Terryn N.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 259
259 AA; 28615 MW; 0464949DB6C619DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TINY-LIKE PROTEIN.
                                                                                                                                                                                                                   259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1245 AA.
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                  Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Conservative
                                                                                                                         70 VEEDINTCIGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : :|: |: :
INDDLMECSSK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 VEEDINTCIGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 >259
  196 AA;
                                   Local Similarity
les 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-COLUMBIA;
 SECUENCE
                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                              024643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09P543
09P543;
                                               datches
                                                                                                                                                                                   RESULT 6
024643
ID 0246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09P543
ID 099
AC 009
DT 001
S
                                                                                             셤
                                                                       à
                                                                                                                       ð
                                                                                                                                             8
                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 EEVRSVAPAGFGRH----GGGVQQHVVKEKFEEVDTVSRAGA-----NHH------ 52
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza,
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Coryas sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
Clone:P0470A12."
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003445; BAB90277.1; -...
SEQUENCE 408 AA; 43466 MW; F7E0297877F6D69C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.0%; Score 86.5; DB 10; Length 408; Best Local Similarity 26.9%; Pred. No. 0.15; Matches 25; Conservative 10; Mismatches 15; Indels 43
    Indels
                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0470Al2.2 protein.
  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11: |||
259 HHYGGATAAAYGNASNKOHFTAAAAGHHSSGGH 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                      408 AA.
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            нн---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                  99 QHHGGTG 105
                                                                                                                                                                                                                                                                                                                                                                                                  56 GHHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ecker J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                         셤
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
WILDRE-94150718; PubMed-7906398;
WILDRE-94150718; PubMed-7906398;
WILDRE-94150718; PubMed-7906398;
WILDRE-94150718; PubMed-7906398;
WILDRE-94150718; PubMed-7906398;
WILDRE-94150718; PubMed-790898;
Craxton M., Dear S., Du Z., Dutbin R., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Dutbin R., Favello A., Fulton L., Joar M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P., Donston B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopea A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Rhomas K., Vaudin M., Vaughan R., Waterston R., Waterston R., Waterson A., Weinstock L., Willkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Willkinson-Sproat J., Wohldman P.;
Water S. M. Dof contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GVQQHVVKEKFEEVDTVSRAGANHHHHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels 25; Gaps
                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF125964; AAD14753.1; -. SEQUENCE 471 AA; 50885 MW; BDF30B59A64A985B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Pauley A., Scheet P., Harper M.;
"The sequence of C. elegans cosmid W03G1.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAV-2002 (TrEMBLrel. 20, Last annotation update)
KIAA1016 protein (Fragment).
                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
W03G1.5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               793 AA
                                                  471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                   PRT;
                                                    PRELIMINARY; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 RSVAPAGFGRHGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 PPHHGHHFF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 -- HHGGHGF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.;
                                                                                                                                                                                                                                                                                                                                                               elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9Y2L9
Q9Y2L9;
                                                                  Q9UAYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
Q9Y2L9
                                                     O9UAYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
MEDLINE-99340003; FUDRWG-1UK31UX-3;
MEDLINE-99340003; FUDRWG-1UK31UX-3;
MAYAJAM N., TABRAWA K., SUYAMA M., GARAIN N., Ohara O.;
MAYAJAM N., TABRAWA M., Kotani H., Nomura N., Ohara O.;
MAYAJAM N., TABRAWA M., Kotani H., Nomura N., Ohara O.;
The complete sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The remptor of the coding sequences of unidentified human genes. XIII.
The coding sequences of unidentified human genes.
The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 EVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEE---VDTVSRAGA-----NHHHHH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheur R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Wamann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHH----HGGH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     At1954990/F14C21_5.
At1954990/F14C21_5.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.9%; Score 86; DB 4; Length 793; 32.8%; Pred. No. 0.37; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.5%; Score 84; DB 10; Length 44 36.8%; Pred. No. 0.31; tive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF424609; AAL11602.1; -
SEQUENCE 441 AA; 48816 MW; 520163FE0A8DE447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0BE99CC48C3BB37C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50021; CH; 1.
PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 1 1
SEQUENCE 793 AA; 87801 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.5%
Best Local Similarity 36.8%
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.9
Best Local Similarity 32.8
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
```

ä;

409 DYISEFV-SLLPKSIRR----VAEEPIPEEVQKVLEEAKAGDDHDHHGHGHAHAGY 460

S

```
RC STRAIN-CV. COLUMBIA;

RA MILE-21016719; PubMed-11130712;

RA Theologia A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Theologia B., Ecker J.R., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Cheasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Cheasy T.H., Dewar R.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Rhan S., Khaykin E.,

A Lin X., Liu S.X., Liu Z.A., Luros G.A., Li J.H., Li Y.-P.,

RA Hiltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

W Uterback T., Van Aken S., Vapberg M., Vysotskala V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
A Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
A Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
A Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
A Kaniya A., Karlin Neumann G., Rawai J., Kim C., Lam B., Lin J.,
A Mayers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Shinozaki K.,
R. Full Length cDNA of gene Atlg54990 (GI:15221965).";
B. Lubmitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC064940; AAG00878.1;
DR EMBL; AV07434; AAG51115.1;
DR EMBL; AV07434; AAG51030.1;
377 DYISEFV-SLLPKSIRR----VAEEPIPEEVQKVLEEAKAGDDHDHHGHGHAHAGY 428
                                                                                                                                                                                                                                          Ol-MAR.2001 (TrEMBLrel. 16, Created)
Ol-MAR.2001 (TrEMBLrel. 16, Last sequence update)
Ol-MAR.2002 (TrEMBLrel. 20, Last annotation update)
Ta24cl0.10 protein (Hypothetical 52.4 kDa protein).
Ta4cl0.10 OR F14c2l.51 OR ATIG54990.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicctyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Federapiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologia A., Shinn P., Summitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.5%; Score 84; DB 10; Length 473; 36.8%; Pred. No. 0.34; Live 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 473 AA; 52419 MW; D09124A11565BB23 CRC64;
                                                                                                                                                                                                        473 AA.
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 36.8 hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                     09FZ33
                                                                                                             RESULT 12
                                                                                                                                               09FZ33
                                                                                                                                                                                     ID DAT THE READ TO THE READ TO THE READ THE READ
```

```
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Ramaratides P.G., Scherer S.E., II P.W., Hoskins R.A., Galle R.F.,
Recorge R.A., Lewiss S.E., Richards S., Ashburner W., Henderson S.N.,
RA Brandon R.C., Rogers Y. H.C., Blazel R.G., Champe M., Feiffer B.D.,
RA Brill J.F., Adbayuni A., An H.J., Andrews Prannkoch C., Baldwin D.,
Ballew R.M., Basu A., Bacendale J., Bayrakaroglu L., Bassley E.M.,
Ballew R.M., Basu A., Bacman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Bayrakaroglu L., Bassley E.M.,
Borkova D., Botchan M.R., Bauler H.J., Andrews Prannkoch C., Baldwin D.,
RA Borson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Baltler H., Cadleu E., Center A., Chandra I.
RA Borkova D., Botchan M.R., Buller H., Cadleu E., Center A., Chandra I.
RA Durbin S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Durbin K.J., Evangelista C.C., Ferrac C., Ferriere S., Pelasforman W.,
RA Baris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kaff C., Kravitz S., Kulp D., Lal Z.,
Lasko P., Lel Y., Lewischy R.A., Li J., Li Z., Linn Y., Lin X.,
Alu X., Mattel B., McIntoon T.C., McIeodo W.P., McPherson D.
RA Ranner R., Realman G.S., Pan S., Pollard J., Honsy C.,
RA Raler R., Reland G.B., McIntoon R., Paceler F., Shen H.,
RA Relart K., Remington K.A., Mayon W. N., Pollard J., Honsy C.,
RA Raler R., Reland G.B., McIntoon R., Strogel R., Welson D.R., Wang X.,
RA Relnert K., Remington K., Strogel W., Strogel R., Raler R., Spier E., Spradling A.C., Stapleron W., Stroge R., Welson D.R., Wang X.,
RA Belazzolo M., Warrey B.W., Rollon W., Strong R., Wang X.,
RA Harliams S.M., Woodage T., Worley C., Wu D., Yang S., Zhu X., Smith H.O.,
RA Bennone sequence of Drosophila melanogaster.";
R. Schence 287:188-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1561 AA; 174616 MW; 10BFD38A3DD4FC4E CRC64;
                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                           PRT; 1561 AA.
                                                                                                                                                                                                                                                                                                                                   MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0025864; Crag.
InterPro; IPR005112; dDENN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005113; uDENN.
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001194; DENN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Conservative
                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                    Ephydroidea; Dro:
NCBI_TaxID=7227;
                                                                                                                                       CRAG protein.
CRAG OR CG12737.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N
STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                         Q9W3D2
RESULT 13
Q9W3D2
```

ä

.,

Matches

g

셤 ð

```
090WV0
                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                 õ
RX MEDLINE-20196006; PubMed-10731132;
RA Adman M.D., Celnikers S.E., Hilp. P.W., Hoskins R.A., Galle R.F.,
RA Adman M.D., Celnikers S.E., Hilp. P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., R. Holted S., Ashburner M., Henderson S.N.,
B. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortnan J.R., Richard Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pefelifer B.D.,
RA Abril J.F., Agbayari A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayari A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendalle J., Baystakaroglu L., Basaley E.M.,
Ballew R.M., Basu A., Baxendalle J., Brokstein P., Borkova D.,
RA Beson K.T., Encos P.V., Berman B.P., Bhandari D., Bacaley E.M.,
Borkova D., Botchan M.R., Buck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawleylstac A., Deng S., Mays A.D., Deller S.M.,
RA Cherry J.M., Cawleylstac C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.J., Evangelistac C.C., Ferraz C., Ferrain S., Rairis M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Marvey D., Heiman T.J., Weir M.-H., Ibeyaman C.
RA Marmel B.E., Kodirac C.D., Kraft C., McLeod M.P., McDherson D.,
RA Metcal B., McIntcsh T.C., McLeod M.P., McDherson D.,
RA Rainet K., Remington K., Sunders R.D., Weisen M., Stupek M., Spupek M., Spupek M., Weisen M., Stupek M., Spupek M., Spupek M., Weisen M., Stupek M., Spupek M., Spupek M., Weisen M., Shupek M., Shupek M., Shupek M., Shupek M., Weisen M., Shupek M., Raunders R., Rainet W., Shupek M., Shupek M., Weisen M., Shupek M., 
                   | : | : | : | : | : | 1.000 ENISSISPSLTGKKSNELIQGSLSSIKSAANSLTKKKFDEIKGVISANSTPTKTNNGHHPH 1149
------ 47
                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY; StapLeton M., Brokstein P., Hong L., Agbayani A., Carlson J., StapLeton M., Brokstein P., Hong L., Dersenk D., Farfan D., Frise E., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., Gorzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                     48 GANH-----HHHHGHHGGHGFVVRE------TRVEEDINTCTGEVHERRES
                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                       168 AA
         12 EEVRSVAPAGFGRHGGGVQQ-----
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20196006; PubMed-10731132; Adams M.D., Celniker S.E., Holt R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome sequence of Dro
Science 287:2185-2195(2000)
                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLEEL. 13,
01-MAY-2000 (TREMBLEEL. 13,
01-JUN-2002 (TREMBLEEL. 21,
                                                                                                                                                                                                                                                                          CG7406 protein (RE04580p). CG7406.
                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                                                                                                                                         Q9VWM5
                                                                                                                                                                                                                            Q9VWM5
                                                                                                                                                                       RESULT 14
```

```
3 YYQEVDYCSEEVRS---VAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 VDYCSEEVRSVAPAGFGRHGGGVQ---QHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGGHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 VKVISEE-----AGHGGWAGGYSGGYAH-APEEVKIVKVISEAGHSHGHDYGHSHGHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Homeobox protein hox4x (Fragment).
Petromyzon marinus (Sea lamprey).
Bukaryota, Metazoa: Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Force A. Amorram.

Force A. Amorram.

**Rocal A. Amorram.

**InterPro; IPR001827; Antennapedia.

InterPro; IPR001827; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                              16.3%; Score 83; DB 5; Length 168; 32.9%; Pred. No. 0.13; Live 9; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                             to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 381 AA; 43860 MW; 4FD20E59DC48E636 CRC64;
Celniker S.;
Submitted (MAR-2002) to the EMBL/GenBank/Lower Submitted (MAR-2002) to the EMBL/GenBank/Lower Submit AE003511; AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.2%; Score 82.5; DB 13;
29.0%; Pred. No. 0.38;
tive 9; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HOMEOBOX.1; UNKNOWN.1
PROSITE; PS50071; HOMEOBOX.2; 1.
HOMEOBOX; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6, 2003, 12:52:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 VVRETRVEEDINTCTGEVH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000010; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00046; homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.2%
Best Local Similarity 29.0%
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                       Query Match 16.3
Best Local Similarity 32.9
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June
Job time : 51 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 DH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GH 61
```

```
.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

ein - pr	OM protein - protein search, using sw model	June 6, 2003, 12:48:33 ; Search time 25 Seconds	(without alignments) 357.620 Million cell updates/sec	US-10-090-035-4	1 MAYYQEVDYCSEEVRSVAPAINTCTGEVHERRESFLARAN 93
OM prot Run on: Title: Perfect Sequence	OM protein - pro	Run on:		t score:	

283224 seqs, 96134422 residues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TINY-like protein delta/xx1/NF-E1/UC related to multifu hypothetical prote hypothetical prote hypothetical prote glycine/proline-ri transcription fact hypothetical prote hypothetical prote abscisic acid-and hypothetical prote hypothetical prote hypothetical prote hypothetical prote transcription fact dve protein - frui CRAG protein - frui hypothetical prote hypothetical prote Zinc finger bindin hypothetical prote hypothetical prote protein corA, cold transcription repr environmental stre Down-syndrome-crit transforming prote probable limonene TINY-like protein Description SUMMARIES Query Match Length DB 17.0 16.5 16.2 16.1 15.9 15.9 15.7 15.7 15.7 15.0 15.0 14.9 Score 92.5 92.5 92.5 86.5 86.5 81.5 81.5 80 80 77 76.5 76.5 76 75.5 75.7 75.7 74.5 74.5 74.5 Result ě. 

hypothetical prote probable Arthook D hypothetical prote hypothetical prote gamma-eminobutyric serine/threonine-s hypothetical prote homeotic protein o ig heavy chain v r phosphopyruvate hy histidine rich callo hypothetical prote cation efflux fami female sterile hom	kakapo gene protei environmental stre
T16440 EB4766 S09880 T02702 T40145 A41145 A41145 T31611 T31611 T31611 T31611 T31611 T3161 T3161 T3181 T3181 T3181 T3181	713/14 709610
ппппппппппппппппппппппппппппппппппппппп	N (N
1147 1285 1285 1583 1583 1585 1585 1388 1388 1388 13	59
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	13.8
73.5 73.5 73.5 73.5 72.5 71.5 71.5 71.5	70.5
	45

## ALIGNMENTS

RESULT

G85435 TINY-like protein (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: G85435 C;Accession: G85435 Safanonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold	A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A:Reference number: A85001; MUID:20083488; PMID:10617198 A:Accession: G85435 A:Status: preliminary A:Molecule true, pass	A;Residues: 1716 CSTO> A;Residues: 1716 CSTO> A;Cross references: GB:NC_001268; NID:97270639; PIDN:CAB80356.1; GSPDB:GN00140 A;Gene: AT4936900 A;Map position: 4	Ouery Match 18.1%; Score 92.5; DB 2; Length 196; Best Local Similarity 33.8%; Pred. No. 0.012; Matches 24; Conservative 12; Mismatches 24; Indels 11; Gaps 5;	21 GFGRHGGG-VQQHVVKEKFEEVDTVSRAGANHHHHHGH-HGGHGFVVRETR 69 		
G85435 TINY-like protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 C;Accession: G85435	A:Title: Sequence and analysis of A:Title: Sequence and analysis of A:Reference number: A85001; MUID A:Accession: G85435 A:Status: preliminary A:Molecule trace, park	A; Residues: 1196 (STO) A; Cross references: GB:NC_001268 C; Genetics: A14g36900 A; Gene: A14g36900 A; Map position: 4	Query Match 18.1%; Best Local Similarity 33.8%; Matches 24; Conservative	21 GFGRHGGG-VQQHVVKEKI     :   : 99 GGGVNGGGDMSAAYIRRK	70 VEEDINTCIGE 80 :: :  : : 159 INDDLMECSSK 169	
0 H O O O W S	A A A A A A A S A S A S A S A S A S A S	A A C C A A S C C A A S C C C A A S C C C A A S C C A A S C C A A S C C A A S C C A A A S C C A A A A	ÕÄÄ	è a	oy Oy	

Sp

RESULT 2

TINY-like protein [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 24-Oct-2000
C;Accession: T52619
C;Accession: T526

Query Match

A; Map position: 4

Length 259; 18.1%; Score 92.5; DB 2; ô

g ŏ 셤

```
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C.; Alon R;Theologis, A.; Ecker, J.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, C.W.; Hughes, B.; Hulzar, L.; Jenkins, D.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jenkins, J.S.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Wonory, T.; Rowley, D.; Sakano, H. Southwick, A.W.; Sun, H.; Tallo A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shino, P.; Southwick, A.W.; Sun, H.; Tallo A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Pauley, A.; Scheet, P.; Harper, M.
R; Pauley, A.; Scheet, P.; Harper, M.
submitted to the EMBL Data library, February 1999
A; Description: The sequence of C. elegans cosmid W03Gl.
A; Reference number: Z21454
A; Accession: T3397
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-471 < PAUJ>
A; Residues: 1-471 < PAUJ>
A; Residues: Lefterences: EMBL:AF125964; PIDN:AAD14753.1; GSPDB:GN00022; CESP:W03Gl.5
A; Cross-references: strain Bristol N2; clone W03Gl
C; Genetics: A; Grame: CESP:W03Gl.5
A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T24C10.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Caenorhabditis elegans
Spate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
Accession: T33997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GVQQHVVKEKFEEVDTVSRAGANHHHHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 471;
A;Molecule type: DNA
A;Residues: 1-1245 <SCH>
A;Cross-references: EMBL:AL356815; GSPDB:GN00116; NCSP:B24H17.10
A;Experimental source: BAC clone B24H17; strain OR74A
                                                                                                                                                                                                                                              Length 1245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86.5; DB 2;
Pred. No. 0.14;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein W03G1.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                              0.21;
                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                       Score 89;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                 ||:| :||!|| || || 901 SRSGTHHHHHHHHHHGHHG 918
                                                                                                                                                                                                                                                                                                                                                                 SRAGANHHHHHHGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.0%;
34.8%;
                                                                                                                                                                                                                                                       17.58;
72.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 RSVAPAGFGRHGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 34.8 nes 24; Conservative
                                                                                                                                                                                                                                                                                 Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ррнн

Ррн

435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --HHGGHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-473 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                  C; Genetics:
A; Gene: NCSP:B24H17.10
                                                                                                                                                                             A; Map position: 6
A; Introns: 6/2; 1141/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                             45
                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
T49815
Telated to multifunctional cyclin-dependent kinase PHO85 [imported] - Neurospora crassa
N.Alternate names: protein B24H17.10
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Accession: T49815
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Bibmitted to the Protein Sequence Database, May 2000
A;Reference number: Z22022
A;Accession: T49815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-414 <FLAA
A; Residues: 1-414 <FLAA
A; Cross-references: GB:W73963; NID:9202270; PIDN:AAA40522.1; PID:9202271
A; Cross-references: GB:W73963; NID:9202270; PIDN:AAA40522.1; PID:9202271
A; Cross-references: GB:W73963; NID:9205271
B; Hariharan, N.; Kelley, D.E.; Perry, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 9799-9803, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 9799-9803, 1991
A; Title: delta, a transcription factor that binds to downstream elements in several poly A; Reference number: A56418; WUID:92052178; PMID:1946404
                                                                                                                                                                                                                                                                                                                                                                                           C;Species; Mus musculus (house mouse)
C;Date: 02-01-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Date: 02-01-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Accession: A48273; A42055; A56418
R;Safrany, G.; Perry, R.P.
Proc. Natl. Acad. Sci. U.S. A: 90, 5559-5563, 1993
A;Title: Characterization of the mouse gene that encodes the delta/YY1/NF-E1/UCRBP trans A;Reference number: A48273; MuID:93296177; PMID:8516301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L13968; NID:g293847; PIDN:AAA40477.1; PID:g293849
A;Cross-references: GB:L13068; NID:g293847; PIDN:AAA40477.1; PID:g293849
F;Planagan, J.R.; Becker, K.G.; Ennist, D.L.; Gleason, S.L.; Driggers, P.H.; Levi, B.Z.;
Mol. Cell. Biol. 12, 38-44, 1992
A;Title: Cloning of a negative transcription factor that binds to the upstream conserved A;Reference number: A42055; MUID:92107191; PMID:1309593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGGHGFVVRETRVEEDINICIGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                       5
                                                                                                            21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-218,'S',220-374,'G',376-414 <HAR>
A;Cross-references: GB:M74590; NID:g192940; PIDN:AAA37521.1; PID:g192941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.0%; Score 92; DB 2; Length 414; 11arity 31.0%; Pred. No. 0.031; Conservative 7; Mismatches 26; Indels
                                24; Indels
        0.016;
     Best Local Similarity 33.8%; Pred. No. 0.01
Matches 24; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 227/1; 281/2; 301/3; 354/3
C; Keywords: transcription factor; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----HSBGGGGGH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 VННИОЕVILVO 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 VHERRESFLAR 91
                                                                                                                                                                                                                                           ::|: |: :
222 INDDLMECSSK 232
                                                                                                                                                                                                        VEEDINTCIGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A42055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 22;
                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

us-10-090-035-4.rpr

ä

```
transcription factor Brn-1 - mouse
N'Alternate names: class III POU domain protein brain-1
C'Species: Mus musculus (house mouse)
C'Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
C'Accession: S31223
R'Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992
A;Title: Structure and evolution of four POU domain genes expressed in mouse brain. A;Reference number: S31223; MUD:9228768; PMID:1565620
A;Ritle: Structure and evolution of four POU domain genes expressed in mouse brain. A;Reference number: S31223; MUD:9228768; PMID:1565620
A;Retus: preliminary
A;Molecule type: DNA
A;Residuss: 1-495 cHRAN
A;Residuss: 1-495 cHRAN
C;Reywords: DNA binding; homeobox; nucleus; transcription regulation
F;27-49/Region: glycine-rich
F;10-117/Pard.c.; glycine-rich
F;10-117/Pard.c.; glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apportetical protein F53A9.6 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Accession: T16437
C; Accession: T16437
C; Accession: The sequence of C. elegans cosmid F53A9.
A; Beference number: 218513
A; Reference number: 2185133
A; Reference number: 2185133
A; Reference number: 2185133
A; Reference 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ë
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 495;
                                                                                                                                                                                                            19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGA----NHHHHHHHHGHHGGHGF
                                                                 Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 81; DB 2; Length 86; 29.5%; Pred. No. 0.089; 1ve 5; Mismatches 24; Indels
                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                            Score 82; DB 2;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHH-
                     16.1%; Sco. No. v. 34.7%; Pred. No. v. 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 GPGLNSHDPHSDEDTPTSDDLEQFAKQFKQRR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 -----FVVRETRVEEDINTCTGEVHERR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
16.0%; Score 81.5; Di
Best Local Similarity 26.1%; Pred. No. 0.5;
Matches 24; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F)101-112/Region: alanine-rich
F;162-180/Region: histidine/proline-rich
F;186-201/Region: alanine-rich
F;236-247/Region: glycine-rich
F;267-291/Region: histidine/proline-rich
F;316-383/Domain: POU domain homology <POU>F;402-458/Domain: homeobox homology <HOX>
                                           Query Match
Best Local Similarity 34.7
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.9
Best Local Similarity 29.5
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:F53A9.6
                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine/prolline-rich protein - Arabidopsis thaliana
N;Alternate names: protein K10A8_130
C;Specias: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51469
R;Sato, S: Nadamura, Y: Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S: Submitted to the Protein Sequence Database, August 2000
A;Reference number: 225394
A;Reference number: 22539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y3986B.gg [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 21-3a1-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C; Accession: T45059
R; Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, Rser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns Nature 368, 32-38, 1994
A; Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; Stock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A; Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A; Reference number: S43531; MUID:94150718; PMID:7906598
                                                                                                                                                                                                                                                                                                                                 ÷
A;Cross-references: GB:AE005173; NID:99857523; PIDN:AAG00878.1; GSPDB:GN00141'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:96434440; PIDN:CAB60938.1; PID:96434473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGH---HGGH 61
                                                                                                                                                                                                                                                                                                                             8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 735;
                                                                                                                                                                                                                                      Length 473;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-735 <MIL>
A;Cross-references: EMBL:AL132896; NID:96434440; PIIC
A;Experimental source: clone Y39868
C;Genetics:
                                                                                                                                                                                                                    16.5%; Score 84; DB 2;
36.8%; Pred. No. 0.26;
Live 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
16.2%; Score 82.5; Di
Best Local Similarity 26.4%; Pred. No. 0.6;
Matches 19; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 GRHGGGVQQHVVKEKFEEVDTVSRAGANHHH---
                                                                                                                                                                                                            Ouery Match
Best Local Similarity 36.8%
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 --- нн сни сен с 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 3
A;Introns: 18/1, 69/1
A;Note: Y39B6B.gg
                                       C;Genetics:
A;Gene: T24C10.10
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
```

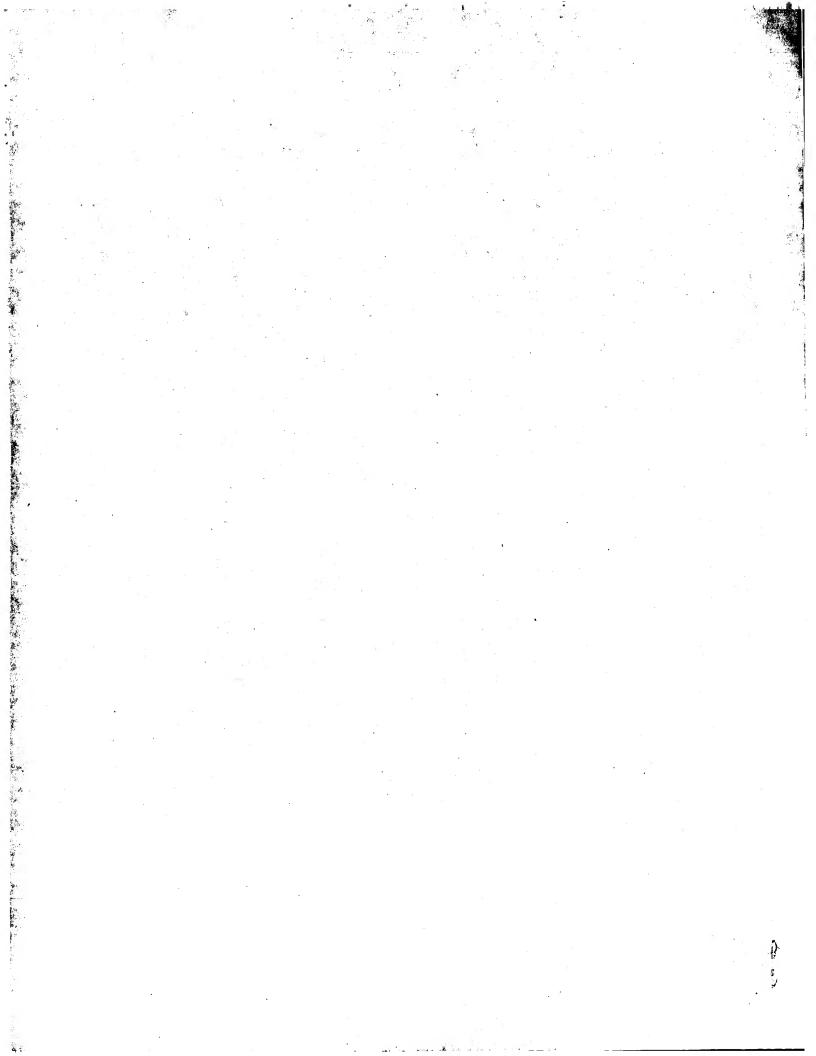
1 MAYYQEVDYCSEEVRSVAPAGFGRHGG-------GVQQHVVKEKFEEVDTVS

ò

```
transcription repressor protein YX1 - human NA1 transcription repressor/activator protein NF-E1 NA1 ternate names: transcription repressor/activator protein NF-E1 C; Species: Homo sapiens (man) control to the sequence_revision 17-Jul-1992 #text_change 08-Oct-1999 C; Accession: A40350; S78494; S33712; A56419 C; Accession: A40350; S78494; S33712; A56419 R; Shi, Y; Seto, E; Chang, L.S.; Shenk, T. Call (F) 377-388, 1991 A; Thitle: Transcriptional repression by XY1, a human GLI-Krueppel-related protein, and A; Reference number: A40350; MUID:92005716; PMID:1655281
                                                                                                                                                                                The comp
                                                                                                         Nomura, N.; Ohara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: proliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1273 ANACA
A; Cross-references: EMBL-AB011142; NID: 93043663; PIDN: BAA25496.1; PID: 93043664
A; Experimental source: brain; clone HH2365
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- 52
C;Species: Homo sapiens (man)
C;Date: 01.Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00338
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.;
R;Nagase, T.; Jalyawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.;
R;Nagase, T.; Jalyawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.;
A;Title: Prediction of the coding sequences of unidentified human genes. IX.
A;Reference number: 214086; MUID:98290545; PMID:9628581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein corA, cold- and drought-regulated - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-204 <LAB>
A; Residues: 1-204 <LAB>
A; Cross-references: EMBL:L03708; NID:g289122; PIDN:AAA99833.1; PID:g289123
A; Cross-references: EMBL:L03708; NID:g289122; PIDN:AAA99833.1; PID:g289123
A; Genetian: CorA
C; Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-414 <SHI>
A;Cross-references: GB:M77698; NID:g186767; PIDN:AAAS9467.1; PID:g186768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.5%; Score 79; DB 2; Length 204; Best Local Similarity 30.4%; Pred. No. 0.37; Matches 24; Conservative 3; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 1273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 GANHHHHHHHGHHGGH--GEVVRETRVEEDINTCTGEVHERRESFLA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GFGRHGGGVQQHV-VKEKFEEVDTV-----SRAGANH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T09592
R;Laberge, S.; Castonguay, Y.; Vezina, L.P.
Plant Physiol. 101, 1411-1412, 1993
A;Title: New cold- and drought-regulated gene from Medicago
A;Reference number: 216754; MUD:94143496; PMID:8310076
A;Accession: T09592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: KIAA0570
C;Superfamily: human hypothetical protein KIAA0570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 GGHGGHGGHGAVQTEDNTQ 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 HHHGHHGGHGFVVRETRVE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.7%;
Best Local Similarity 33.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-204 <LAB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A40350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Medicago sativa (alfalfa)
C.Species: Medicago sativa (alfalfa)
C.Species: Medicago sativa (alfalfa)
C.Species: Medicago sativa (alfalfa)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Jun-2000
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Jun-2000
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Jun-2000
R.Jul-1996 #sequence in the Jul-1998 #text_change 02-Jun-2000
R.Jul-1999 #sequence in the Jul-1999 #text_change 02-Jun-2000
R.Jul-1999 #sequence in the Jul-1999 #text_change 02-Jun-2000
R.Jul-1999 #text_change 02-Jun-2000
R.Jul-1999 #sequence in the Jul-1999 #text_change 02-Jun-2000
R.Jul-1999 #text_change 02-Jul-1999
R.Jul-1999 #text_cha
                                                                                                                                                                                                                                                                                                                                                                            abscistc acid-and environmental stress-inducible protein - alfalfa (fragment)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A42844
R;Luo, M.; Liu, J.H.; Mohapatra, S.; Hill, R.D.; Mohapatra, S.S.
J; Biol. Chem. 267, 15367-15374, 1992
A;Title: Characterization of a gene family encoding abscisic acid- and environmental str
A;Reference number: A42844; MUID:92348382; PMID:1379227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GFGRHGGGVQQHV-VKEKFEEVDTV-----SRAGANH-----HHHHGHH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----Н 52
                                         A; Molecule type: mRNA
A; Residues: 1-191 <-LUO>
A; Cross-references: GB:S40947; NID:g252396; PIDN:AAB22713.1; PID:g252397
A; Cross-references: GB:S40947; NID:g252396; PIDN:AAB22713.1; PID:g252397
A; Note: sequence extracted from NCBI backbone (NCBIN:109886, NCBIP:109889)
C; Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: mRNA
A; Residues: 1-133 <LUO>
A; Cross-references: EMBL:M74190; NID:g166373; PID:g166374
A; Experimental source: cultivar Ank
C; Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFGRHGGGVQQHV-VKEKFEEVDTV------SRAGANH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGHGGTVDTVLFKLTTLKTDHNDIIMHHALFLS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 GGHGFVVRE--TRVEEDINTCTGEVHERRESFLA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 80; DB 2;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 81; DB Pred. No. 0.213; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGHGGHGGHGADQTEDNTQNDHN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 HHHGHHGGHGFVVRETRVEEDIN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein KIAA0570 - human
                                                                                                                                                                                            ::|| || ||||||||| 52 ННDSHHRGGHHGGHHGGH
                                                                                                                                                      46 RAGANHH--НННGНHGGH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.7%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%;
ilarity 30.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A42844
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                          g
                                                                                                                                                             ç
                                                                                                                                                                                                                                 셤
```

```
A; Experimental source: HeLa cells
A; Note: the authors translated the codon CGC for residue 371 as Lys, CGA for residue 375
A; Note: the authors translated the codon CGC for residue 371 as Lys, CGA for residue 375
B; Whiteon, R.H.; Huang, T.; Dang, J.; Itakura, K.
B; Data Library, July 1992
A; Description: Observed and predicted DNA binding of a zinc finger protein which recogning A; Reference number: S78494
A; Accession: S78494
                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-195, 'G', 197-414 <WHI>
A; Residues: 1-195, 'G', 197-414 <WHI>
A; Cross-references: EMBLE 214077; NID:938010; PIDN:CAA78455.1; PID:938011
A; Proc. Natl. Acad. Sci. U.S.A. 88, 9804-9808, 1991
A; Title: Isolation of a candidate repressor/activator, NF-E1 (YY-1), delta, that binds A; Reference number: A56419; MUID:92052179; PMID:1946405
A; Accession: S33712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGGH-GFVVRETRVEEDINTCTG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: mRNA
A; Residues: 1-64, R', 66-195, 'G', 197-414 <PAR>
A; Residues: 1-64, R', 66-195, 'G', 197-414 <PAR>
A; Cross-references: GB:M76541; NID:g189173; PIDN:AAA59926.1; PID:g189174
C; Keywords: DN binding: transcription regulation; zinc finger
F; 298-320/Region: zinc finger CCHH motif
F; 317-347/Region: zinc finger CCHH motif
F; 385-377/Region: zinc finger CCHH motif
F; 385-407/Region: zinc finger CCHH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 2; Length 414;
Pred. No. 0.78;
6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.2%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|| :| | :
96 QVHHHQEVILVQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 EVHERRESFLAR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

Search completed: June 6, 2003, 12:53:25 Job time : 26 secs



```
sequence 17, Appl. Sequence 15, Appl. Sequence 13, Appl. Sequence 17, Appl. Sequence 17, Appl. Sequence 113, Appl. Sequence 11, Appl. Sequence 1, Appl. Sequence 14, Appl. Sequence 3, Appl. Sequence 34, Appl. Sequence 2739, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 14, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 13, Appl. Sequence 17, Appl. Sequence 143, Appl. Sequence 15, Appl. Appl. Sequence 15, Appl. Sequence 15, Appl. Sequence 15, Appl. Appl. Sequence 15, Appl. Sequence 15, Appl. Sequence 15, Appl. Sequence 15, Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl. Appl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Appl
Sequence 457, App
Sequence 6480, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10090035
Fatent No. US202020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/24990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 05.202
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                             US-10-090-035-17
US-10-090-035-7
US-10-090-035-15
US-10-090-035-21
US-10-090-035-23
US-10-090-035-23
US-10-090-035-18
US-09-923-876-2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-938-842A-457
US-09-918-995-6480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-052-798-6
US-10-052-798-7
US-10-278-173-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         თ თ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3e-58
510.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25309
8979
3309400
1458
1519
                                                                                                                                                                                                                                           3966
10062
1602
1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (96)...(374)
US-10-090-035-3
                                                              TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (96)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-10-090-035-3
499.5
499.5
277.5
258
251
251
251
251
251
351
362.5
88.5
88.5
80
78.5
                                                                                                                                                                                                                                                                                                                                                                                                                                            75.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:

"MODEL-frame+_p2n.model -DEV-x1h
-0-/cggr2_L/USPTO_spool_VG1090035/runat_06062003_105507_11116/app_query.fasta_1.526
-0-/cggr2_L/USPTO_spool_VG1090035/runat_06062003_105507_11116/app_query.fasta_1.526
-DB-published_Applications_NA -OFMT-fastap -SUFERIX-rnpb -MINARTCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-b1s -START-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_NIN-0 -ALIGN-15 -MODEL-LOCAL -OOTFMT-ptc -NORM-ext -HEAPSIZE-500 MINLEN-0
-MAXLEN-2000000000 -USER-US10090035_GCGN_1_L176_Grunat_06062003_105507_1116
-NCPU-6 -LCPU-3 -NO_MMAP -LARGEQUERY -NGG_SCORES-0 -WAIT -DSPBLOCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDC-10 -XGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                                                                                                   (without alignments)
1077.357 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Sequence 5, Sequence 1, Sequence 1,
                                                                                                                                                                                                                                         1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/DCG_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
                                                                                                                     June 16, 2003, 11:41:43; Search time 125 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2059716
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                             nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                     1029858 seqs, 724030393 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-3
US-10-090-035-5
US-10-090-035-1
US-10-090-035-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                     Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                US-10-090-035-4
510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ОВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574
577
676
529
                                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0
100.0
100.0
99.4
                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                               OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
```

à 셤

g à

ð

g δy

```
; sequence 1, Application US/10090035; sequence 1, Application US/10090035; sequence 1, Application US/10090035; patent No. US20020170089A1; sequence No. US20020170089A1; simmons, Carl R.; TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof; TITLE OF INVENTION: Proteins and Uses Thereof; TITLE OF INVENTION: PROTEINS US/10/090,035; CURRENT FILING DATE: 2002-02-28; CURRENT FILING DATE: 2002-02-28; PRIOR FILING DATE: 02/28/2001; NUMBER OF SEQ ID NOS: 25; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 1; LENGTH: 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-9
(Sequence 9, Application US/10090035)
(Sequence 9, Application US/10090035)
(SEMERAL OUS/20010/0089A1)
(SEMERAL INFORMATION:
TITLE OF INVERVION: Nucleic Acids Encoding Defense Inducible TITLE OF INVERVION: Proteins and Uses Thereof
FILE REPERENCE: 35718/242990
(CURRENT APPLICATION UNMERR: 2002-02-28)
(CURRENT FILING DATE: 2002-02-28)
(CURRENT PRICE OF UNMERR: 2002-02-28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676
93
0
0
                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-4 (1-93) x US-10-090-035-1 (1-676)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                              1.59e-58
510.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (89)...(367) US-10-090-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                     279
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                    VESTION 1900-035-5

Sequence 5, Application US/10090035

TILLE OF INVENTION: No.1eic Acids Encoding Defense Inducible TILLE OF INVENTION: Proteins and Uses Thereof

TILLE OF INVENTION: Proteins and Uses Thereof

CURRENT APPLICATION UNBER: US/10/090,035

CURRENT FILING DATE: 2002-02-28

SETOR PAPLICATION NUMBER: 60/272,227

PRIOR FILING DATE: 20/2/28/2001

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 5

LENGTH: 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                577
93
0
0
0
                                                                                                                                                                                                                                                                                          000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
              Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-090-035-4 (1-93) x US-10-090-035-5 (1-577)
                                                                US-10-090-035-4 (1-93) x US-10-090-035-3 (1-574)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.31e-58
510.00
100.00%
100.00%
                100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (99)...(377)
US-10-090-035-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays
                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                     216
                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                   RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
```

g

δ

g δ 염 ď

ò

m

236

```
1 MetalaTyrTyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaProAla 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                                              41 ValaspThrvalSerargalaGlyalaasn---Hishishishishishishishiy
                                                                                                                                                                            Sequence 7, Application US/10090035
; Patent No. US20020170089A1
; General Information:
GENERAL INFORMATION:
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272.227
FRIOR FILING DATE: 002/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                 580
0
1
1
                 0 4 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
              Mismatches:
Indels:
Gaps:
                                                    US-10-090-035-4 (1-93) x US-10-090-035-17 (1-524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-090-035-4 (1-93) x US-10-090-035-7 (1-580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.24e-57
499.50
98.94%
98.94%
             98.94%
97.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:

; NAME/KEY: CDS

; LOCATION: (99)...(380)

US-10-090-035-7
            Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                        US-10-090-035-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                         ö
                                                                                              g
                                                                                                                     ò
                                                                                                                                       g
                                                                                                                                                               ð
                                                                                                                                                                                   윱
                                                                                                                                                                                                         ð
                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                        Sequence 17, Application US/10090035
Patent No. US20020170089A1
SEGNERAL INFORMATION:
TERENT: SIMMONS, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 3578/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 05/10/2027
PRIOR FILING DATE: 202/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 524
                                                                                                                                               529
1
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                81 ValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                             293 GTCCACGAGGCAGGGAGAGCTTCCTCGCCAGGGCTAAC 331
                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
                                                                                                                                                                                                                  US-10-090-035-4 (1-93) x US-10-090-035-9 (1-529)
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 9
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: CDS
NAME/KEY: CDS
NAME/KEY: (57)...(338)
NAME/KEY: (1)...(524)
CACTION: (1)...(524)
US-10-090-035-17
                                                                                                                                           2.93e-58
507.00
100.00%
98.92%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.85e-57
499.50
98.94%
                                                                                   ; NAME/KEY: CDS
; LOCATION: (53)...(331)
US-10-090-035-9
                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                        TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-17
                                                                            FEATURE:
                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                    a
```

```
Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 AACGACTACCTGATGGTGCGCGAGACCAAGGTGGAGGAGGACTTCAACACCTGCACCGGC 291
1719 GGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGACATCAACACCTGCACCGGC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGly
                                                                                                                                  sequence 15, Application US/10090035
sequence 15, Application US/10090035
sequence 15, Application US/10090035
general incommarion:
TILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 35718/242906
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 2022-02-28
SOFTWARE: FALSE OF TO NOS: 25
SOFTWARE: FALSE OF TO NOS: 25
SED ID NO 15
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: SIGMONS, Carl R.
ITILE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 GAGITCCGCGAGCGAAGCTTCCTGCTCCAAGTCCGAC 333
                                             80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-090-035-4 (1-93) x US-10-090-035-15 (1-591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4e-30
295.00
75.53%
60.64%
57.84%
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (61)...(333)
NAME/KEY: Misc_feature
LOCATION: (1)...(591)
OTHER INFORMATION: n = A
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-090-035-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-15
                                                                                                                               US-10-090-035-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                          g
                                                      ö
```

```
165 CAGGAGTICGACACCICCGGCCGC------CGCCACGGICACCACGGICACCAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPhe--- 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 GluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 ThrCysThrGlyGluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NS-10-090-035-19
Sequence 19, Application US/10090035
Sequence 19, Application US/10090035
Sequence 19, Application US/10090035
Sequence 10, Application US/10090035
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof TITLE OF INVENTION: UNMER: 2090
CURRENT APPLICATION NUMBER: 20/2-28
PRIOR PILING DATE: 2002-02-28
PRIOR FILING DATE: 02/28/2001
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                              436
60
12
13
13
                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-090-035-4 (1-93) x US-10-090-035-21 (1-436)
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 436
LENGTH: 436
                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - A, T, C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Triticum aestivum
                                                                                                                                                                         ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                  277.50
73.478
61.228
54.418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (46)...(321)
NAME/KEY: misc_feature
                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (54)...(326)
US-10-090-035-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(584)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Fast
SEQ ID NO 19
LENGTH: 584
                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                            FEATURE
```

us-10-090-035-4.rnpb

Db 283 GAGTTTCGCGAGCGC 297 RESULT 12 US-09-923-876-2788 ; Sequence 2788, Application US/09923876	Db 46 ATGGCGCACTTCCAGGAGGTGGACTACTGCTGGAGGAGGAGGGGGGGG
80	
7	US-10-090-035-4 (1-93) x US-10-090-035-23 (1-584)
Qy 60 GlyHisGlyPheValValArgGluThrAr	Gaps:
Qy 40 GluValAspThrValSerArgAlaGlyAle	Score: 258.00 Matches: 58 Percent Similarity: 72.73% Conservative: 14 Best Local Similarity: 58.59% Mismatches: 13 Query Match: 50.59% Indels: 14
Db 112 GGCGCTTCCTCGCCGCGCGCGTGCAC	ent Scores: 3.13e-25 Length:
Qy 20 AlaGlyPheGlyArgHisGlyGlyGlyWa	
Qy 1 MetalanyrTyrGlnGluValaspTyrCyt	
US-10-090-035-4 (1-93) x US-10-090-035-13 (	
251.00 larity: 70.59% imilarity: 60.00%	SOFTWARE: FattSEQ for Windows Version 4.0
	; PRIOR APPLICATION NUMBER: 60/272,227 ; PRIOR FILING DATE: 02/28/2001
; OTHER INFORMATION: n = A,T,C or G US-10-090-035-13	CURRENT APPLICATION NUMBER: US/10/090,035 CURRENT FILING DATE: 2002-02-28
; ;	<ul> <li>GARGAL INCHAILOR.</li> <li>TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible</li> <li>TITLE OF INVENTION: Protectins and Uses Thereof</li> <li>FILE REPERENCE: 35718/2242940</li> </ul>
: LENGTH: 348 : TYPE: DNA : ORGANISM: Oryza sativa : FFRATHRE:	RESULT 10 US-10-090-035-23 ; Sequence 23, Application US/10090035 ; Patent No. US20020170089Al
FRIOR FILING DATE: 02/28/2001 FRIOR FILING DATE: 02/28/2001 SOFTWARE: FESTSEQ for Windows Version 4.0	Oy 75 AsnThrCysThrGlyGluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93 
; TITLE OF INVENTION: Proceins and Uses T. FILE REFERENCE: 35718/242990 ; CURRENT APPLICATION NUMBER: US/10/090,03: CURRENT FILING DATE: 2002-28	<pre>Qy 58 H18GlyGlyH18GlyPheValValArgGluThrArgValGluGluAspIle 74                                     </pre>
GENERAL INFORMATION: ; APPLICANT: Simmons, Carl R. ; TITLE OF INVENTION: Nucleic Acids Encodi	<pre>Qy 39GluGluValAspThrValSerArgalaGlyAlaAsnHisHisHisHisGlyHis 57 :::                                   </pre>
RESULT 11 US-10-090-035-13 ; Sequence 13, Application US/10090035	Oy 20 AlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPhe 38
Oy 75 ASHTHICLYSTHIGLYGLUVALHISGLUAR.	Qy . 1 MetalatyrTyrGlnGluValaspTyrCysSerGluGluValargSerValalaPro 19       :::::
dy 58 HisGlyGlyHisGlyPheVa	10-090-035-4 (1-93) x US-10-090-035-19 (1-584)
157 GTGCAGGAGTTCGA	Percent Similarity: 72.73% Conservative: 14 Best Local Similarity: 58.59% Mismatches: 13 Query Match: 50.59% Indels: 14 DB: 6200
	is Length: 5

```
AlvalargGluThrargValGluGluAspIle 74
                                                                                                                                                                                                                 AlGINGINHISVAlValLysGluLysPheGlu 39
                                                                                                                                                                                                                                                   ling Defense Inducible Thereof
                                                                                                                                                                           ngth:
tches:
nservative:
smatches:
dels:
                                                                                                                                                                                                         (1-348)
                                                                                          35
                                                                                                                0
```

12 24 11 5

52

69

9

```
208 CATCATCATCAACATCAACGTGGTAATCATAACGTAGATAATCATAGTGATTATCGT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyPheGlyArgHisGlyGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                  21 GlyPheGlyArgHisGlyGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 HisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 CATCATCATCAACATCAACGTGGTAATCATGATTACGTAGATAATCATAGTGATTATCGT
                                                                                                                                                                                       53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ValAspThrValSerArgAlaGlyAla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-090-035-4 (1-93) x US-09-938-842A-1858 (1-591)
                                                                                                                                                                                                                                                                                                                                          70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                   US-10-090-035-4 (1-93) x US-09-924-035A-17 (1-328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STARES, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1858, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.50
50.70%
33.80%
18.14%
50.70%
33.80%
18.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 Glu-----
 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-842A-1858
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-938-842A-1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                    ŏ
                                                                                                                                                                                         ò
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                            APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Braddey K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: 08/09/933,876
CURRENT PILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR PILING DATE: 1998-05-05
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 6332
LENGTH: 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 ValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHisGlyGly 60
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Griach, Jrn
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIOR FILING DATE: 1999-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-090-035-4 (1-93) x US-09-923-876-2788 (1-237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09924035A Patent No. US20020142319A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.24e-20
213.00
81.67%
80.00%
41.76%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.00126
92.50
   Patent No. US20020013958A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-924-035A-17/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-924-035A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores
                                                                                                                                                                                                                                                                                            IYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
```

PLANTS, TRANSGENIC PLANTS CONTAINING

354

591 24 12 24 11 5

52

```
---CAC 322
                                                                                                                   APPLICANT: Friedrich, Glenn
APPLICANT: Sandrowicz, Brian
APPLICANT: Sandrowicz, Brian
APPLICANT: Sandrowicz, Brian
APPLICANT: Sandrowicz, Brian
TITLE OF INVENTION: Animals
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
FURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,358
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 817
LENTH: 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 AsnHisHisHisHisGlyHisHisGlyGlyHisGlyPheValValArgGluThrArg 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 ValGluGluAspIleAsnThrCysThrGlyGluValHisGluArgArgGlu------ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546
119
11
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
US-10-090-035-4 (1-93) x US-09-728-445-817 (1-546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: June 16, 2003, 13:51:21
Job time : 130 secs
                                                                         Sequence 817, Application US/09728445 Patent No. US20020102543A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 GGCACATTCATAGAACAAGCC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 ---SerPheLeuAlaArgAla 92
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA

ORGANISM: Mus musculus

FRATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(546)

OTHER: INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.00804
88.50
51.06%
40.43%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
Percent Similarity;
Best Local Similarity:
Query Match:
DB:
                                           RESULT 15
US-09-728-445-817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      red. No.:
                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

			. ,
	die		
			·
M.			7
	ż		
	1 7		
	* * * * * * * * * * * * * * * * * * * *		· ·
•			
			. +
			•
			9
N.			
		·	
E.		·	
			į
3			
2			

```
Sequence 6, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 9, Appli
Sequence 10, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl
Appl
Appl
Appl
Appl
Appl
                                                                                    June 6, 2003, 12:52:33 ; Search time 29 Seconds (without alignments) 331.081 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               US-10-090-035-4
510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8,
Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22
Sequence 20
Sequence 24
Sequence 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      /egn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/egn2_6/ptodata/2/pubpaa/DECT_NEW_PUB.pep:*
/egn2_6/ptodata/2/pubpaa/NS06_NEW_PUB.pep:*
/egn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/egn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/egn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/egn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/egn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/egn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/egn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/egn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/pubpaa/US10_PUBGOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /ptodata/2/pubpaa/US10_NEW_PUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-090-035-2
US-10-090-035-4
US-10-090-035-6
US-10-090-035-10
US-10-090-035-18
US-10-090-035-18
US-10-090-035-16
US-10-090-035-22
US-10-090-035-24
US-10-090-035-24
US-10-090-035-24
US-10-090-035-24
US-10-090-035-14
US-10-090-035-14
US-10-090-035-14
US-10-090-035-14
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      392085 seqs, 103240269 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_AA:
                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507
499.5
499.5
295
277.5
273
258
                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
```

4 Q (4	201, 11, Al 225, Al 135, Al	Sequence 120, App Sequence 317, App Sequence 317, App Sequence 126, App Sequence 71, App1 Sequence 71, App1 Sequence 69, App1 Sequence 20, App1 Sequence 20, App Sequence 200, App Sequence 200, App Sequence 199, App	
US-09-876-904A-627 US-09-824-735-3 US-09-801-368-338 US-10-052-798-11 US-10-052-798-11	20222	0.5-10-044-692-317 0.5-10-044-692-317 0.5-10-270-333-126 0.5-10-108-605-71 0.5-10-108-605-71 0.5-09-738-186-69 0.5-09-738-197-20 0.5-09-975-719-201 0.5-09-975-719-201 0.5-09-975-719-201 0.5-09-975-719-1990 0.5-09-853-386-70	
1201	210000000000000000000000000000000000000	100000000000000000000000000000000000000	
19 633 633 310	532 3132 623 726 257 257 139	510 530 530 1207 1207 507 507 608 643	
14.3 14.3 14.0	20000000000000000000000000000000000000	13222222222222222222222222222222222222	
73 73 71.5 71.5	6 69 69 67 57 57 57 57 57 57 57 57 57 57 57 57 57	67.5 67.5 67.5 67.5 67.6 67.6 67.6 67.6	
222 232 24	25 26 27 28 30 33 33 33	6 K K K K K K K K K K K K K K K K K K K	

## ALIGNMENTS

```
1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                               GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
GURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION WHORER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 510; DB 9; Length 93; Best Local Similarity 100.0%; Pred. No. 5e-45; Matches 93; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. US2020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10090035
Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10090035 Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
US-10-090-035-2
-10-090-035-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-090-035-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
```

US-10-052-798-9 US-10-052-798-10

ö

```
US-10-090-035-18
NOMBER SOFTWARE: FAST SOFTWARE: FAST SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-10-090-035-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
LENGIH: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHHGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10090035; Sequence 6, Application US/10090035; Patent No. US20020170089A1; GENERAL INFORMATION:
TOTAL OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: NUMBER: US/10/090,035; CURRENT FILING DATE: 2002-02-28; PRIOR FILING DATE: 2022-02-28; PRIOR FILING DATE: 2022-02-28; SOFTWARE: PASCEC for Windows Version 4.0; SED ID NO 6
                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/10090035
Sequence 10, Application US/10090035
Patent No: US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/742990
CURRENT APPLICATION UNMBER: US/10/090,035.
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 510; DB 9; Length 93; Best Local Similarity 100.0%; Pred. No. 5e-45; Matches 93; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Length 93;
                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 510; DB 9; Length 9
Best Local Similarity 100.0%; Pred. No. 5e-45;
Matches 93; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
  FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Zea mays US-10-090-035-6
                                                                                                                                                                                           TYPE: PRT CORGANISM: Zea mays US-10-090-035-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-090-035-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-10-090-035-6
                                                                                                                                                       SEO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
÷
                                                                                                                                                                                  ö
                                                                                                                                                                                                                      1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGG 60
                                                                                                                                                                                                                                             1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGAN-HHHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/10090035

Sequence 18, Application US/10090035

Sequence 18, Application US/10090035

Sequence 18, Application:
GENERAL INFORMATION:
TITLE OF INVENTION: Motified Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
CURRENT APPLICATION UNBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28

SEQUENCE FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 18

LENGTH: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SIMMONS. Carl R. APPLICANT: SIMMONS. Carl R. TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                  Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 499.5; DB 9;
Pred. No. 5.9e-44;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                  Score 507; DB 9;
Pred. No. 1e-44;
1; Mismatches
                                                                                                                                                                                                                                                                                                   61 HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
NUMBER OF SEQ 1D NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10090035
Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.9%;
                                                                                                                                                  ch 99.4%;
1 Similarity 98.9%;
92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                          Query Match
Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Zea mays US-10-090-035-8
                                                                              ; TYPE: PRT
; ORGANISM: Zea mays
US-10-090-035-10
```

Mon Jun 16 14:55:57 2003

13; Gaps

```
1 MAYYQEVDYCSEEVRSVA-PAGFGRHGGGVQQHVVKEKF-EEVDTVSRAGANHHHHGHH 58
                                                                     1 MAYYQEVDYCSEEVRSVA-PAGFGRHG-GGVQOHVVKEKF-EEVDTVSRAGANHHHHHGH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Simmons, Call R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proceeding and Uses Thereof
FILE REPRENDENCE: 33718/242990
CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/272,227

PRIOR PELLING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 92
                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
File Reference: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEO ID NOS: 25
SOFTWARE: FRSELEGO FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 53.5%; Score 273; DB 9; Length 92; Similarity 61.6%; Pred. No. 7e-21; 11; Conservative 12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.6%; Score 258; DB 9; Length 92; 58.6%; Pred. No. 2.4e-19; 1ve 14; Mismatches 13; Indels
                                                                                                                     59 G---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                           58 HG---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                         Sequence 20, Application US/10090035 Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
                      12;
                      60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Triticum aestivum
US-10-090-035-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Triticum aestivum US-10-090-035-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.6%
Matches 58; Conservative
                                                                                                                                                                                                                       US-10-090-035-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-090-035-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 24
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                    а
                                                                                                                   à
                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                    23
                                                                                                                                           1 MAYYQEVDYCSEEVRSVAP-AGFGRHGGGYQQHVVKEKFEEVDTVSRAGANHHHHHHHGHHG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGAN-HHHHHGHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                 ï
                                                                                                                                                                                                                                                                                    VS-10-090-035-16

Sequence 16, Application US/10090035

Fatent Wo. US/20020170089A1

GENERAL INFORMATION:
TITLE OF INVENTION: Proteins and Uses Thereof

FILE REFERENCE: 35148/242990

CURRENT APPLICATION NUMBER: US/10/090,035

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 02/28/2001

NUMBER OF SEQ ID NOS: 25

SOFFWARE: FEASTSEQ for Windows Version 4.0
                                                              Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE REFERENCE: 3718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER: OF TELEME DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 57.8%; Score 295; DB 9; Length 91
Best Local Similarity 60.6%; Pred. No. 4e-23;
Matches 57; Conservative 14; Mismatches 19; Indels
                                                         Score 499.5; DB 9;
Pred. No. 5.9e-44;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 277.5; DB 9;
Pred. No. 2.4e-21;
                                                                                                                                                                                        60 GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                            60 GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 91
                                                     97.98;
; ORGANISM: Triticum aestivum
US-10-090-035-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.4%;
61.2%;
                                                                                    93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Triticum aestivum
US-10-090-035-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-090-035-16
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-090-035-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                    Matches
                                                                                                                     ð
                                                                                                                                                   8
                                                                                                                                                                                        õ
                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

۲,

14; Gaps

14;

```
175 ADDMGAGHHHGAНHTAННННSANHHHHHHHHHGGSG 210
                                                                                                                         Sequence 64, Application US/09888615
Patent No. US20020064856A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ucery match
Best Local Similarity 33.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.3
Best Local Similarity 29.9
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-232-563-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                  GENERAL INFORMATION:
49 A---
                                                                                              RESULT 13
US-09-888-615-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-232-563-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                g
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 MSGYQH--HLNPEALNLTPEDAVETLIGSGHHGAHHGAHHPAAAAYEAFRGQNFASGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAYYQEVDYCSEEVRSVAP----AGFGRHGGGVQQH-----VVKEKFBEVDTVSRAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAYYQEVDYCSEEVRSVAP-AGFGRHGGGVQQHVVKEKFFEEVDTVSRAGANHHHHHGHHG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/10232563;
Sequence 7, Application US/10232563;
Publication No. US20030087394A1
GENERAL INFORMATION:
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
GURRENT APPLICATION NUMBER: US/10/232,563
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US/10/32,563
PRIOR PELLING DATE: 2001-08-31
NUMBER OF SEQ 1D NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: SImmons, Carl R.
TITLE OF INVENTION: Nucleal Acids Encoding Defense Inducible
TITLE OF INVENTION: Deteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 9; Length 359;
Pred. No. 1.4;
7; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
                      HG---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                             54 HGRGSGH-FEVRESKLEEDINTRTGEFHERKGNFSSKAD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 245; DB 9;
Pred. No. 5.4e-18;
9; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
LOCATION: (1)...(99)
CHER INFORMATION: Xaa = Any Amino Acid
MS-10-090-035-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GHGFVVRETRVEEDINTCTGEVHER 84
                                                                                                                                                              Sequence 14, Application US/10090035 Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26.0%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.8%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus US-10-232-563-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 7
LENGTH: 359
TYPE: PRT
                                                                                                                                               US-10-090-035-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -10-232-563-7
                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                     q
                                  δ
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHG--GHG-----FVVRETRVEED 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches 19; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10232563
Sequence 2, Application US/10232563
Publication No. US20030087394A1
GERERAL INFORMATION:
TITLE OF INVENTION: INSULIN RELATED TRANSCRIPTION FACTOR AND TITLE OF INVENTION: USSE THEREOF FILE REPERSOR: 10276-072001
CURRENT FILING DATE: 2002-08-30
PRIOR PILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.3%; Score 78; DB 9; Length 352; 29.9%; Pred. No. 2.1; tive 7; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 GANHHHHHHHHGH--GFVVRETRVEEDINTCTGEVHERRESFLA.90
GENERAL INFOGRATION:
GENERAL INFOGRATION:
APPLICANT: WHYTE, DAVID
APPLICANT: GENERAEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: WINNING, GERARD
APPLICANT: WINNING, GERARD
APPLICANT: WINSENAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: 05/214,047
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 64
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD_RES
LOCATION: (1891)
CTHER INFORMATION: Any amino acid
US-09-888-615-64
```

```
| No. 10 | N
```

Search completed: June 6, 2003, 13:02:10 Job time : 29 secs

Sequence 603, App Sequence 201, App Sequence 200, App Sequence 199, App Sequence 253, App Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli Sequence 1, Appli

US-08-974-549A-603 US-09-199-637A-201 US-09-199-637A-199 US-09-199-637A-259 US-08-291-394-2 US-08-991-804-4 US-08-991-804-4 US-09-011-769A-60 US-09-011-769A-60 US-09-011-769A-60 US-09-011-769A-60 US-08-279-270A-1 US-08-279-270A-1 US-08-279-270A-1 US-08-279-270A-1 US-08-650-000-4 US-08-680-770-761A-7 US-08-980-755-457-1 US-08-981-709A-50

133.2 1123.3 1122.9 1122.9 1122.8 1122.8 1122.8 122.6 123.6

-

```
6, 2003, 12:49:03 ; Search time 18 Seconds (Without alignments) 152.018 Million cell updates/sec
                                                                                                                                                                                                          510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: ./cggl_6/ptcdata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/laa/pcTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/laa/pcTUS_COMB.pep:*
    5.1.6
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     262574 seqs, 29422922 residues
GenCore version
Copyright (c) 1993 - 2003
                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum.Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                          US-10-090-035-4
                                                                                                               June
                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                Scoring table:
                                                                      OM protein
                                                                                                                                                                                                                            Seguence:
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                         Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## No. Score Match Length DB ID 1 79 15.5 414 5 PCT-US92-06840-2 Sequence 2, 27 15.1 763 2 US-09-252-571-2 Sequence 2, 27 15.1 763 3 US-09-252-571-2 Sequence 2, 27 15.1 763 4 US-08-010-2 Sequence 2, 27 15.1 763 4 US-08-079-029-9 Sequence 3, 27 15.1 763 4 US-08-079-029-9 Sequence 3, 27 14.3 617 1 US-08-137-614A-26 Sequence 2, 27 14.3 617 1 US-08-137-614A-26 Sequence 4, 27 14.3 617 1 US-08-137-614A-26 Sequence 4, 27 14.3 617 1 US-08-137-614-6 Sequence 6, 27 14.3 617 3 US-08-072-064-6 Sequence 6, 27 14.3 617 3 US-08-072-064-6 Sequence 1, 27 14.3 617 3 US-08-072-064-6 Sequence 1, 27 14.3 617 3 US-08-072-064-6 Sequence 1, 27 14.3 617 5 US-08-072-064-6 Sequence 2, 27 15.1 17

Appli

	ALIGNMENTS		
M O M A A A A A A A A A A A A A A A A A	PETUTI 1  FCT-1052-06840-2  Sequence 2, Application PC/TUS9206840  GENERAL INFORMATION:  GENERAL INFORMATION:  APPLICANT: Seto, Edward  APPLICANT: Shenk, Yang  APPLICANT: Shenk, Thomas  TITLE OF INVENTION: YIT TRANSCRIPTION FACTOR AND METHODS OF  TITLE OF INVENTION: ISOLATING SAME  NUMBER OF SEQUENCES: 10  CORRESPONDENCE ADDRESS:  ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  STREE: Ostrolenk, Faber, Gerb & Soffen  GITY: New York  COUNTRY: USW YORK  STATE: New YORK  STATE: New YORK  STATE: New YORK  COUNTRY: USW YORK  COUNTRY: USW YORK  COUNTRY: USW YORK  COUNTRY: USW COMPATIBLE  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: PATENTION PREABSE #1.0, Version #1.25  CURRENT APPLICATION NAMER: PCT/US92/06840  ELLING DATE: 19920814  CLASSIFICATION NUMBER: PCT/US92/06840  ELLING DATE: 1006-1991  APPLICATION NUMBER: US 07/746,485  FLING DATE: 1006-1991  APPLICATION NUMBER: M-12594 CIP (1570-8)  TELECHMUNICATION INFORMATION:  TEL		
J ÖME	Query Match 15.5%; Score 79; DB 5; Length 414; Best Local Similarity 29.2%; Pred. No. 0.088; Matches 21; Conservative 6; Mismatches 25; Indels 20;	Gaps	ë

```
11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA-----GANHHHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09434065
; Sequence 2, Application US/09434065
; Patent No. 6107074
; GENERAL INFORMATION:
APPLICANT: SONG, HO Yeong
APPLICANT: ROTHE, Mike
TITLE OF INVENTION: TRAF2-Associated Kinase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, 34th floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Indels
Albritton & Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSIEM: PC-DOS/MS-DOS
PatentIn Release #1.0, version #1.30
                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77; DB 2;
Pred. No. 0.33;
4; Mismatches
ADDRESSEE: Flehr, Hohbach, Test, Albritte
STREET: 4 Embarcadero Center, 34th floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                       NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: T96-005/A63613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 781-1899
TELEFAX: 415 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/434,065
                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/677,862
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.1%;
Best Local Similarity 33.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415 398-3249
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 11
615 HHHHHG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 HHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                       94111
                                                                    CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-434-065-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-571-2
                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GVQQHVVKEKFEEVDTVSRA-----GANHHHHG 56
            21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGHHGGH-GFVVRETRVEEDINTCTG 79
                                     14; Gaps
                                                                                                                                                                                                RESULT 2
US-08-677-862-2
| Sequence 2, Application US/08677862
| Sequence 2, Application US/08677862
| Patent No. 5874230
| GENERAL INFORMATION:
| APPLICANT: SONG, HO Yeong
| APPLICANT: ROTHE, Mike
| TITLE OF INVENTION: TRAF2-Associated Kinase
| TITLE OF INVENTION: TRAF2-ASSOCIATED KINASE
| ORRESPONDENCES: 2
| CORRESPONDENCES: 2
| CARDESSEE: Flehr, Hobbach, Test, Albritton & Herbert STRRET: 4 Embarcadero Center, 34th floor
| CITY: SON FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 77; · DB 2; Length 763;
Pred. No. 0.33;
4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09252571
Sequence 2, 581250
CENERAL INFORMATION:
APPLICANT: SONG, Ho Yeong
APPLICANT: SOTHE, Mike
TITLE OF INVENTION: TRAF2-Associated Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSLFICATION:
ATTORNEY/ABORNT INFORMATION:
NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFERENCE/POCKET NUMBER: T96-005/A63613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415 398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ucuely match
Best Local Similarity 33.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 SEEVRSVAPAGFGRHGG-
                                                           55 GGGDHGGG-----
                                                                                                                            :|| :| : | 3
96 QVHHHQEVILVQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                 80 EVHERRESFLAR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 HHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-252-571-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-677-862-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                              g
                                                                                                     ò
                                                                                                                                        g
```

14; Gaps

us-10-090-035-4.rai

```
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Palleja, Estivill Xavier
APPLICANT: Palleja, Estivill Xavier
APPLICANT: Pritcherd, Melanie
APPLICANT: Vilato, Jordi Guimera
TITLE OF INVENTION: Human Gene Sequence of the Down Syndrome Critical
Patent No. 635164
TITLE OF INVENTION: Region of Human Chromosome 21, Coding for A Serine-
TITLE OF INVENTION: Threonine Protein Kinase (MNB), Expressed in the
TITLE OF INVENTION: Nouronal Regions Affected in Down Syndrome
FILE REFERENCE: U 011114-4
CURRENT APPLICATION NUMBER: US/08/789,275A
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
LENGTH: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA-----GANHHHHG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 763;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
15.1%; Score 77; DB 3; Length 763
Best Local Similarity 33.3%; Pred. No. 0.33;
Matches 22; Conservative 4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77; DB 4; Length 763;
Pred. No. 0.33;
4; Mismatches 26; Indels
                                     ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: T96-005/A63613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 781-1989
APPLICATION NUMBER: 08/677,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08789275A
Patent No. 6251664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08789275A Patent No. 6251664 GENERAL INFORMATION:
                                                                                                                                                                TELEFAX: 415 398-3249
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 15.1%;
Best Local Similarity 33.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-434-065-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  615 ННИНЬ 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 HHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615 ННИНЬ 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 HHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-789-275-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-789-275-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-789-275-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  င်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHG 56
APPLICANT: Pritchard, Melante
APPLICANT: Pritchard, Melante
APPLICANT: Vilaro, Jordi Gulmera
TITLE OF INVENTION: Human Gene Sequence of the Down Syndrome Critical
Patent No. 6251664
TITLE OF INVENTION: Region of Human Chromosome 21, Coding for A Serine-
TITLE OF INVENTION: Threonine Protein Kinase (MNB), Expressed in the
TITLE OF INVENTION: Neuronal Regions Affected in Down Syndrome
CURRENT APPLICATION NUMBER: US/08/789,275A
CURRENT FILING DATE: 1997-01-28
NUMBER OF SEO ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
15.1%; Score 77; DB 4; Length 763;
Best Local Similarity 33.3%; Pred. No. 0.33;
Matches 22; Conservative 4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09086010
Patent No. 6274338
| GENERAL INCEMATION:
APPLICANT: Glimcher, Laurie H. et al.
TITLE OF INVENTION: Human c-Maf Compositions and
TITLE OF INVENTION: Hethods of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/030,579
FILING DATE: 2-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: HUI-027CP
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Rat norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 HHHHHG 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 HHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                      SEQ ID NO 5
LENGTH: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-789-275-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-09-086-010-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
```

Adams, Camilia W.

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fitzgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Martin, Mark T.
APPLICANT: Martin, Mark T.
APPLICANT: Milliams, Richard C.
APPLICANT: Mark T.
APPLICANT: Milliams, Richard C.
APPLICANT: Mark T.
APPLICANT: Mark 
                                                                                                                                                                                                            11 SEEVRSVAPAGFGRHGGGVQQH-----VVKEKFEEVDTVSRAGANHHHHGHHGGH 61
                                                                                                                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.4%; Score 73.5; DB 2; Length 40; Best Local Similarity 34.8%; Pred. No. 0.024; Matches 16; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 HVVKEKFEEVDTVSRAGANHHHHHHGHHGGHGFVVRETRV--EEDIN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AAEOKLISEEDLN 37
                                                         14.9%; Score 76; DB 4; Length 400; 31.6%; Pred. No. 0.2; tive 8; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39, Application US/08273146
Patent No. 5855885
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 9, Application US/09079029; Patent No. 6342369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith, Rodger
McCafferty, John
Chiswell, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 40 amino acids
                                                                         Query Match 14.99
Best Local Similarity 31.69
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-273-146-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-079-029-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-273-146-39
US-09-086-010-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                        ð
```

```
256 EADYYCNSRDSS-----2NHVVFGGGTKL-----TVLGAAAHHHHHG---- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 EVD-YCSEEVRSVAPAGFGRH---GGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHHHGHHGGH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.4%; Score 73.5; DB 4; Length 309; 32.9%; Pred. No. 0.29; Live 6; Mismatches 14; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z1F: 3*coc
COMPUTER READBLE FORM: 1.44 Mb floppy disk
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                               COMPUTER PARADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIBLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapal, Anan
APPLICANT: Chuntharapal, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA MAY
CITY: South San Francisco
STARET: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Genentech)
CURRENT. APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
                                                        TITLE OF INVENTION App-2 Receptor NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEE Genentech, Inc. STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-079-029-10; Sequence 10, Application US/09079029; Sequence 10, Application US/09079029; Patent No. 6342369; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-5416
TELEPHONE: 650/255-5416
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                      Chuntharapai, Anan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :: |||:|
294 ---AAEQKLISEEDLN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GFVVRETRV--EEDIN 75
                                                                                                                                                          STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 32.99
Matches 25; Conservative
                                              Kim, Kyung J.
                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                   94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-079-029-9
APPLICANT:
APPLICANT:
                                                 APPLICANT:
```

```
GENERAL INFORMATION:

APPLICANT: Berl, Rajindar K.

APPLICANT: Carling, David

APPLICANT: Carling, David

APPLICANT: Carling, David

APPLICANT: Forder, Robert A.

TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NGAP/PHM37588/UST

CURRENT APPLICATION NUMBER: US/08/557,006C

CURRENT FILING DATE: 1994-05-20

PRIOR PRILING DATE: 1994-05-20

PRIOR PPLICATION NUMBER: GB 9318010.7

PRIOR FILING DATE: 1993-05-21

PRIOR FILING DATE: 1993-06-31

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1

LENGTH: 633
                                                                                                                          413 VGPGGPGGGGGV-----NVGVGMGMGPEHGHGHGHGHGHPAPSHGHPHAPKQTVSNRP 462
                                                                                      17 VAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGHHG----CHGFVVRET----
                                                       22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                   Best Local Similarity 27.8%; Pred. No. 0.78;
Matches 20; Conservative 7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 4; Length 633;
Pred. No. 0.81;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08072064
Patent No. 6008046
GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
CORRESPONDENCE: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION: (1)..(633)
COTHER INFORMATION: Yeast SNF1 polypeptide
US-08-557-006C-43
                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/08557006C Patent No. 6258547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%;
76.9%;
                                                                                                                                                                                                                463 IGFSNIQQNVGT 474
                                                                                                                                                                                 69 ----RVEEDINT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 инниннинсенс 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||| || |||
21 нняннянняндя
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Yeast
                                                                                                                                                                                                                                                                                        RESULT 12
US-08-557-006C-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-072-064-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || | |:||||||
----TVLGAAAHHHHHG---- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 EVD-YCSEEVRSVAPAGFGRH---GGGVQQHVVKEKFEEVDTVSRAGANHHHHGHHGGH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/08137614A

Sequence 26, Application US/08137614A

Septent No. 5487976

GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Milpple, Douglas C.
APPLICANT: Henderson, Joseph E.
TITLE OF INVENTION: Gene Encoding An Insect
TITLE OF INVENTION: Gamma-Aminobutyric Acid (GABA) Receptor Subunit NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: ALXON, HAIGTAVE, DEVANS & DOYLE
                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.4%; Score 73.5; DB Best Local Similarity 32.9%; Pred. No. 0.29; Matches 25; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 EADYYCNSRDSS-----GNHVVFGGGTKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%; Score 73;
APPLICATION NUMBER: US/09/079,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/137,614A
FILLING DATE: 15-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19603/120
                                   CLASSIFICATION:
NAME: MAIGHARY, INFORMATION:
NAME: MAIGHARY, DAIRE L.
REGISTRATION NUMBER: 35,600
REFERENCE, DOCKET NUMBER: F1101
TELECHONICATION INFORMATION:
TELEPHONE: 650/255-5416
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENTH: 312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFRENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1636
TELEFAX: (716)263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 ---AAEQKLISEEDLN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GEVVRETRV--EEDIN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEO ID NO. 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          : 312 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-137-614A-26
                                                                                                                                                                                                                                                                                                                       Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -08-137-614A-26
                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-09-079-029-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

ö

Gaps

```
17 VAPAGEGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHG---GHGFVVRET---- 68
                                                                                                                                                                                                                                                                                17 VAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHG---GHGFVVRET----
                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
                                                                                                                                                                       DB 3; Length 637;
                                                                                                                                                                                                                 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER, READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/072,064
FILIG DATE: 19930602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PETER G. CARROLL STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California COUNTRY: United States of America ZIP: 94104
                                                                                                                                                                         Score 73; DB 3;
Pred. No. 0.81;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%; Score 73; DB.:
11larity 27.8%; Pred. No. 0.81;
Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPHD-00574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19930602
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08072064
Patent No. 6008046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                           14.3%;
nilarity 27.8%;
Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 637 amino acids
AMINO ACID
                                                              : 637 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                  484 IGFSNIQQNVGT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                 434 VGPGGPGGPGGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415/397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide US-08-072-064-6
                                                                                                                                                                                                                                                                                                                                       69 ----RVEEDINT 76
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 20; Conserve
                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-072-064-6
                                                                                                                                          US-08-072-064-4
                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NVGVGMGMGPEHGHGHGHAHSHGHPHAPKQTVSNRP 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 VAPAGEGRHGGGVQQHVVKEKFEEVDIVSRAGANHHHHHHHHGHHG---GHGFVVREI----- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73; DB 3; Length 637;
Pred. No. 0.81;
7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: PETER G. CARROLL
STREET: 220 Montégomery Street, Suite 2200
CITY: San Francisco
STREE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,064
FILLIG DATE: 19930602
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOSOME/SEGMENT: III; polytene subregion 66F MAP POSITION: approximately map unit 26
                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 0PHD-00574
TELECHMUNICATION INFORMATION:
TELECHMONE: 415/705-8410
TELEFRAX: 415/397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPHD-00574
                                                                                                                                                                                                                                                                                                                                                                                                 OKNANISM: Drosophila melanogaster POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
              APPLICATION NUMBER: US/08/072,064
FILING DATE: 19930602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08072064 Patent No. 6008046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: OF FELECOMMUNICATION INFORMATION: TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                              TELEFAX: 415/39/-b330
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 antho acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.8%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 VGPGGPGGPGGGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 IGFSNIQQNVGT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 ----RVEEDINT 76
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                       FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-072-064-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-072-064-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

ë,

22; Gaps

69 ----RVEEDINT 76 ::::: | 484 IGFSNIQQNVGT 495

Oy Op

Search completed: June 6, 2003, 12:54:08 Job time: 19 secs

The state of	4	,		Andrew CA	* 1		5.7	THE PARTY OF THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO	1 1 1 T	.7		
	∢.		٠.	*	Sec.			) /200		÷.		
	*				ega Nor			to pro-				
7				A 2								
100 m								÷ .	i		•	
			at at	*					,			. *
			,									
			,						•			
•												
a Poo			, ·	* *								at .
			= :									
												1
		•		3,4			7.4					
	٠.	*,	× , .	<u> </u>								
				¥ <sup>2</sup>			•					4
												<u>:</u>
												•
2						•					3	
	•											
												1
				• 10					1.8			. 1
												ş <del>a</del>
									· .	. 5		V
				•				•				
		•		7 * "						•)(=		
								4				
				* *								
	17	4									*	
*												
1												
de i						-	ċ.			•		
3				•							٠.	
										•		
												,
<b>Q</b> .					•			• •				
ľ												
L												
												t in
								•				<u>.</u>
*												, , ,
- 3												
		•										
e Fr			*					. 9				
1											•	and the same of th
■報,							**3	\$			 غي	A STATE OF THE STA

```
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Drosophila melanog
Drosophila melanog
ScFv 1b4 antibody
Drosophila melanog
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                          June 6, 2003, 12:42:12 ; Search time 31.5 Seconds (Without alignments) 393.407 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Sinos2/godata/geneseq/geneseqp-embl/AA1980_DAT:*
| Sinos2/godata/geneseq/geneseqp-embl/AA1981_DAT:*
| Sinos2/godata/geneseq-embl/AA1981_DAT:*
| Sinos2/godata/geneseqy-embl/AA1981_DAT:*
| Sinos2/godata/geneseqy-embl/AA1991_DAT:*
| Sinos2/godata/geneseqy-embl/AA20000_DAT:*
| Sinos2/godata/geneseqy-embl/AA2001_DAT:*
                                                                                                                                                                                                                                                                                                              1 MAYYQEVDYCSEEVRSVAPA......INTCTGEVHERRESFLARAN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG26460
AAG26459
AAG26458
ABB66445
ABB63257
AAG6039
ABB67674
AAG13903
AAG13903
                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                            US-10-090-035-4
510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.5
16.5
16.5
16.5
16.0
15.8
15.8
                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ģ
```

21 AAB41548 Human ORFX ORF1315 22 AAB94344 Human protein sequ			
AAB41548 Human OAFX ORF			
AAB41548	95	14.	45
	95 2	14.	44
ABB60446	37 2	14.	<b>4</b> .
AAB93737 Human profe	37 2	14.	7 .
AAU74634	49 2	7	4.
ABB71938	ď	14.	<b>4.</b>
ABB74382	34 2	14.	n .
ABB69230	015 2	7	200
ABB58402	534 2		ì (
ABB61798	4	1	) (
ABB92962	000		יי
ABB69373		1.	* L
AAY31232	400	7	0 6
ABB61038	~	6.5 15.	2.0
AA017154	288 2	15	31
ABB57155	33	77 15	30
AAU02222		15	29
AAIIO221	· ·	15	28
AAW41734		15	27
ABB67228		15	26
ADD 0.040		15	52
ADD04202	000	77 15	24
	••	77.5 15.2	23.
ABB65863			25
ABB71829	2:	7 5 15	210
AAB90775	414	15	5
3 AAW65406	14	15	976
I AAR32020		15	77
2 AAB11466		15	19
2 AAB11465		9 15	CT.
3 AAU82706		15	4.
L AAG49723	405	0.5 15	13
1 AAG49724		2 12	77
1 AAG13901 Arabidons		CT C'O	11
	396		

## ALIGNMENTS

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 30923.
      AAG26460
ID AAG26460 standard; Protein; 441 AA.
                                                                                                                                                                                                          990S-0121825.
990S-0123180.
990S-0123548.
990S-0125788.
                                                                                                                                                                                                                                              990S-0126264.
990S-0126785.
990S-01287462.
990S-0128234.
990S-0128714.
990S-0130077.
                                                                                                                                                                                       25-FEB-2000; 2000EP-0301439
                                                     17-OCT-2000 (first entry)
                                                                                                                               Arabidopsis thallana,
                                                                                                                                                  EP1033405-A2
                                                                                                                                                                                                                  05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                         25-FEB-1999
                                                                                                                                                                                                                                                                                             16-APR-1999;
19-APR-1999;
                                                                                                                                                                    06-SEP-2000
                                     AAG26460;
RESULT 1
```

PR 21-APR-1999; 99US-0130449. PR 23-APR-1999; 99US-0130891. PR 32-APR-1999; 99US-0131449. PR 30-APR-1999; 99US-0131449. PR 30-APR-1999; 99US-0131449. PR 65-MAY-1999; 99US-0132486. PR 65-MAY-1999; 99US-0132486. PR 14-MAY-1999; 99US-0132486. PR 14-MAY-1999; 99US-0132486. PR 14-MAY-1999; 99US-0134219. PR 14-MAY-1999; 99US-0134219. PR 14-MAY-1999; 99US-0134219. PR 14-MAY-1999; 99US-0134219. PR 20-MAY-1999; 99US-0134219. PR 21-MAY-1999; 99US-0134219. PR 21-MAY-1999; 99US-013422. PR 10-UNN-1999; 99US-013422. PR 10-UNN-1999; 99US-013442. PR 10-UNN-1999; 99US-013442. PR 10-UNN-1999; 99US-013442. PR 10-UNN-1999; 99US-0133442. PR 10-UNN-1999; 99US-014083. PR 10-UNN-1999; 99US-014433. PR 10-UNN-1999; 99US-0				
21-APR-1999 23-APR-1999 28-APR-1999 30-APR-1999 30-APR-1999 30-APR-1999 30-APR-1999 30-APR-1999 30-APR-1999 30-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 44-APR-1999 46-AP	S-0130449 S-0130510 S-0130891 S-0130891 S-0132049 S-0132407 S-0132487 S-0132487 S-0132487 S-0132487 S-0132885	S-0134218 S-0134218 S-0134278 S-0134278 S-0134278 S-0134278 S-013428 S-013632 S-013632 S-013632 S-013752 S-013752 S-013752 S-013752 S-013752 S-013752 S-013752 S-013752 S-013752 S-013762	US-013945 US-013945 US-013946 US-013946 US-013946 US-013946 US-013976 US-013975 US-013976 US-013976 US-013976 US-014035	102-01428 103-01429 103-01435 103-01436 103-01440 103-01443 103-01443 103-01443 103-01443 103-01443 103-01443
	21-APR-1999 23-APR-1999 28-APR-1999 28-APR-1999 30-APR-1999 04-MAY-1999 06-MAY-1999 06-MAY-1999 06-MAY-1999	14 MAY - 1995 14 MAY - 1995 14 MAY - 1995 14 MAY - 1995 16 MAY - 1995 20 MAY - 1995 21 MAY - 1995 22 MAY - 1995 25 MAY - 1995 26 MAY - 1995 27 MAY - 1995 27 MAY - 1995 28 MAY - 1995 27 MAY - 1995 28 MAY	18 - JUN - 199 18 - JUN - 199 22 - JUN - 199 23 - JUN - 199 24 - JUN - 199 25 - JUN - 199 26 - JUN - 199 27 - JUN - 199 28 - JUN - 199 29 - JUN - 199 20 - JUN - 199 21 - JUN - 199 22 - JUN - 199 23 - JUN - 199 24 - JUN - 199 25 - JUN - 199 26 - JUN - 199 27 - JUN - 199 28 - JUN - 199 29 - JUN - 199 20 - JUN - 199	08-JUL-199 09-JUL-199 13-JUL-199 14-JUL-199 16-JUL-199 19-JUL-199 19-JUL-199 19-JUL-199 19-JUL-199 19-JUL-199 19-JUL-199 19-JUL-199 19-JUL-199

```
PR 20-JUL-1999; 99US-0144832.
PR 20-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145146.
PR 22-JUL-1999; 99US-0145146.
PR 22-JUL-1999; 99US-0145218.
PR 22-JUL-1999; 99US-0147302.
PR 03-AUG-1999; 99US-0147302.
PR 03-AUG-1999; 99US-0147720.
PR 13-AUG-1999; 99US-0147720.
PR 13-AUG-1999; 99US-0147720.
PR 13-AUG-1999; 99US-0147720.
PR 13-AUG-1999; 99US-0149772.
PR 13-AUG-1999; 99US-0149772.
PR 13-AUG-1999; 99US-0149772.
PR 13-AUG-1999; 99US-0149772.
PR 22-AUG-1999; 99US-015206.
PR 22-SEP-1999; 99US-015206.
PR 23-SEP-1999; 99US-015206.
PR 23-S
```

```
99US-0132485.
99US-0132486.
99US-0132487.
99US-0132863.
99US-0134256.
99US-0134219.
                                                          990S-0134221
990S-0134370.
990S-0134768.
990S-0134941.
990S-0135124.
990S-01355353.
                                                                                                                                   990S-0137222
990S-0137528
990S-0137502.
990S-0137724.
990S-0138094.
                                                                                                              99US-0136021.
99US-0136392.
99US-0136782.
                                                                                                                                                                              99US-0138847.
99US-0139119.
99US-0139452.
99US-0139453.
99US-0139454.
99US-0139455.
                                                                                                                                                                                                                                              9903-0139459.
9903-0139460.
9903-0139460.
9903-0139461.
9903-0139462.
                                                                                                                                                                                                                                                                                          99US-0139750.
99US-0139763.
99US-0139817.
                                                                                                                                                                                                                                                                                                               99US-0139899.
99US-0140353.
99US-0140354.
                                                                                                                                                                                                                                                                                                                                                                                                     99US-0142920.
99US-0142977.
99US-0143542.
99US-0143624.
                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0144005
99US-0144085
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0144086
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0144325
99US-0144331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0145086.
99US-0145088.
99US-0145085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0144332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0144333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0144335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0144352
        05-MAY-1999;

06-MAY-1999;

07-MAY-1999;

11-MAY-1999;

14-MAY-1999;

14-MAY-1999;

14-MAY-1999;

14-MAY-1999;

19-MAY-1999;

20-MAY-1999;

21-MAY-1999;

22-MAY-1999;

22-MAY-1999;

23-MAY-1999;

25-MAY-1999;
                                                                                                                                                      07-70N-1999;
08-70N-1999;
10-70N-1999;
10-70N-1999;
                                                                                                                                          03-JUN-1999;
         3,
                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                   8 DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHH----HGGH 61
                                                                                                                                                                                                 8; Gaps
                                                                                                                                                                            'Match 16.5%; Score 84; DB 21; Length 441; Local Similarity 36.8%; Pred. No. 0.064; nes 21; Conservative 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 30922.
                                                                                                                                                                                                                                                         AAG26459 standard; Protein; 473 AA.
 990S-0159331.
990S-0159637.
990S-0159538.
990S-0160741.
990S-0160767.
990S-0160767.
990S-0160767.
                                                                                                     990S-0161405
990S-0161406
990S-0161369
990S-0161360
990S-0161320
990S-0161992
990S-0161993
                                                                                99US-0160981.
99US-0160989.
99US-0161404.
                                                                                                                                                                                                                                                                                                                                                                                                          99US-0121825.
99US-0123180.
99US-0123788.
99US-0125788.
99US-0126264.
99US-0126785.
99US-0126785.
99US-012845.
99US-0130077.
99US-013010.
99US-013010.
99US-0131449.
99US-0131449.
                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                Arabidopsis thallana
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                              EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1999;
05-MAR-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
                                                                                                                                                                                                                                                                                      17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1999,
23-APR-1999,
                                                                                                                                                                            Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                         AAG26459;
                                                                                                                                                                                                                       377
```

g ð

```
PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145224.

PR 23-JUL-1999; 99US-0145224.

PR 23-JUL-1999; 99US-0145224.

PR 23-JUL-1999; 99US-0145224.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145918.

PR 02-ANG-1999; 99US-0145918.

PR 02-ANG-1999; 99US-0147302.

PR 03-ANG-1999; 99US-0147302.

PR 10-ANG-1999; 99US-0147302.

PR 10-ANG-1999; 99US-0147302.

PR 11-ANG-1999; 99US-0147302.

PR 11-ANG-1999; 99US-0149302.

PR 11-ANG-1999; 99US-0149302.

PR 11-ANG-1999; 99US-0149302.

PR 12-ANG-1999; 99US-0149302.

PR 13-ANG-1999; 99US-0149302.

PR 23-ANG-1999; 99US-015303.

PR 23-SEP-1999; 99US-015303.

PR 23-
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                        8 DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGH---HGGH 61
                                                                                                                                                 Gaps
                                                                                                                               16.5%; Score 84; DB 21; Length 473; 36.8%; Pred. No. 0.07; ive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 30921.
                                                                                                                                                                                                                         AAG26458 standard; Protein; 488 AA
                                                                                                                                                                                                                                                                                                                                                                                        99US-0121825.
99US-0123548.
99US-0123548.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0127462.
99US-0128714.
99US-013077.
99US-013077.
99US-0130449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0132484.
990S-0132485.
990S-0132486.
990S-0132863.
990S-0134218.
            9905-0160815.
9905-0160980.
9905-0160981.
9905-0160981.
9905-0161404.
9905-0161405.
9905-0161359.
9905-0161360.
9905-0161360.
9905-0161360.
9905-0161361.
                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0132407
                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                     Query Match 16.5
Best Local Similarity 36.8
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 - ARR - 1999;
28 - APR - 1999;
30 - APR - 1999;
30 - APR - 1999;
05 - MAY - 1999;
06 - MAY - 1999;
06 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                          EP1033405-A2
                    22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                           06-SEP-2000
                                                                                                                                                                                                                                            AAG26458;
                                                                                                                                                                                                           RESULT 3
AAG26458
                                                                                                                                                                                                                              g
                                                                                                                                                                      ğ
```

•	
- SUG SUG-	990x-0138847 99us-0139845 99us-0139452 99us-0139452 99us-0139456 99us-0139456 99us-0139460 99us-0139460 99us-0139461 99us-0139461 99us-0139461 99us-0139461 99us-0139461 99us-0139750 99us-0139750 99us-0139750 99us-013989 99us-013989 99us-013989 99us-0140991 99us-014091 99us-014086 99us-014384 99us-014384 99us-014384 99us-014384 99us-014384 99us-014384 99us-0144086 99us-0144086 99us-0144086 99us-0144331 99us-0144331 99us-0144331 99us-0144331 99us-0144331 99us-0144332 99us-0144332 99us-0144332 99us-0144332 99us-0144333 99us-0144334 99us-0144336 99us-0144336 99us-0144336 99us-0144336 99us-0144336 99us-0144336 99us-0144336 99us-0144336 99us-0144336 99us-0144336 99us-0144336 99us-0145086 99us-0145086
14 - MAY - 1999; 14 - MAY - 1999; 18 - MAY - 1999; 20 - MAY - 1999; 21 - MAY - 1999; 25 - MAY - 1999; 27 - MAY - 1999; 03 - JUN - 1999; 04 - JUN - 1999; 04 - JUN - 1999; 08 - JUN - 1999; 08 - JUN - 1999;	PR 10-JUN-1999; PR 16-JUN-1999; PR 16-JUN-1999; PR 16-JUN-1999; PR 18-JUN-1999; PR 23-JUN-1999; PR 20-JUN-1999; PR 13-JUN-1999; PR 20-JUN-1999; PR 20-JUN-1999; PR 20-JUN-1999; PR 20-JUN-1999; PR 22-JUN-1999; PR 23-JUN-1999; PR 23-JUN-1999

9905-0145913.
9905-0145913.
9905-0145919.
9905-0145919.
9905-0146386.
9905-0146386.
9905-0146386.
9905-0147102.
9905-0147102.
9905-0147102.
9905-0147102.
9905-0147103.
9905-0147103.
9905-0147303.
9905-0147303.
9905-0147303.
9905-0147303.
9905-0147303.
9905-0147303.
9905-0147303.
9905-0147303.
9905-0147303.
9905-0147303.
9905-0155659.
9905-0155659.
9905-0155659.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.
9905-015773.

27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 03-AUG-1999; 04-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999; 14-AUG-1999; 15-AUG-1999; 16-AUG-1999; 17-AUG-1999; 18-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 47

```
GANH-----HHHHGHHGGHGFVVRE--------TRVEEDINTCTGEVHERRES
                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
--HVVKEKFEEVDTVSRA-
                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 16563.
                                                                                                                        ABB63257 standard; Protein; 168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 DVKIIKVIQEEGHSHGHGH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VVRETRVEEDINTCTGEVH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.3%;
32.9%;
   12 EEVRSVAPAGFGRHGGGVQQ-
                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 32.9
Matches 26; Conservative
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
N-PSDB; ABL07360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 AA;
                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interactions -
                                                                                                                                                                                                                                                                         WO200171042-A2.
                                                                                                                                                                                                                            pharmaceutical
                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                               27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                ABB63257;
                                                 48
                                                                                                                  ABB63257
                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                 ö
                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is
                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from brosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                 Gaps
                                                                                                                                                    8 DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGH---HGGH 61
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 26127; 21pp + Sequence Listing; English.
                                                                                                                                  ..
œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.5%; Score 84; DB 22; Length 1561; Best Local Similarity 23.9%; Pred. No. 0.32; Matches 28; Conservative 17; Mismatches 30; Indels 4
                                                                                                          Length 488;
                                                                                                                                  18; Indels
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 26127.
                                                                                                            DB 21;
                                                                                                              16.5%; Score 84; DB 21 36.8%; Pred. No. 0.073; iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                     ABB66445 standard; Protein; 1561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                   99US-0161992.
99US-0161993.
99US-0162142.
                                  99US-0161360
99US-0161361
             99US-0161406
                          99US-0161359
                                                          99US-016192(
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1561 AA;
                                                                                                                        1 Similarity
21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABL10548
                                                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                           pharmaceutical
                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                     26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
                                                                                           29-0CT-1999
                                                                      28-OCT-1999
                                                                                 28-OCT-1999
                           -OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                               ABB66445;
                                                                                                                 Query Match
                                                                                                                             Local
                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                  RESULT 4
ABB66445
                                                                                                                                                                                                                                                    g
     PR
PR
PR
PR
PR
PR
                                                                                                                                                              ò
```

```
ò
                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VDYCSEEVRSVAPAGFGRHGGGVQ---QHVVKEKFEEVDTVSRAGANHHHHHGHHGGHGF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 VKVISEE-----AGHGGWAGGYSGGYAH-APEEVKIVKVISEAGHSHCHDYGHSHGHGS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences (ABLO1840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 16563; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 168; 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 83; DB 2
pred. No. 0.025
9; Mismatches
Myers EW;
```

27-FEB-2002

AAG66039;

RESULT 6

15-NOV-2001.

Synthetic.

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHH-------HHHGHHGGHGFVVRETR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA Sequences (ABL16175) and the encoded proteins (ABB7737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 29814; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 13565.
                                                                           Drosophila melanogaster polypeptide SEQ ID NO 29814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.5; DB 22;
Pred. No. 0.13;
9; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG13903 standard; Protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 VNEDADLEDDOAESOLDSF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 VEEDINTCTGEVHERRESF 88
                                                                                                                                                                                                                                                                                                                                                                                                                                            L1 PWD,
                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 15.8%;
Local Similarity 26.6%;
Les 21; Conservative
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL1177;
                                                                                                                                                                                                                    WO200171042-A2.
                                                                                                                                          pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interactions -
                                     26-MAR-2002
                                                                                                                                                                                                                                                         27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-0CT-2000
  ABB67674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG13903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ryk protein; anglogenesis; variant; receptor tyrosine kinase; cytostatic; antidiabetic; ophthalmological; cardiant; vulnerary; antianglogenic; gene therapy; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding the protein and expressing the protein in vivo. (I) is used as an immunogen to produce an antibody against it. The antibodies are useful for modulating angiogenesis at a site. Polynucleotides encoding (I) is useful in gene therapy technique for treating above mentioned medical conditions. The present sequence represents the scrv 1b4 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to modulating anglogenesis at a site by supplying a composition comprising a variant Ryk protein (I) (a member of the receptor tyrosine kinese family), or modulating formation of calls into capillary-like structures by contacting the calls with a composition comprising (I). The method is useful modulating anglogenesis at a site (endothelia) cells of human origin) into capillary-like structure. The condition e.g. cancer, metastasis, diabetic retinopathy, macular condition e.g. cancer, metastasis, diabetic retinopathy, macular condition involving anglogenesis in the reproductive system, including protein is supplied to the individual an individual. The variant production is supplied to the individual as a source of polynocleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating anglogenesis at a site, for treating or preventing cancer, metastasis, diabetic retinopathy, cardiovascular disease, wound by supplying composition comprising variant Ryk protein to the site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 EVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roczniak S, Dubois-Stringfellow NA, Zolotorev A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 81.5; DB 23;
Pred. No. 0.071;
9; Mismatches 21;
                               AAG66039 standard; Protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examples; Page 79-80; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB67674 standard; Protein; 347 AA.
                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-2001; 2001WO-US15043.
                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2000; 2000US-0568783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.0%;
34.0%;
                                                                                                                                                     scFv 1b4 antibody fragment.
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 16.0°
Best Local Similarity 34.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-049443/06.
N-PSDB; AAI67770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AA;
                                                                                                                                                                                                                                                                                                                WO200185789-A2.
```

1;

Sequence

225

à 셤 RESULT 7 ABB67674 ID ABB(

```
MAY ARABIdopais thaliana.

MAY ARABIdopais thaliana.

MAY 25-778-1200.

MAY 1999.

MAY 1
```

9903-0145085. 9903-0145087. 9903-0145192. 9903-0145145. 9903-014518.

99US-0144814. 99US-0145086. 99US-0145088.

99US-0140991.
99US-0141842.
99US-0142184.
99US-0142184.
99US-0142390.
99US-0142390.
99US-014230.
99US-014337.
99US-0144332.
99US-0144335.
99US-0144335.
99US-0144335.
99US-0144335.

990S-0145224. 990S-0145276. 990S-0145913. 990S-0145918. 990S-0145919. 990S-0148565. 990S-0148568. 990S-0149368. 990S-0149378. 990S-014972. 990S-014972. 990S-0149929. 990S-0149909. 990S-015966. 990S-015966. 990S-0150866. 990S-0150866. us-10-090-035-4.rag

```
990S-0131449.
990S-0132048.
990S-0132407.
990S-0132484.
990S-0132485.
 25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0138094.
99US-0138540.
99US-0138847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0139119.
99US-0139452.
99US-0139453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0139492.
990S-0139454.
990S-0139456.
990S-0139456.
990S-0139459.
990S-0139469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   990S-0139462.
990S-0139463.
990S-0139763.
990S-0139763.
990S-0139819.
990S-0140353.
990S-0140353.
990S-0140823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0142055.
99US-0142390.
99US-0142803.
                                                                 23-MAR-1999;
25-MAR-1999;
26-MAR-1999;
01-APR-1999;
08-APR-1999;
16-APR-1999;
16-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 SNGVREMVRCG-GIFGGGFWIMTSSSSSSSSSWSSSAEHHHHNHNMGHG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match Match 15.8%; Score 80.5; DB 21; Length 384; Local Similarity 36.5%; Pred. No. 0.15; Length 384; les 19; Conservative 4; Mismatches 28; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 13564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG13902 standard; Protein; 388 AA
9905-0154019
9905-0154039
9905-0154039
9905-0155486
9905-0155659
9905-015659
9905-0157117
9905-0157117
9905-0157117
9905-015929
9905-015929
9905-015929
9905-015929
9905-0159330
9905-0159331
9905-0159331
9905-0159331
                                                                                                                                                                                                                                                                                                                                                                                                               99US-0160989.
99US-0161404.
99US-0161405.
                                                                                                                                                                                                                                                                                                                                                                         99US-0160815.
99US-0160980.
99US-0160981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990s-0161359
990s-0161360.
990s-0161361.
990s-0161920.
990s-0161992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0161406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0161993
99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thàliana
                                                                                                                                                                                                                                                                                                                    21-0cr-1999;
21-0cr-1999;
21-0cr-1999;
22-0cr-1999;
22-0cr-1999;
22-0cr-1999;
25-0cr-1999;
25-0cr-1999;
25-0cr-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S1
Matches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG13902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
```

AAG13902

g ð

. 990S-0142977. 990S-0143542. 990S-0144005. 990S-0144086. 990S-0144086.

99US-0144331 99US-0144332

19-JUL-1999

99US-0142920

99US-0144352. 99US-0144632. 99US-0144884.

990S-0144814 990S-0145086 990S-0145088 990S-0145088

> 21-JUL-1999; 21-JUL-1999; 22-JUL-1999;

-JUL-1999

20-JUL-1999; 20-JUL-1999; 21-JUL-1999;

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                 282 SNGVREMVRCG-GIFGGFMIMTSSSSSSSSSWVSSSSAEHHHHNHNMGHG 332
                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                       11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGGHG
                                                                                                                                                                                                                                                                                                                                     Length 388;
                                                                                                                                                                                                                                                                                                                                    Query Match
15.8%; Score 80.5; DB 21; Length
Best Local Similarity 36.5%; Pred. No. 0.15;
Matches 19; Conservative 4; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 62934.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG49725 standard; Protein; 388 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
                                                                                                                                                                                                                                                                        990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
                                                                               990S-0159294.
990S-0159295.
990S-0159330.
990S-0159331.
990S-0159331.
990S-0159534.
990S-0160741.
990S-0160767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                         99US-0160814.
99US-0160815.
99US-0160980.
                                                                                                                                                                                                                                              99US-0161405.
99US-0161406.
99US-0161359.
99US-0156458.
99US-015696.
99US-0157117.
99US-015785.
99US-0158823.
99US-0158329.
                                                                                                                                                                                                                                                                                                                       99US-0162142
                                                                                                                                                                                                                              99US-0160989
99US-0161404
                                                                                                                                                                                                                     99US-0160981
                                                                        99US-0159293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
28-SEP-1999;
29-SEP-1999;
04-0CT-1999;
06-0CT-1999;
06-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
                                                                                                                                                                                                            22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
                                                                                                                                                                                                                                                         25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000
                                                                                                                                                       1-OCT-1999;
                                                                                                                                                                                                                                                                                                              28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                  21-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                                                                        25-0CT-1999;
25-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG49725;
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                 ğ
                                                                                                                                                                                                                                                                                                                                                                                             셤
```

990S-0145087.
990S-0145089.
990S-014518.
990S-0145218.
990S-0145218.
990S-0145218.
990S-0145218.
990S-0145918.
990S-0145918.
990S-0145918.
990S-0145918.
990S-0145918.
990S-014738.
990S-014738.
990S-0147302.
990S-0147303.

05-AUG-1999; 05-AUG-1999;

10-AUG-1999 11-AUG-1999

09-AUG-1999

13-AUG-1999 13-AUG-1999

6-AUG-1

12-AUG-1

26-JUL-1999; 27-JUL-1999; 27-JUL-1999;

-AUG-1999

02-AUG-1

99US-0149902. 99US-0150566. 99US-0150884. 99US-0151065. 99US-0151066.

> 26-AUG-1999; 27-AUG-1999; 27-AUG-1999;

5-AUG-1999

90S-0149929

17-AUG-1999; 18-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 99US-0151303 99US-0151438

27-AUG-1999; 30-AUG-1999; 31-AUG-1999;

01-SEP-1999

99US-0154779. 99US-0155139. 99US-0155486. 99US-0155659.

> 23-SEP-1999 24-SEP-1999

99US-0153758. 99US-0154018. 99US-0154039.

99US-0153070

99US-0152363

ï

```
990S-0144325.
990S-0144331.
990S-0144332.
990S-0144334.
990S-0144334.
990S-0144335.
990S-0144335.
990S-0144884.
990S-0144884.
990S-0145085.
990S-0145085.
990S-0145087.
990S-0145087.
990S-0145087.
990S-014518.
990S-014518.
990S-014518.
990S-014518.
990S-014518.
990S-014518.
990S-014733.
990S-014733.
990S-014733.
990S-014865.
990S-014866.
990S-0149175.
990S-0151303.
       19-70L-1999)
19-70L-1999)
19-70L-1999)
19-70L-1999)
20-70L-1999)
21-70L-1999)
21-70L-1999)
22-70L-1999)
22-70L-1999)
22-70L-1999)
22-70L-1999)
23-70L-1999)
24-70L-1999)
26-70L-1999)
26-70L-1999)
27-70L-1999)
27-70L-1999)
28-70L-1999)
28-70L-1999)
28-70L-1999)
28-70L-1999)
28-70L-1999)
28-70L-1999)
28-70L-1999)
28-70L-1999)
                                                                                                                                                                                                                                                                                                                                           23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
        990S-0126785.
990S-012845.
990S-0128134.
990S-0128134.
990S-013945.
990S-0130409.
990S-0130409.
990S-0131449.
990S-0131449.
990S-0131449.
990S-0131449.
990S-013485.
990S-013486.
990S-013945.
990S-013945.
990S-013945.
990S-013945.
990S-013946.
990S-014083.
990S-014083.
990S-014083.
990S-014083.
29-MAR-1999;
01-APR-1999;
08-APR-1999;
16-APR-1999;
21-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
11-MAY-1999;
                                                                                                                                                                            1-MAY-1999;
4-MAY-1999;
5-MAY-1999;
7-MAY-1999;
                                                                                                                                                                                                                                                 0-JUN-1999;
0-JUN-1999;
4-JUN-1999;
                                                                                                                                                                                                                                                                                           18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                      16-JUN-19
16-JUN-19
17-JUN-19
                                                                                                                                                                                                                                                                                                                                                                             21-JUN-19
22-JUN-19
23-JUN-19
23-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-19
30-JUN-19
01-JUL-19
01-JUL-19
02-JUL-19
                                                                                                                                                                                                                                                                                                               -JUN-1
```

```
99US-0137528.
99US-0137502.
99US-0137724.
   9905-0130891.
9905-0131449.
9905-0132407.
9905-0132484.
9905-0132485.
9905-0132487.
9905-0132487.
9905-0134286.
9905-0134286.
9905-0134286.
9905-0134286.
9905-0134289.
9905-013429.
                                                                                                                                    99US-0136392.
99US-0136782.
99US-0137222.
                                                                                                                                                                           99US-0138094
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                        Score 80.5; DB 21; Length 388;
Pred. No. 0.15;
4; Mismatches 28; Indels 1
                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 13563.
                                                                                                                                                                                                                                                                        AAG13901 standard; Protein; 396 AA
                                                                                                                                                                                                                                                                                                                                                                                                       99US-0121825.
99US-0123180.
99US-012548.
99US-0125788.
99US-01264.
99US-012765.
99US-012874.
99US-012874.
99US-012874.
                                                                                           990S-01660814
990S-01660815
990S-0166080-
990S-0160980-
990S-0161404-
990S-0161405-
990S-0161405-
990S-0161360-
990S-0161360-
990S-0161360-
990S-0161360-
990S-0161360-
990S-0161360-
990S-0161360-
990S-0161360-
990S-0161360-
                                                                                                                                                                                                  Query Match
Best Local Similarity 36.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000EP-0301439
                     990S-0159295.
990S-0159329.
990S-0159330.
                                         99US-0159331.
99US-0159637.
99US-0159638.
  99US-0158369
99US-0159293
               99US-0159294
                                                                                                                                                                                                                                                                                                   (first entry)
                                                             99US-0159584
                                                                    99US-0160741
                                                                          99US-0160767
                                                                                      99us-0160770
                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                   EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1999;
19-APR-1999;
21-APR-1999;
  12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
                                                                                                                                    25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                   17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1999
25-MAR-1999
                                                                                                                 2-OCT-1999;
2-OCT-1999;
5-OCT-1999;
                                                                                                                                                                                                                                                                                      AAG13901;
                                                                                                                                                                                                                                                             RESULT 11
AAG13901
                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                         g
```

```
RR 20-7111-1999 9945-0146642
RR 21-711-1999 9945-0146642
RR 21-711-1999 9945-01466484
RR 21-711-1999 9945-01466484
RR 21-711-1999 9945-0146666
RR 22-711-1999 9945-0145086
RR 22-711-1999 9945-0145086
RR 22-711-1999 9945-0145218
RR 22-711-1999 9945-0152234
RR 22-711-1999 9945-0152324
RR 22-711-1999 9945-0152324
```

```
ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 SNGVREMYRCG-GIFGGFMINTSSSSSSSSSWVSSSSAEHHHHNHNMGHG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thallana protein fragment SEQ ID NO: 62933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 15.8%; Score 80.5; DB 21; Local Similarity 36.5%; Pred. No. 0.15; es 19; Conservative 4; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG49724 standard; Protein; 396 AA.
990S-0159637.
990S-0159584.
990S-0160741.
990S-0160767.
990S-01607767.
990S-0160767.
990S-016098.
990S-016098.
990S-016098.
990S-0161360.
990S-0161360.
990S-0161361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990S-0121825.
990S-0123548.
990S-0125788.
990S-0125788.
990S-0126785.
990S-0127462.
990S-0128714.
990S-0128714.
990S-0130871.
990S-0130871.
990S-0130891.
990S-013081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thallana
14-0CT-1999;
14-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
13-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG49724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG49724

ID AAG49724

XX AAG49724

XX DT 18-0C7

XX DT 18-0C7

XX C ACADIC

XX C A
  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
```

```
PR 06-MAY-1999; 99US-0132486.

PR 11-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134219.

PR 18-MAY-1999; 99US-0134219.

PR 21-MAY-1999; 99US-013522.

PR 01-UN-1999; 99US-013522.

PR 18-UN-1999; 99US-013942.

PR 18-UN-1999; 99US-013943.

PR 18-UN-1999; 99US-013949.

PR 18-UN-1999; 99US-014433.

PR 18-UN-1999
```

PR 22-JUL-1999; 99US-0145089.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145214.

PR 23-JUL-1999; 99US-0145214.

PR 23-JUL-1999; 99US-0145218.

PR 27-JUL-1999; 99US-0145218.

PR 27-JUL-1999; 99US-0145318.

PR 02-AUG-1999; 99US-0145318.

PR 02-AUG-1999; 99US-0145318.

PR 02-AUG-1999; 99US-0145319.

PR 02-AUG-1999; 99US-0147302.

PR 03-AUG-1999; 99US-0147302.

PR 03-AUG-1999; 99US-0147302.

PR 04-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147303.

PR 10-AUG-1999; 99US-0147303.

PR 11-AUG-1999; 99US-0147303.

PR 11-AUG-1999; 99US-0147303.

PR 12-AUG-1999; 99US-0147303.

PR 12-AUG-1999; 99US-0147303.

PR 12-AUG-1999; 99US-0149319.

PR 23-AUG-1999; 99US-0151066.

PR 23-AUG-1999; 99US-0151066.

PR 23-AUG-1999; 99US-0151070.

PR 23-AUG-1999; 99US-0151303.

PR 23-AUG-1999; 99US-0151303.

PR 23-AUG-1999; 99US-0151307.

PR 23-AUG-1999; 99US-0151307.

PR 23-EEP-1999; 99US-0151307.

PR 23-EEP-1999; 99US-015307.

PR 24-EEP-1999; 99US-015307.

PR 24-EEP-1999; 99US-015307.

PR 25-EEP-1999; 99US-015307.

PR 26-CCT-1999; 99US-015307.

PR 27-EEP-1999; 99US-015307.

PR 27-EEP-1999; 99US-015307.

PR 28-EEP-1999; 99US-015307.

PR 28-EEP-1999; 99US-015307.

PR 28-EEP-1999; 99US-015307.

PR 28-EEP-1999; 99US-015307.

PR 29-EEP-1999; 99US-015307.

PR

```
990S-0134370.
990S-0134768.
990S-0135124.
990S-0135129.
990S-0135622.
990S-0137528.
990S-0137528.
990S-0137528.
990S-0137528.
990S-0137528.
990S-0137528.
990S-013452.
990S-0139455.
990S-0139455.
990S-0139455.
990S-0139456.
990S-0139456.
990S-0139459.
990S-0139459.
990S-0139460.
990S-0139460.
990S-0139463.
990S-0139463.
990S-0139463.
990S-0139463.
990S-0139463.
                                                                                                                                                                                                                                                                                                                                                                                                                                    990S-0142920.
990S-0142977.
990S-0143542.
990S-0144005.
990S-0144085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9905-0144335
9905-0144331
9905-0144333
9905-0144334
9905-0144335
9905-0144352
9905-014484
9905-0144884
9905-014684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0145276
99US-0145913
         14 - MAY - 1999;

18 - MAY - 1999;

20 - MAY - 1999;

21 - MAY - 1999;

24 - MAY - 1999;

25 - MAY - 1999;

26 - MAY - 1999;

27 - MAY - 1999;

30 - JUN - 1999;

30 - JUN - 1999;

31 - JUN - 1999;

32 - MAY - 1999;

33 - JUN - 1999;

34 - JUN - 1999;

35 - JUN - 1999;

36 - JUN - 1999;

36 - JUN - 1999;

37 - JUN - 1999;

38 - JUN - 1999;

39 - JUN - 1999;

30 - JUN - 1999;

30 - JUN - 1999;

31 - JUN - 1999;
                                                                                                                                                                                                                                                                                                              21-JUN-1999;
22-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                    29-JUN-19
30-JUN-19
01-JUL-19
         ;
                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                           Gaps
                                                                                                                                                                                                 290 SNGVREMYRG-GIFGEFMINTSSSSSSSSSSAVSSSAEHHHHNHNMGHG 340
                                                                                                                                                                                       11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHHGHHGGHG 62
                                                                                                                                                                           1;
                                                                                                                                                         Length 396
                                                                                                                                                                           indels
                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 62932.
                                                                                                                                                   Ouery Match 15.8%; Score 80.5; DB 21;
Best Local Similarity 36.5%; Pred. No. 0.15;
Matches 19; Conservative 4; Mismatches 28;
                                                                                                                                                                                                                                                       AAG49723 standard; Protein; 405
 990S-0160814.
990S-0160815.
990S-0160980.
990S-0160989.
990S-0161404.
990S-0161405.
990S-0161360.
990S-0161359.
990S-0161360.
990S-0161360.
990S-0161360.
                                                                                                                                                                                                                                                                                                                                                                                                                                              990S-0121825.
990S-0123180.
990S-0123784.
990S-0125785.
990S-0126785.
990S-01287462.
990S-0128714.
990S-0128714.
990S-0132845.
990S-0132485.
990S-0132485.
990S-0132485.
990S-0132486.
990S-0132486.
990S-0132486.
990S-0132486.
                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                           18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thallana
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                       EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
04-MAY-1999;
06-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                                                                                                                          AAG49723;
                                                                                                                                                                                                                                      RESULT 13
AAG49723
 ò
                                                                                                                                                                                                    8
```

```
990S-0148341.
990S-0148565.
990S-0148684.
990S-0149368.
990S-0149175.
                                                                                                                            99US-0149722.
99US-0149723.
99US-0149929.
                                                                                                                                                                                                                                                                                                                                                                                                           99US-0161405
                                                                                                                                                                                                                                                      99US-0156458
                                                                                                                                                                                                                                                            99US-0156596
                                                                                                                                                                                                                                                                                       90S-0158232
                                                                                                                                                                                                                                                                                                  90S-0159293
                                                                                                                                                                                                                                                                                                                                                               99US-0160768
                                                                                                                                                                                                                                                                      99US-0157753
                                                                                                                                                                                                                                                                           99US-0157865
                                                                                                                                                                                                                                                                                                                        99US-0159330
                                                                                                                                                                                                                                                                                                                                                                                                      99US-0161404
                                                                                                                                                                                                                                                                                                        99US-0159294
                                                                                                                                                                                                                                                                                                                                    99US-0159637
                                                                                                                                                    99US-0149930
                                                                                                                                                                               99US-0151080
                                                                                                                                                                                                          99US-0153070
                                                                                                                                                                                                                                                                 99US-0157117
                                                                                                                                                                                                                                                                                                                              90S-015933
                                                                                                                                                                                                                                                                                                                                                          990S-016076
                                                                                        99US-0148319
                                                                                                                                                              990S-0150884
                                                                                                                                                                                                                                                                                                              99US-015929
                                                                       99US-0147493
                                                                                                                                                                                                                                     990S-015
                                                                                                                                                                                         99US-01
                                                                                                                                                                                                                      99US-01
                                                                                                                                                                                                                                99us-01
                                                                                                                                                                                                                                                99US-01
                                                                                                                                                                                                99US-01
                                                                                                                                                                                                                990S-01
                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
                          02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
                                                           06-AUG-1999;
06-AUG-1999;
                                                                                                           16-AUG-1999;
                                                                                                                              20-AUG-1999
                                                                                                                                         20-AUG-1999
                                                                                                                                                                                                                                                                                                                                    4-0CT-1999
                                                                                                  13-AUG-1999
13-AUG-1999
                                                                                                                                                                   27-AUG-19
27-AUG-15
27-AUG-19
                                                                                                                                                                                                                                                                                                                                        14-0CT-19
18-0CT-19
21-0CT-19
21-0CT-19
                                                                                                                                                                                                                                                                                                                        -0CT-1
                                                                                                                                                                                                                                                                                                              13-0CT-1
14-0CT-1
                                                                            09-AUG-19
                                                                                                                                                          -AUG-1
                                                                                                                                                               26-AUG-1
                                                                                                                                                                                         1-AUG-1
                                                                                                                                                                                                                                                      -SEP-
                                                                                                                                                                                                                                                                                   -OCI
                                                                                             12-AUG-1
                                                                                                                         18-AUG-1
                                                                                                                                                                                                                                                            29-SEP-
                                                                                                                                                                                                                                                                                                        3-0CT-
                                                                                                                                    20-AUG-
                                                                                                                                                                                                     07-SEP-
                                                                                                                                                                                                                           SEP-
                                                                                                                                                                                                                                 20-SEP-
                                                                                                                                                                                                                                            33-SEP-
```

```
The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. rheumatord arthritis and psorlasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, hypertension, psychotic disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias.

The nucleic acids and polypeptides are also useful for treating viral
                                                                                                                                                                     ï
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; path; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                    1;
                                                                                                                                                                                                  11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                     Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sudarsanam S, Manning G, Caenepeel
                                                                                                                                                                       Indels
                                                                                                                                                                       28;
                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of novel human protease #5.
                                                                                                                                       Score 80.5; DB Pred. No. 0.16; 4; Mismatches
                                                                                                                                                                                                                                                                                                                 AAU82706 standard; Protein; 3353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claim 6; Fig 2B-C; 313pp; English.
                                                                                                                                          15.8%;
ilarity 36.5%;
Conservative 4
               99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161993.
99US-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2000; 2000US-214047P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2001; 2001WO-US20171
 39US-0161406
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-139913/18.
N-PSDB; ABK31748.
                                                                                                                                        Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200200860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plowman G, Wl
Charydczak G;
                                                                           28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                     23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                     AAU82706;
                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                      엄
      PR
PR
PR
PR
PR
                                                                                                                                                                                                               õ
```

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (I) comprising at least two cytomegalovirus (CWV) p52 peptide sequences of up to 60 amino acids, each sequence including a segment of at least 18 amino acids between positions 264 and 293 of the CWV p52 antigen. (I) is useful as an immunoassay reagant for determining the presence and/or amount of CMV antibodies or antigens, especially for diagnosis of primary or secondary CMV infections or for detecting reactivation of cMV after minon amples, especially for diagnosis of primary or latency. (I) is a more specific and sensitive immunoassay reagent than monomeric CMV p52 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel multimeric cytomegalovirus (CMV) antigen
infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multimeric cytomegalovirus antigen useful as an immunoassay reagent, and which comprises at least two p52 peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                       CMV-p52 antigen; multimeric; immunoassay; IgM; immunoglobulin M; diagnosis; infection; reactivation.
                                                                                                                                          5
                                                                                                       Score 80; DB 23; Length 3353;
Pred. No. 2.7;
9; Mismatches 19; Indels
                                                                                                                                                                                  48 GANHHHHHHGHHGGH--GEVVRETRVEEDINTCTGEVHERRESFLA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 79; DB 22; Length 87;
Pred. No. 0.035;
5; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                         Human cytomegalovirus dimeric p52 antigen protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ŀ.
                                                                                                                                                                                                                                                                 AAB11465 standard; Protein; 87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                                     6
                                                                                                      15.7%;
ilarity 33.3%;
Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Fig 2; 18pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.5%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99DE-1019121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99DE-1019121
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.5 Best Local Similarity 32.1 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-041727/06.
N-PSDB; AAC81969.
                                                                         3353 AA;
                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE19919121-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1999;
                                                                                                                                                                                                                                                                                                                              01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-2000.
                                                                         Seguence
                                                                                                                                                                                                                                                                                                AAB11465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                        AAB11465
8 \times 8 \times 8 \times 8
                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                    ð
```

Search completed: June 6, 2003, 12:50:08 Job time: 32.5 secs

1;

Gaps

10;

17 VAPAGFGRHGGGVQQHVVKEKFEEVDIV-----SRAGANHHHHGHHGGHG 62 

ò g

		inger () mar distribution of Albrich Banding		41 S	47- <b>5</b> 7		The state of the s		
***					200				
					- 1		*		
2	. Y	*	0		1.3	1. Sept. 1			
									4
1									
			•						
		* :					*		
P.									
		•					•		\$
		water			. ,				
	. *						•		
								*	
	**								
	*								
	Ę								
N.									
	*								
	E	· · · · ·							,
	No. 2 1. 1								
	0,								
7	, <b>, ,</b> , , , , , , , , , , , , , , , ,								
								· ·	
	· ·			•.					•
				•					
						*1			
5		•							
	Ÿ.								
							· ·		
		•							
		•							
							•		
6	•			*.					
ř.	•								
* 	•	•							
k.				•					
羅		•							
<del>"</del>			•						
			•						
									•
-	•								
				•					•
									. •
					•				
4					•				
1	•			14 14 14 14 14 14 14 14 14 14 14 14 14 1					ĠV.

-

```
June 16, 2003, 01:55:01; Search time 40.4096 Seconds (without alignments) 4356.204 Million cell updates/sec
                                                                                                                              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                          441362 seqs, 153338381 residues
                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                         Sequence:
                                                                                                                                                                                                                         Searched:
                                                                           Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appli Sequence 10, Appli Sequence 10, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 7, Appli Description Sequence Sequence Sequence Sequence 5 4 US-09-103-840A-1
1 US-08-103-840A-1
1 US-08-103-840A-1
1 US-08-103-813-10
2 US-08-25-913-1
2 US-08-25-913-1
1 US-08-440-856A-2
1 US-08-440-856A-1
1 US-08-440-856A-1
1 US-08-103-840A-2
1 US-08-103-840A-2
1 US-08-103-840A-2
1 US-08-103-840A-2
1 US-08-103-840A-2
2 US-09-103-840A-2
1 US-08-31-25-1
1 US-08-31-25-1
1 US-08-31-25-1
1 US-08-471-601-23
1 US-08-470-354-23
1 US-08-470-382-23 US-08-479-041-23 US-08-819-646-23 US-09-197-649-7 SUMMARIES 390 4 U 4403765 4 4211529 4 2244 5 P 2244 5 P 2334 1 U 2334 5 P 4411529 4 7559 1 U 1256 1 U Query Match Length DB Result No. υυ

223 CGGTCTCACGCGCCGCCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCT 282 

q οŽ

ò g

Sequence 23, Appl Sequence 32, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 16, Appl Sequence 17, Appl	ion by Reverse Translation	Artificial Sequence  RMATION: Description of Artificial Sequence: Sequence  RMATION: having a 120 repeat of Acc flanked by flxed  RMATION: having a 120 repeat of Acc flanked by flxed  RMATION: fragments having NcoI restriction sites.  10.9%; Score 62.6; DB 4; Length 390;  imilarity 52.0%; Pred. No. 0.00014;  Conservative 0; Mismatches 129; Indels 0; Gaps 0;  ACTACCAGAGGACTACTACTGCTGGAGGAGGAGGTGGTGGCCCCGGCGCGCCGCCGCCGCGCGCG
4 US-09-195-716-23 4 US-09-105-537-32 4 US-09-105-537-5-5 4 US-09-320-878-19 5 PCT-US92-06840-1 1 US-08-19-5-31-58-5-3 2 US-08-265-310-5-3 3 US-08-951-742-5 4 US-09-951-742-5 4 US-09-951-742-5 4 US-09-951-742-5 2 US-08-951-742-5 3 US-08-951-742-5 4 US-08-951-742-5 4 US-08-317-942-1 5 US-08-317-942-1 5 US-08-317-942-9 4 US-08-317-942-9 4 US-08-765-9078-7	ALIGNMENTS 9197649 Lic Polypeptide Evolution 08/09/197,649 1-23 07/829,461 07/739,055 3-01 07/7551,968	ce 100 of Artificial Sequence 120 repeat of ACG flankee 8 having Ncol restriction 7 Score 62.6; DB 4; Ler 9 Pred. No. 0.00014; 0; Mismatches 129; Ir 17 CTGCGAGGGGTGAGGTGGGTGGGTGGGTGGGTGGGTGGGAGGTGGGGGG
6 8.0 1485 8 8.0 38578 8 8.0 38578 9 7.9 2353 4 7.7 1777 4 7.7 1342 4 7.7 1342 6 7.6 291 6 7.6 291 6 7.6 291 6 7.6 291 6 7.6 4896 4 7.6 4041	ton US/0  rry  raig  raig  onathan i  Systema i  Systema i  1998-1  NUMBER:  1992-0  NUMBER:  1992-0  1990-0  1990-0  1990-0	ORGANISM: Artificial Sequence FEBAUGE: OTHER INFORMATION: Description OTHER INFORMATION: having a 120 OTHER INFORMATION: fragments has 9-197-649-7 10.9%; S st Local Similarity 52.0%; S st Local Similarity 52.0%; S t Local Similarity 60; O; Conservative 0; O; Conservative 10; Co
0 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	RESULT 1  US-09-197-649-7  Sequence 7, Applicat  Patent No. 6194550  GENERAL INFORMATION: APPLICANT: Gold, La APPLICANT: Tuerk, C APPLICANT: Prithnow, APPLICANT: Smith, W TITLE OF INVENTION: FILE REFERENCE: NEX CURRENT APPLICATION CURRENT APPLICATION EARLIER APPLICATION BARLIER PILING DATE BARLIER PILING DATE BARLIER PPLICATION BARLIER PILING DATE BARLIER PILING D	ORGANISM: ORGANISM: COTHER INFO OTHER INFO O

```
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
1..2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
US-08-476-519-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-476-519-10
                                                                                                                                                                                                                                                                                                                                              329
                                                                                                                                                              g
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 CACGGGGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 GCCCGGCCGGCTTCGGCCGCCACGCGGCGCGTCCAGCACGTCGTCGTCAAGGAAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 IICGAGGAGGICGACGGTCICACGCGCGCGCGCCAACCACCACCACCATGGICAC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENSER, Claire M.
APPLICANT: VENSER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                         APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT FILING DAIE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53.2; DB 4; Length 4
Pred. No. 0.028;
0; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1191389 GGCGGCAACGCCGGCAACGGCGAACGGC 1191360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 ACCGGCGAGGTCCACGAGCGCAGGGAGAGC 356
                              343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371
                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                   Sequence 2, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.3%;
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                      JS-09-103-840A-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
                                                                                                                        RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                å
                                                                    a
                                   ò
```

```
3932728 CCCCACCGGCATCGGCGGCACCGGCGGCACGGGAAAGGCGGCGCGGCGGGGCCGG 3932787
                                                                                                                                                                                                                                                                                                                          3932848 cédcédachadécegedecedededecreecedecedecedecedecentaric 111 111 111 1332907
                                                                                                                                                                                                                                                                                      269 CGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGAGACATCAACACCTGCAC
                                                                                           149 CCCGGCCGGCTTCGGCCGCCACGGCGGCGTCCAGCAGCACGTCGTCAAGGAAAGTT
                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
TITLE OF INVENTION: No. 5750876el Isoamylase Gene, Compositions
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
NUMBER OF SEQUENCES: 11
Length 4411529;
Score 53.2; DB 4; Length 4 Pred. No. 0.028; 0; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5750876th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-UL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
NAME: Bonner, Grace 132,963
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-21(13577)A
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08476519
Patent No. 5750876
                                                                                                                                                                                                                                                                                                                                                                                                                                               3932908 CGCCGCCCGCC 3932921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (314)537-7286
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2244 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
          Query Match 9.3%;
Best Local Similarity 54.6%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                              CGGCGAGGTCCACG 342
```

g ò 셤 õ g ö 8

```
Sequence 1, Application US/08476519
Patent No. 5750876
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
TITLE OF INVENTION: No. 5750876e1 Isoamylase Gene, Compositions
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: ADDRESSE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5750876th
STREET: AL Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,519
FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51.8; DB 1; Pred. No. 0.025; 0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38-21(13577)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (314)537-7286
TELEFAX: (314)537-76647
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.5%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 GCGAGGTCCAC 341
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                       US-08-476-519-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-09323-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-476-519-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                   151 CGGCCGGCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCG 210
                                                                                                                                                    211 AGGAGGTCGACACGGTCTCACGCGCCGGCCCAACCACCACCACCACGATGGTCACCACG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1877 CGGCCAGCGACACCAACGCAACGTGATGGACCAGTTGCGCTGCTTCAAGCCCGACGGCG 1936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997 ACGCAGCGAGTTCGGCGACAGCGCCATCTACGTCGCCTACAACGGCTGGTCCG 2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 AGGAGGTCGACACGGTCTCACGCGCCGGCCCAACCACCACCACCACCATGGTCACCACG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 GCGGCCACGGCTTCGTGGTGCGGGGGCTCGAAGAGGACATCAACACCTGCACCG 330
                                                                                                                                                                                                                                 271 GCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCG
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Novel Isoamylase Gene, Compositions
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   ö
9.0%; Score 51.8; DB 1; Length 2244;
54.5%; Pred. No. 0.025;
Live 0; Mismatches 87; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
9.0%; Score 51.8; DB 5; Length 2244;
Best Local Similarity 54.5%; Pred. No. 0.025;
Matches 104; Conservative 0; Mismatches 87; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US95/09323
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application PC/TUS9509323 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-7UL-1994
INFORMATION FOR SEQ ID No: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2244 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                  Best Local Similarity 54.5
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                        2057 GCGCGTCGAC 2067
                                                                                                                                                                                                                                                                                                                GCGAGGTCCAC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCGGTCGAC 2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGAGGTCCAC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: CDS
; LOCATION: 1..2
PCT-US95-09323-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US95-09323-10
                                                                                                                                                                                                                                                                                                             331
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
```

```
2029
ö
                                                                                                               2089
                                                                                                                                                   151 CGGCCGGCTTCGGCCGCCGCCGCGCGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCG 210
                                                                                   270
                                             211 AGGAGGTCGACACGGTCTCACGCGCCGCGCCAACCACCACCACCACCATGGTCACCACG
                                                                                                                                  271 GCGGCCACGCCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGAGACATCAACACCTGCACCG
                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS9509323 GENERAL INFORMATION:
APPLICANT:
```

ò g ð පු ð 8 ö

```
3748947 CTCGGCGGTGGCAACCTCGGCGGGAACCTGGGGTTGGGCAACCTCGGGGAAC 3748388
236 CGGCGCCAACCACCACCACCATGGTCACCGGGGGGGCCACGGCTTCGTGGTGCGGGA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 CACCACCATGGTCACCACGGGGGCCACGGCTTCGTGGTGCGGGACCAGGGTCGAAGAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 CGGCGTCCAGCACCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGC
                                                                                         Gaps
                                                            192 GTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCCAACCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                               13-08-440-856A-9
Sequence 9, Application US/08440856A
Sequence 9, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELLAPORTA, STEPHEN L.
APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: PARTEILS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/440,856A FILING DATE: 15-MAY-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%; Score 50.2; DB 1; ilarity 43.9%; Pred. No. 0.05; Conservative 20; Mismatches 123;
                                                                                                                                                                                                                                                  312 GACATCAACACCTGCACCGGCGAGGTCCACG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REGISTRATION NUMBER: 05463-20001.00
REFRENCE/COMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2000 PENNSYLVANIA AVE. N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 887-15
(202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1288 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 112; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-440-856A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                        .
B
                                                                                                               ద
                                                                                                                                                     δ
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                        d
                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 GAGGTGAGGTCGGTGGCCCCGGCTTCGGCCGCCGCGGCGGCGGCGTCCAGCAGCAC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09103840A

Sequence 1, Application US/09103840A

Patent No. 6294328

GENERAL INFORMATION:

APPLICANT: FIEISCHMAN, Robert D.

APPLICANT: WHITE, Owen R.

APPLICANT: VENERR, John C.

TITLE OF INVENTION: TUBERCULOSIS

TITLE OF INVENTION: TUBERCULOSIS

TITLE OF INVENTION: TUBERCULOSIS

TITLE OF INVENTION NUMBER: US/09/103,840A

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ INOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1.2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 CGGCCGGCTTCGGCCGCCACGGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 AGGAGGICGACACGGICTCACGCGCCGCGCCCAACCACCACCACCACCATGGICACCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 GCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1970 cecccaccaccaccaacecaacercaresaccacrrecrecrecresaccccaacece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                      Novel Isoamylase Gene, Compositions
Containing It and Methods of Using Isoamylases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9%; Score 51; DB 4; Length 4411529;
ilarity 52.6%; Pred. No. 0.078;
Conservative 0; Mismatches 100; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51.8; DB 5; Length 2. Pred. No. 0.025; 0; Mismatches 87; Indels
                          TITLE OF INVENTION: Novel Isoamylase Gene, Compositions TITLE OF INVENTION: Containing it and Methods of Using NUMBER OF SEQUENCES: 11
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-UUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2334 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2150 ececeerceac 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 GCGAGGTCCAC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-103-840A-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-09323-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

ద ò

g à 엄 ç

ò

ö

ð

```
exon
2153..2332
                                                                                                                                                                                                                                                                                                                        exon
2437..2832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
4492..4596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
5198..6196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
3901..4120
                                                                                                                                                                                                                                                                                                                                                                                 exon
2944..3027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
4723..4812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
6294..6680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
4946..5099
                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
3900..4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
4945..5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
2154..2331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
4724..4811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1ntron
2438..2831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
2945..3026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
6789..7079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intron
4493..4595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
5199..6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
6295..6679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
6790..7078
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
LOCATION:
FEATURE:
LOCATION:
                                                                                                                                                                                             NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                            RESULT 10
US-08-250-848-2
US-08-250-848-2
Sequence 2, Application US/08250848
Sequence 2, Application US/08250848
Sequence 2, Application US/08250848
Sequence 3, Security 17
Sequence 2, Application US/08250848
Sequence 3, Security 18
Sequence 3, Security 18
Sequence 3, Security 18
Sequence 4, Security 10
Sequence 18

296 GACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAG 355
                             COUNTRY: USA
ZIP: 91009-7068
COMPUTER READABLE FORM:
MEDIUW TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/250,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATOONEY/AGENT INFORMATION:
NAME: Sharp Esq., Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: P114:25992/JAS
TELEPHONE: (818) 795-5843
TELEPHONE: (818) 577-1769
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7559 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: NOCHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
                                                                                                                  994 GGACATCGCCGAGGC 1008
                                                                               356 CTTCCTCGCCAGGGC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
2153..2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
2437.:2832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
2944..3027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
4492..4596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
4723..4812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
3900..4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2ев шаув
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                 g
                                                                                                            g
    à
                                                                             ò
```

```
296 GACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAG 355
                                                                                                                                                                                                                           176 CGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGC 235
                                                                                                                                                                                                                                                                                                                          236 CGGCGCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/08133711
Patent No. 5525463
GENERAL INFORMATION:
APPLICANT: 2019, Werner
TITLE OF INVENTION: Methods and reagents for detection of
TITLE OF INVENTION: pathogens using superoxide dismutase gene
TITLE OF INVENTION: targeting
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            ö
                                                                                                                                                      Length 1236;
                                                                                                                                                        Query Match

8.5%; Score 48.6; DB 1; Length 1
Best Local Similarity 49.4%; Pred. No. 0.1;
Matches 126; Conservative 0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSE: Hoffmann-La Roche Inc.
SIREET: 340 Kingsland Street
CITY: Nutley
STATE: Nutley
STATE: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92810780.4
FILING DATE: 13-0CT-1992
ATTORNEY AGENT INFORMATION:
NAME: PALTICIA S. ROCHA
REGISTRATION NUMBER: 31,054
REFERENCE/DOCKET NUMBER: 4095/95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (201) 235 5000
TELEFAX: (201) 235 3500
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERIŞTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 CTTCCTCGCCAGGGC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 983 GGACATCGCCGAGGC 997
                                                  LENGTH: 1236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 base pairs
TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-133-711-44
                                                                                                          ,
TOPOLOGY:
US-08-440-856A-1
                                                                           TYPE:
                                                                                                                                                                                                                                                                                                              δŏ
                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2670 CACCGAGTCCGACATCGAGGAGACGTCCAAGCGCCTCGTGTCCGAGGTCGGCAAGTCCCC 2729
                                                                                                                                                                                                                                                                                                                                                                                         2490 GAAGCTGGGGCGAAGCTCACGGGGCTGGCCCCGCCGACGCATCCTCGT 2549
                                                                                                                                                                                                                                                                                                                                                                                                                                            170 CGGCGGCGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 GCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACGGCGAGGTCCACGAGCGCAG :349
                                                                                                                                                                                                                                                                                                                                                                      230 ACGCGCCGGCCCAACCACCACCACCATGGTCACCACGCGGCCACGGCTTCGTGGT
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                               Query Match 8.6%; Score 49.2; DB 2; Length 7559; Best Local Similarity 49.6%; Pred. No. 0.094; Matches 126; Conservative 0; Mismatches 128; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: DELLAPORTA, STEPHEN L.

APPLICANT: DELLAPORTA, STEPHEN L.

TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING

TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MILLAAN, ROBERTA A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEPHONE: (202) 887-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER STREET: 2000 PENNSYLVANIA AVE. N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-440-856A-1; Sequence 1, Application US/08440856A; Patent No. 5750873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2730 CGAGGAGGTGTTCG 2743
                                                                     prim_transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 GGAGAGCTTCCTCG 363
                                                                                                                                                                             TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
               polyA_site
7314..7319
                                                                                                                                                                                                                                                 2153..7079
                                                                                                                           promoter
1..2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20037
                                                                 NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                  ;
US-08-250-848-2
                                                                                                                                                                                                                                     NAME/KEY:
               NAME/KEY:
                                LOCATION:
FEATURE:
                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
```

```
3921983 CCG 3921985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 CGG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4403765
                                                                                                                                                                                                                                                                                                                                                             US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                               셤
                                                                                           ò
                                                                                                                    엽
                                                                                                                                                     ò
                                                                                                                                                                            g
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                 ö
                                                                                                                                                                                               206
                                                                                                                                                                                                      207 TTCGAGGAGGTCGACACGGTCTCACGCGCGGCGCCAACCACCACCACCACCATGGTCAC 266
                                                                                                                                                                                                                                                                                                                        CACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGACGACATCAACACCTGC 326
                                                                                                                                                                                    147 GCCCCGGCCGGCTTCGGCCGCCGCGCGCGCGCGTCCAGCAGCACGTCGTCAAGGAGAAG
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                          Query Match

8.4%; Score 48; DB 1; Length 491;
Best Local Similarity 50.9%; Pred. No. 0.13;
Matches 114; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 47.6%; Pred. No. 0.14;
Matches 141; Conservative 0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                             327 ACCGGCGAGGTCCACGAGGCAGGGAGGCTTCCTCGCCAGGGC 370
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
; TYPE: nucleic acid
; STRANDENNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Actinomyces viscosus/SOD gene
US-08-133-711-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05463-20001.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORRISON & POERSTER STREET: 2000 PENNSYLVANIA AVE. N.W. STREET: D.C. STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08440856A Patent No. 5750873 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-440-856A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-440-856A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                      g
                                                                                                                                                                                     õ
                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
3921803 GCGGGATCGGCGGTGCCGGCGGGCGGCGGCCGGCACGGCGGCCATG 3921862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGA 138
                                                                                                                                                                                     258
                                                                                                                                                                                                                                                                 259 ATGGTCACCACGCCGCCACGCCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCA 318
                                                                                                                                        654
                                                                                                                                                                                                      715 TCTCCCCTTCGGCGTCGCCACCCGATGCTCAACGCCTGGCGCCAGGGCCACGACG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 CGGCCGGCTTCGGCCGCCGCCGCGGCGCGCCAGCAGCACGTCGTCAAGGAGAAGTTCG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AGGAGGTCGACACGGTCTCACGCGCCGCGCCAACCACCACCACCATGGTCACCACG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
COTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                        535 AGCACGCGCGCTCGCCATGACCCAGCGCGGCGGCAGCATCATCATCGTCGCCAGCG
                                                                                     139 GGTCGGTGGCCCCGGCCTTCGGCCGCCACGGCGGCGCGTCCAGCAGCACGTCGTCA
                                                                                                              199 AGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCACCA
                                                                                                                                                                                                                                                                                                                                                      319 ACACCTGCACGGCGAGGTCCACGAGGGAGGGAGGGTTCCTCGCCAGGGCTAAC 374
                                                                                                                                                                                                                                                                                                                                                                                271 GCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFWARE: PALENTIN VET: 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%; Score 47.8; DB 4; Length 4403765;
49.8%; Pred. No. 0.34;
tive 0; Mismatches 122; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/09103840A
; Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, RODERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.81
Matches 121; Conservative
```

```
169 ACGCCGCCGCCGCCACCACCACCTCCTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 CACGCGCCGGCGCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                    Sequence 4, Application US/09249585A

Sequence 4. Application US/09249585A

Patent No. 6417002

GENERAL INFORMATION:
APPLICANT HOLICK, Robert

TITLE OF INFORMATION:
FILE REFERENCE: 0867/0D905

CURRENT APPLICATION NUMBER: US/09/249,585A

CURRENT FILING DATE: 1999-02-11

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                             Score 47.2; DB 4; Length 1926;
Pred. No. 0.21;
0; Mismatches 123; Indels 0
                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; LOCATION: (1)..(1926); OTHER INFORMATION: template strand of EBNA-1 DNA US-09-249-585A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: June 16, 2003, 03:58:13
Job time: 81.4096 secs
                                                                                                                                                                                                                                                                                                                                  Query Match 8.2%;
Best Local Similarity 49.6%;
Matches 121; Conservative
                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Epstein Barr Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 GGGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||
684 AGGA 681
RESULT 15
US-09-249-585A-4/C
                                                                                                                                                                                 SEQ ID NO 4
LENGTH: 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

G-protein co

Run on:

```
S. Chrysomallus ac Mycobacterium tube Sequence encoding Wheat inositol 1,3 Wheat Scip-1 ortho Streptomyces nours Streptomyces nours Streptomyces nours Streptomyces nours Malze phosphenolpy Malze phosphenolpy Malze T92 cDNA nuc Streptomyces nours Streptomyces nours Streptomyces nours Streptomyces nours Streptomyces nours Streptomyces nours Trehalose-releasin Trehalose-releasin
                                                            Mature isoamylase
Flavobacterium iso
Isoamylase gene.
Full length Flavob
                     Human DNA for pote
Micromonospora DNA
                                                   Human adenosine Al
                                                                                                                                                                                                                                                                                                                                                                               Streptomyces galil
M. capsulatus gene
TGF-57-Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wild type TGF-alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nitric oxide synth Wheat raffinose sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nitric oxide synth
Bovine endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                            rGF-57-PE40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Systematic polypeptide evolution by reverse translation; SPERT; ligand binding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New method of systematic polypeptide evolution by reverse translation – by linking each polypeptide in sample mixt, tindividualised mRNA allowing further synthesis of selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Randomising oligonucleotide used in SPERT mRNA prepn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                   AAH44082
AAV45824
                                                                                                                                                                                                                                               AAV82011
AAS54218
AAT45060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT16858
AAT16857
                                                                                                                                               AAN70566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
 91WO-US05463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-0561968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ21833 standard; DNA; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUN-1992 (first entry)
                            109519
                                                                                                                                                                                                                                                                                          27541
125401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COLS ) UNIV OF COLORADO.
                                                                                                                                                                                                                                                                                                                                                                             14806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-080018/10.
                                                                                                                                                                                                                                                                                                                                                4 m m u u u u u u u u u u u u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gold L, Tuerk C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9202536-A
                                                                                                                                         47.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ21833;
AAQ21833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer for 5' Sequence containin Oligo #7 for cloni Mycobacterium tube Nycobacterium tube DNA encoding G pro Human orphan G pro Human G protein co
                                                                               June 15, 2003, 23:41:35; Search time 188.272 Seconds (without alignments) 6855.849 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Randomising oligon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                  | SIDSZ/godatu/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSZ/godatu/geneseqn/geneseqn-embl/NA1981.DAT:*
| SIDSZ/godatu/geneseqy/geneseqn-embl/NA1981.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1981.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1981.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1985.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1986.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1986.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1989.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1989.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1989.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1989.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1989.DAT:*
| SIDSZ/godatu/geneseqyfeneseqn-embl/NA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | SIDS2/goddata/geneseqy seussequ embl./NA1991.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl./NA1991.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl./NA1993.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl./NA1993.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl./NA1995.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl./NA1995.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl./NA1995.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl./NA1999.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl./NA1999.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl.NA1999.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl.NA2001.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl.NA2001.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl.NA2001.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl.NA2001.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl.NA2001B.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl.NA2001B.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl.NA2001B.DAT:*
                                                                                                                                                                      Description
 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                            2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ21833
AAQ36859
AAF76910
AAI72775
AAI99683
AAI99683
AAI90682
AAZ10560
AAD01125
                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H
                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_101002
                                                                                                                                            US-10-090-035-3
574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %
Query
                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 622.6
622.6
523.2
523.2
523.2
523.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                       Seguence:
                                                                                                                                                                                                                                            Searched:
```

S

Result

ş

98798

000

O

Mycobacterium tube

```
(GOLD/) GOLD L.
(TUER/) TUERK C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-1990;
01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6194550-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF76910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF76910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                  임
                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
ò
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                     283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACGGGGGGGTCCACG 342
                                                                                                                                                                                                                                                                                                                                                  163 GCCGCCACGGCGCGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA 222
                                                                                                                                                                                                                                                                    168
                                      The sequence is that of an example randomising oligonucleotide which is used in the prepn. of mRNA encoding candidate polypeptides for the method of systematic polypeptide evolution by reverse translation (SPERT). The method provides a rapid way of isolating and identifying polypeptide ligands which bind to target mols. The polypeptide ligands can be used in e.g. assay methods, diagnostic procedures, cell sorting, as activators or inhibitors of target mol. function, as probes, as sequestering agents, drug delivery vehicles, modififers of hormone action and as catalysts. See also AAQ21830-Q21832.
                                                                                                                                                                                                           103 ACTACCAGGAGGTGGACTACTGCTCGGÀGGAGGTGAGGTCGGTGGCCCCGGCCGGCTTCG
                                                                                                                                                                                                                               223 CGGTCTCACGCGCGGCGCCAACCACCACCACCATGGTCACCACGGCGGCGCCACGGCT
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Systematic peptide evolution by reverse translation; SPERT; ligand; specific; inhibitors; probes; assay; cell sorting; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Systematic polypeptide evolution by reverse translation - used for prodn. of polypeptide ligand specific for desired target molecule
                                                                                                                                                                                        ;
0
                                                                                                                                                                  Query Match
10.9%; Score 62.6; DB 13; Length 390;
Best Local Similarity 52.0%; Pred. No. 0.0016;
Matches 140; Conservative 0; Mismatches 129; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer for 5' fixed sequence contg. T7 promoter and RBS.
                                                                                                                                               Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            349 ACGACGACGACGACGACGCCATGGTT 377
                                                                                                                                                                                                                                                                                                                                                                                 343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuerk C;
                        Example; Page 55; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gold L, Pribnow D, Smith JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ36859 standard; DNA; 390 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-US00801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0739055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYRE-) UNIV RES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-076529/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9303172-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ36859;
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
AAQ36859
                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                              g
        ŏ
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                    à
```

```
SPERT is used to select novel polypeptides that bind the antibody of the epitope commonly recognised by the antisera from autoimmune of the epitope commonly recognised by the antisera from autoimmune of the antisera from autoimmune of the allowan epitope composed of a Tormonol. 144, 4633, 1990). The known epitope consists of ca. 10 amino acids at the N-terminus of the histone H2B consists of ca. 10 amino acids at the N-terminus of the histone H2B consists of a Tormoner sequence and a ribosome binding sequence composed of a Tormoner sequence and a ribosome binding stee which is recognised by both prokaryotic and autonome binding stee which is restriction endonuclease site is synthesised and cloned terminating in a restriction endonuclease site is synthesised and cloned is placed into a restriction site to provide an mRNA encoding the C-is placed into a restriction site to provide an mRNA encoding the C-is placed into a restriction site is provided so that cDNA synthesis can be accomplished on the mRNA recovered from partitioned ribosome complexes. See also AAQ36845-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACCGGCGAGGTCCACG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ligand isolation; systemic polypeptide evolution by reverse translation; SPERT; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 ACTACCAGGAGGIGGACTACTGCICGGAGGAGGIGAGGICGGIGGCCCCGGCCGGCTICG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 CGGTCTCACGCGCGGCGCCAACCACCACCACCATGGTCACCACGGCGCCCACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence containing a 120 repeat of ACG flanked by fixed fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
10.9%; Score 62.6; DB 14; Length 390;
Best Local Similarity 52.0%; Pred. No. 0.0016;
Matches 140; Conservative 0; Mismatches 129; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 AGCGCAGGGAGGCTTCCTCGCCAGGGCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGACGACGACGACGACGACGCCATGGTT 377
Example 1; Page 84; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0829461.
90US-0561968.
91US-0739055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0197649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF76910 standard; DNA; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
```

22-FEB-2001; 2001US-0790399.

US2002038000-A1.

Synthetic.

8-MAR-2002.

```
The present sequence was used in an example illustrating an invention relating to a method for isolating a polypeptide ligand for a desired target molecule. The method involves synthesising a nucleic acid mixture comprising mRNA having translatable each on-translatable regions and a mixture of nucleic acid polypeptide coopolymers, each comprising the mRNA and a polypeptide encoded by its associated mRNA. The copolymers are partitioned relative to their affinity to the target. The method is termed systemic polypeptide evolution by reverse translation (SPERT). The polypeptide solution by reverse translation (SPERT). The polypeptide solution by reverse translation of target molecule function, as probes, as drug delivery vehicles and modifiers of target molecules include natural and synthetic polymers. The target target molecules include natural and synthetic polymers, including proteins, hormones, receptors and cell surfaces, nucleic acids and small concludes such as drugs, metabolites, cofactors and toxins. Polypeptide
                                                                                                                                                          Isolating a polypeptide ligand to a target molecule, useful for diagnostic assays, comprises partitioning candidate mixtures comprised of ribosome complexes or mRNA.polypeptide copolymers relative to their affinity to the target molecule
                                                                             Smith JD;
                                                                                                                                                                                                                                                                          Example; Column 39; 35pp; English.
                                                                        Tuerk C, Pribnow D,
                                                                                                                 WPI; 2001-243412/25.
    (PRIB/) PRIBNOW D. (SMIT/) SMITH J D.
                                                                   Gold L,
```

Ouery Match 10.9%; Score 62.6; DB 22; Length 390; Best Local Similarity 52.0%; Pred. No. 0.0016; Matches 140; Conservative 0; Mismatches 129; Indels 0; Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;

223 CGGTCTCACGCGCCGCGCGCACCACCACCACCATGGTCACCACGGCGGCCACGGCT 282 283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACG 342 163 GCCGCCACGGCGCGCGCGCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA 0; Gaps 343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371 g à 셤 ò g ç Q ð 셤

AAI72775 standard; DNA; 390 22-JUL-2002 (first entry) AAI72775; RESULT 4 AAI72775 

Oligo #7 for cloning T7 promoter and RBS containing mRNA.

17 promoter; ribosome binding site; RBS; prokaryotic; eukaryotic; ribosome; mRNA.circle-solid.polypeptide copolymer; mRcs.pC; SPERT; Systematic Polypeptide Evolution by Reverse Translation; assay; diagnosis; cell sorting; inhibitor; probe; sequestering agent; ribosome complex; ss.

```
The sequences given in AA172769-81 are oligonucleotides which were used to make mRNA encoding a candidate polypeptide, a 5' fixed sequence composed of a T7 promoter sequence and a Thosome binding site which is recognised by both prokaryotic and eukaryotic ribosomes, terminating in a restriction endonuclease site. The resulting nucleic acid was used in a restriction endonuclease site. The resulting nucleic acid was used in the method of the livention for preparing ligands of target molecules in which mixtures of ribosome complexes or mRNA.circle-solid.polypeptide on which mixtures of ribosome complexes or mRNA.circle-solid.polypeptide amplified to create candidate mixtures enriched in ribosome complexes command the account of the livention of the target, are new. The methods are useful for isolating polypeptide in ribosome complexes or mRNA.circle-solid.polypeptide except molecules. The polypeptide products are useful for assay methods, diagnostic procedures, cell sorting, as inhibitors of the sperm methods diagnostic procedures, cell sorting, as inhibitors of target molecule function, as probes, as sequestering agents and the carget molecule function, so probes, as sequestering agents and the carget molecule function, so property of the invention can have catalytic activity. Target molecules include natural and synthetic polymers, including proteins, polysecthatides, plysoproteins, bormones, creeptors and cell surfaces, nucleic acids, and small molecules such acting sequence of that polypeptide. The candidate mixture of polymetres including proteins, polysecthatics, of binding to a given desired target molecule. The partitioned according to their property of binding to append according to their property of binding to a given desired cach man acid sequence of that polypeptide. The candidate mixture is linked to an individualized mixture mixture and the mans for further amplifying it by an in vitro process. Content and the mans for further amplifying it by an in vitro process. It has the mean according to polypep
                                                                                                                                                                                                                                                                                                                                                                                                                                New methods (termed SPERT (Systematic Polypeptide Evolution by Reverse Translation)) for selecting high-affinity polypeptide ligands that specifically bind target molecules, e.g. proteins, carbohydrates, toxins, drugs and receptors
                                                                                                                                                                                                                                                                                                                                                           Smith JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 21; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                       Tuerk C, Pribnow D,
                                                                                                                                                                          98US-0197649.
90US-0561968.
91US-0739055.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-329128/36.
                                                                                                                                                                                                                                                       GOLD L.
TUERK C.
PRIBNOW D.
                                                                                                                                                                                                                01-AUG-1991;
                                                                                                                                                                            23-NOV-1998;
                                                                                                                                                                                               02-AUG-1990;
                                                                                                                                                                                                                                                                        (TUER/)
(PRIB/)
(SMIT/)
                                                                                                                                                                                                                                                                                                                                                   Gold L,
                                                                                                                                                                                                                                                       (COLD/)
```

Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;

ö 10.9%; Score 62.6; DB 24; Length 390; 52.0%; Pred. No. 0.0016; 1.ve 0; Mismatches 129; Indels 0 Query Match 10.9 Best Local Similarity 52.0 Matches 140; Conservative

ö

Gaps

ö

Length 4403765;

22; 98;

В

Score 53.2; DB Pred. No. 0.28; Mismatches

9.3%;

ö

112; Conservative

Query Match Best Local Matches 147

ð g ö

207

g

267

à

a δ

> ద ò

g ò g ò

셤 ö

ğ

Indels

1191449 gacgecegercegecegerrererereseancegesegecegecegecegeseges 1191390

1191389 GGCGCCAACGCCGGCAACGCGCAACGCC 1191360

327 ACCGGCGAGGTCCACGAGCGCAGGGAGAGC

CACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGC

GCCCCGGCCGGCTTCGGCCGCCGCCGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAG

TTCGAGGAGGTCGACACGGTCTCACGCGCCGCCCAACCACCACCACCACCATGGTCAC

326

```
The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, why cobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37RV (AA199682). The method is useful for evaluating strain of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                             168
                                                         222
                                                                                                                  282
                                                                                                                                   342
                                                                                                                                                                                          Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                           TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACGGCGAGGTCCACG
GCCCCCACGCCGCCGCCCTCCAGCACCACGTCGAGGAGAAGTTCGAGGAGGTCGACA
                                                                                    CGGTCTCACGCGCCGGCGCCAACCACCACCACCATGGTCACCACGGCGCCACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; d
                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; SEQ ID NO 2; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC;
                                                                                                                                                                                                                                      343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371
                                                                                                                                                                                                                                                                 ACGACGACGACGACGACGCCATGGTT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser CM,
                                                                                                                                                                                                                                                                                                                            AAI99683/c
ID AAI99683 standard; DNA; 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0103840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0103840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White OR,
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-647261/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fleischmann RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6294328-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-2001
      103
                                                               163
                                                                                           169
                                                                                                                          223
                                                                                                                                                                                                                                                                                                                                                                         AA199683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
```

```
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen.

Mycobacterium tuberculosis or related Wycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1531 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in th genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
                                                                                                                                                              Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds
                                                                                                                                  strain H37Rv genome SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser CM,
                               BP.
                             AA199682 standard; DNA; 4411529
                                                                                                                                                                                                                                                                                                                                  98US-0103840.
                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                         White OR,
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-647261/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fleischmann RD,
                                                                                                                                                                                                                                                                                                                                    24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                      24-JUN-1998;
                                                                                                    15-JAN-2002
                                                                                                                                                                                                                                                                                                 25-SEP-2001.
                                                                     AAI99682;
RESULT 6
                  AA199682
```

Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1..

662 216

603

543

```
97 TGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGTGAGGTCGGTGGCCCCGGCCG 156
                                                                                                                                                                                                 217 TCGACACGGTCTCACGCGCCGGCGCCACCACCACCACCACCATGGTCACCACGCGGCC 276
                                                                                                                                                                                                                                                                               277 ACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGG 336
                                                                                                                                                                                                                                                                                                           542 GGGCGCCGCTCCTGCTCCAGGCCCCACGTCCTCGTCGTCGCCCCCCCGCG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; orphan G protein-coupled receptor; GPCR; hGPCR27; drug screening;
transmembrane receptor; expressed sequence tag; EST; signal cascade; ss.
                                                                                                                                                                                                                         721 rescencecceceres de consecue de la respecta del respecta de la respecta de la respecta del respecta de la respecta della respecta della respecta de la respecta de la respecta de la respecta della respecta della respecta de la respecta de la respecta della respecta della respecta della respecta de la respecta della r
                                                                                                                    GCTTCGGCCGCCGCGGCGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                                                                                                661 GCACCAGGCGCGCGGGCCGCATCTTGCGGC-GGTCGTGAAGAGAGAGCAGGCGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Human orphan G protein-coupled receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human orphan G protein-coupled receptor hGPCR27 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "hGPCR27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..1128
                                                                                                                                                                                                                                                                                                                                                                                          TCCACGAGCGCAGGGAGAGC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD01125/c
ID. AAD01125 standard; cDNA; 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0157294.
99US-0416760.
99US-0417044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0121852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0136439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0137127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0157280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0156634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0156653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40200031258-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-0CT-1999;
12-0CT-1999;
                                                                                                                  157
                                                                                                                                                                                                                                                                                                                                                                337
                                                                                                                                                                                                                                                                                                                                                                                                       482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD01125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                         원
                                                                                                                                                    셤
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                              3932728 CCCCACCGGCATCGGCGGCACCGGCGGGGGAAGGCGGCGCGGCGGCGGG 3932787
                                                                                                                                                                                    3932788 CGGCGCGGCGGTAGCAGCGGTGCCGGCGCACCAACGGCTCTGGTGGCGCGCAC 3932847
                                                                                                                                                                                                                                                                  3932848 CGGCGGACAAGCGGCGCGCGCGCGCGCGCGCCGATAACCCCACCGGCAT 3932907
                                                     ö
                                                                             149 CCCGGCCGGCTTCGCCCCCCCCGCGGCGCCTCCAGCACCACCACCACGAAAGTT 208
                                                                                                                                                             209 CGAGGAGGICGACACGGICTCACGCGCCGGCGCCAACCACCACCACCATGGICACCA 268
                                                                                                                                                                                                                                            CGGCGGCCACGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACTGCAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor proteins expressed in the central nervous system and genes encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a G protein-coupled receptor protein, designated SREB1. The protein is expressed in the central nervous system. The SREB products are used for the diagnosis and treatment of diseases of the central nervous system, including inflammatory disorders of immunological origin.
    Score 53.2; DB 22; Length 4411529;
Pred. No. 0.28;
0; Mismatches 88; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor protein; SREB1; central nervous system;
inflammatory disorder; immunological; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding G protein-coupled receptor protein designated SREBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
9.2%; Score 52.8; DB 20; Length 1128;
Best Local Similarity 52.7%; Pred. No. 0.15;
Matches 137; Conservative 0; Mismatches 122; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kamohara M;
                                               88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsumoto M, Sugimoto T, Takasaki J, Saito T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 47-49; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualiflers
1..1128
/*tag= a
/product= "SREB1"
                                                                                                                                                                                                                                                                                                                                                                                                                      3932908 CGCCGCCCCCC 3932921
9.3%;
                                                                                                                                                                                                                                                                                                                              CGGCGAGGTCCACG 342
            Best Local Similarity 54.69
Matches 106; Conservative
                                                                                                                                                                                                                                            269
                                                                                                                                                                                                                                                                                                                            329
Ouery Match
                                                                                                                  a
                                                                                                                                                          ò
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                       ç
                                                                                                                                                                                                                                                                                                                                                              g
```

```
20-APR-2000
                                                                                                                                                                                                                                                                                                                    MAR-1
                                                                                                                                                                                                                                                                                                                                                                                           MAR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 - AUG - 1
                                                                                                                                                                                                                                                                                                                                            MAR-1
                                                                                                                                                                                                                                                                                                                                                                        MAR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                    corpus of protein-coupled receptor (GPCR), expressed in foetal brain, putamen, pitulitary gland and caudate nucleus. The hGPCR27 cDNA was identified using EST (expressed sequence tag) AA775870 as a probe. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular c-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the cidentification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 recentactaccageaegregactactecresageaegreaegresereseres 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 TCGACACGGTCTCACGCGCCGGCGCCAACCACCACCACCATGGTCACCACGGCGCCC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 ACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              721 rescescesceresces resces resces researes respected resces respected rescess respected respec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 GCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 GCACCAGGCGCGCGGCGCGCATCTTGCGGC-GGTCGTGGATGAAGAAGAGAGCAGGCGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602 TAGACGAGGTGCGTGGCGCCCACCACGACCAGCAGCAGCAGGAAGCCCAGCGCGCCG
                                                                                                                                                                                        Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G protein coupled receptor hGPCR27 encoding cDNA SEQ ID NO:17
                                                                                                                                                                                                                                                                                                                      present sequence is a cDNA encoding hGPCR27, an endogenous human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G protein coupled receptor; GPCR; transmembrane receptor;
identification; agonist; screening; therapeutic; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52.8; DB 21; Length 1128;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                        Claim 29; Page 61-62; 102pp; English
                                                                    Lin I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 TCCAGCACTGGCGGGAAGGC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 TCCACGAGCGCAGGGAGAGC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA46026 standard; cDNA; 1128 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.2%;
52.7%;
                                                                  Liaw CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                (AREN-) ARENA PHARM INC
                                                                                                                WPI; 2000-400068/34.
P-PSDB; AAY71298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                  Dang HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200022131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA46026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                    Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA46026/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 ACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 TGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGGCCCCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                721 rescencecceccestesces and respect to the contract of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTTCGGCCGCCGCCGCCGCCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 TCGACACGGTCTCACGCGCCGCCGACCACCACCACCACCATGGTCACCACGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor, inverse or partial agonists useful as therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-endogenous, human G protein-coupled receptors for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dang HT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
9.2%; Score 52.8; DB 21;
Best Local Similarity 52.7%; Pred. No. 0.15;
Matches 137; Conservative 0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Behan DP, Lehmann-Bruinsma K, Chalmers DT, (
Gore M, Liaw CW, Lin I, Lowitz K, White C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 91-92; 187pp; English.
                                                                                                                                                                                                                                       99US-0123946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0141448
                                                   99US-0121852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0156633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0137131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0137567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0136437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0137127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                       99US-012
                                                                                                                                                                                                                                                                                                                                                                                                                    99US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-317986/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB02832.
                                                                                                                                                                             MAR-1999
6-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
```

ij

156 662 216 603

```
RESULT 11
AAS98049/c
88888888
                                                                                                                                               a
                                                                                                                             à
                                                                                                                                                                        ö
                                                                                                                                                                                             셤
                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of identifying an agent that binds to and/or modulates activity of human G-protein coupled receptor (GPCR) 14266. The invention also provides a method for modulating the level or activity of the GPCR in cells in vivo or in vitro, or in a subject disorders. Detecting 14266 polypeptides or neutrophil deficiency disorders. Detecting 14266 polypeptides or nucleic acids in specific biological samples is useful in disease disponais. Modulating level or activity of the GPCR polypeptide or polynuclectide is useful for treating spleen (e.g. splenomegaly, neoplasms); lung (e.g. pulmonary hypertension, emphysema); colon (e.g. disarhoea and disease); liver (e.g. hepatic injury, viral hepaticis); uterus and endometrium (e.g. endometricasis, endometrial adgemention); caute meningitis, multiple sclerosis, splinocerebellar degeneration); T-cells (e.g. vitiligo, acanthosis nigricans); heart (e.g. heart failure,
                                                                                                                                                                        Human; G-protein coupled receptor; GPCR 14266; haematopoietic disorder; neutrophil deficiency disorder; splenomegaly; pulmonary hypertension; colon; diarrhoea; hepatic injury; idiopathic inflammatory bowel disease; uterus; endometriosis; brain; acute meningitis; multiple sclerosis; T-cell; systemic lupus erythematosus; skin; vitiligo; heart failure; angina pectoris; atherosclerosis; haemolytic anaemia; thymic cyst; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying compound that binds to and/or modulate activity of the polypeptide for treating splenomegaly, emphysema and multiple sclerosis, comprises using human G-protein coupled receptor 14266
                                                                                                                                                                                                                                                                                                                                          /*tag= b
103..1125
/*tag= c
/product= "Mature GPCR 14266"
                                                                                                                                                     Human G-protein coupled receptor 14266 DNA.
                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "GPCR 14266"
1..102
                                                                                                                                                                                                                                                                                  Location/Qualiflers
  TCCACGAGCGCAGGGAGAGC 356
                 AAD27892 standard; DNA; 1128 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2001; 2001WO-US24835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2000; 2000US-0634392.
                                                                                                                             31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-217181/27.
P-PSDB; AAE14597.
                                                                                                                                                                                                                                                                                                                                                                                                   WO200212344-A2
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                       mat_peptide
  337
                                                                                                        AAD27892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weich NS;
                                                           RESULT 10
                                                                                            8
  à
```

```
97 TGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCG 156
                                                                                                                                                                                                                                                                                                                                                                   662
                                                                                                                                                                                                                                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 ACGGCTTCGTGGTGCGGGGGCCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542 GGGGGCGTCGGGCCGCTGCTCCAGGCGCACGGCGCGTCCTCGTCGTCGCCACCGCCG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzeaner's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease; multiple sclerosis; osteoarthritis; popporosis; parkinson's disease; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; thormonal release disorder; memory disorder; anorexia; brimonal release disorder; cardiovascular activity disorder; pain perception disorder; diabetes; obesity; diabetes; obesity; diabetes; besity;
angina pectoris); blood vessels (e.g. atherosclerosis, Raynaud disease, thalassaemia syndromes, haemolytic anaemia) and disorders of the thymus (e.g. thymic systs, Hodgkin's disease). The present sequence is human GPCR 14266 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful
                                                                                                                                                                                                                                                                                                                                                       721 TGGCGGCCGCTGGCCGGTGGCCCCGGGCCGTGGAAGGTCCAGTCGTGGCTGACGCGG
                                                                                                                                                                                                                                                                                                                                                                                                               157 GCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGACACGGTCTCACGCGCCCGGCGCCAACCACCACCACCACCATGGTCACCACGGCGCC
                                                                                                                                                                                                    Length 1128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pritchard
                                                                                                                                                                                                                                                         Indels
                                                                                                                                 Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human DNA for potential G protein-coupled receptor #7.
                                                                                                                                                                                           9.2%; Score 52.8; DB 24;
52.7%; Pred. No. 0.15;
11ve 0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fabre-Suver C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 TCCACGAGCGCAGGGAGAGC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown JP, Miller M, Burmer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS98049 standard; DNA; 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-2001; 2001WO-US15332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-2000; 2000US-203217P.
                                                                                                                                                                                         Query Match
Best Local Similarity 52.7<sup>1</sup>
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-066595/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200185791-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS98049;
```

```
/*tag= o
/product= "Evd1"
complement (10232..10235)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "No start codon"
complement (12108..13022)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "EvdL"
complement (13027..13030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "EvrC"
complement (17870..18934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (14410..15363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (15369..15373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (15380..16414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (9463..10224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "EvrB"
complement 16419..17873
                                                Micromonospora carbonacea var. africana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omplement (3867..3870)
                                                                                                                                                                                                              complement (1389..1394)
                                                                                                                                                                                                                                                                       complement (1490..2611)
                                                                                                                                                                                                                                                                                                                        /product= "EvdB"
complement (2618..2622)
                                                                                                                                                                                                                                                                                                                                                                                                           complement (2622..3860)
                                                                                                       Location/Qualifiers
complement (132..1382)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product- "EvrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "EvrD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product= "EvdK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= q
product= "EvdJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "EvdH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "EvdE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "EvdF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "EvdG"
                                                                                                                                                                                 product- "EvdA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "EvdC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "EvdD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g= p
4..11176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2027..12455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7*tåg= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3342..9364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8333..8336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143..5312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34..4138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226..6229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309..6235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= m
                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tad=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
fermentation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                             Key
                                                                                                                                                                                                                          RBS
                                                                                                                                                                                                                                                                                                                                                              RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RBS
                                                                                                                              The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G nucleic acid molecule that is at least 80% identical to the G nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polymorleotides included in the specification.

Also included are probes based on the GPCR sequences (including attisense probes), a host cell comprising an expression vector comprising the GPCR sequence, antibodies raised against the polypeptides. The Compounds which polypeptides are useful for identifying modulator compounds which polypeptides are useful for identifying modulator compounds which of the novel GPCR polypeptides including the GAL4 polypeptide. The antibodies and nucleic acids and are used to detect the presence of the polypeptides and nucleic acids and are used to diagnose a variety of diseases as described above can be used to diagnose a variety of diseases or disorders in which GPCRs are involved c.g., Alzhelmer's disease, amyotrophic lateral sclerosis, asthma, chonic obstructive pulmonary disease, carcinoma, cardiomyopathy, chondrosarcoma, chronic obstructive pulmonary disease, acarcinom, pulmonary disease, carcinom, melanoma, melanoma, melanoma, procederosis, past became to the propession, epilepsy, macular degeneration, lymphoma, melanoma, procederosis, past became to the propession, epilepsy, macular degeneration, lymphoma, melanoma, procederosis, past probes and antibodies are also useful for diagnosing cognition and memory disease, and antibodies are also useful for diagnosing cognition and memory disease, and antibodies are also useful for diagnosing and memory disease, and antibodies are also useful for diagnosing and antipolation and memory disease and antibodies are also useful for diagnosing and anti-private and antipolation and and antipolation and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 TGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 TAGACGAGGTGCGTGGCGCCCACCACCACGCCAGCAGCAGGAAGCCCAGCGCGCGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 ACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilsorders, anorexia, hormonal release disorders, cardiovascular activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 GCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   721 TGGCGCCCGCCTGGCCGCTGGCGCCCTGGAAGGTCCAGTCGTGGCTGACGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 TCGACACGGTCTCACGCGCGCGCGCCAACCACCACCACCACCATGGTCACCACGGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
           for treating Alzheimer's disease, psoriasis, melanoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52.8; DB 24; Length 1128;
Pred. No. 0.15;
0; Mismatches 122; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Everninomicin; antibiotic; bottle-neck gene; orthomicin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
                                                                                           Disclosure; Page 116-117; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 TCCACGAGCGCAGGGAGAGC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482 TCCAGCACTGGCGGGAAGGC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS08693 standard; DNA; 109519 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.7%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS08693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS08693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XX DX DX XXX
```

g ò 임 ò g à 셤 ò a

1937420906	/rtag= z /product= "EvrE" 2106422542	/"tag= aa /product= "EvrF" 2105622542	/*tag- ab 2274824172	/*teg= ac /product= "EvrG" 2273622740	/*tag= ad complement (2417725223) /*tag= ae	/product="EvrH" complement (2523025233)	/*Lay= ai 2555026626 /*tag= ag	/product="EvrI" 26685.30479 /*tag= ah	/product= "EvrJ" 2667226676	/*tag= a1 complement (3055731876) /*tag= a4	/product= "EvrK" complement (3188531888)	/*tag= ak complement (3194132882) /*tag= a	5 8	/product- "EvrM" complement (3441434418	/*tag= an complement (3444935210) /*tag= ao	/product= "EvrN" complement (3521935221)	/ .cay= ap complement (3529436238) /*taq= aq	/product="Evro" complement (3623536963) /*tag= ar	/product="Evrp" complement (3699838026)	/product="EvrO" complement (3807238566) /*tag= at	/product="EvrR" complement (3889240163) /*tag= au	/product="Evrs" complement (4021640890)	/product= "EvrT" complement (4089940902)	/*tag= aw complement (4088741576) /*tag= av	<u>ب</u> و ب	/ complement (4271442717)	/*tag= az complement (4281043799)
CDS	cos	RBS	CDS	RBS	cps	RBS	CDS	CDS	RBS	CDS	RBS	CDS	CDS	RBS	cos	RBS	CDS	CDS	cos	cos	CDS	CDS	RBS	CDS	CDS	RBS	, sac

```
The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene
con-coding regions of RNAs carcinomes on borders, the
initiation codons, genomic flanking regions, intron-exon borders, the
confidence diseases, conditions or mixtures. The antisense oligonucleotides
common diseases, conditions or mixtures. The antisense oligonucleotides
common genence AAX55180-271, can be used for the
antisense treatment of diseases and conditions. Typical diseases and
conditions are those associated with impaired respiration and
conditions are those associated with impaired respiration and
conditions allergic rhinitis, acute asthma, allergies, asthma, impeded
respiration, including lung disease, pulmonary vasoconstriction,
conditions allergic rhinitis, acute asthma, allergies, asthma, impeded
respiration, allergic rhinitis, acute asthma, allergies, asthma, impeded
conditions allergic rhinitis, acute asthma, allergies, acute
conditions allergic rhinitis, acute asthma, allergies, asthma, impeded
conditions are those associated with impaired respiration, painconstriction,
confidence associated with impaired solutions, paincers, lung cancer,
confidence associated to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                          Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vascoonstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vascoonstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                    Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 37; 120pp; English.
                                           AAX53491 standard; DNA; 114955 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0093972.
97US-0059160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US19419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEC-) UNIV EAST CAROLINA
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-1998;
                                                                                                                                     05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09913886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                          AAX53491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nyce JW;
RESULT 13
                        AAX53491
```

```
103427 CGCNNHNNNSACGCCCCCAVGACGCCCCCCCNHNNNSCACGCCCCCAVGACGCCCCC 103368
                                                                                                                                                                                                  103187 CCAVGACGCCGCCNNHNNNSCCGGCCCGACGCCCCAVGACGCCGCGCNNHNNNSCC 103128
                                                                                                                                            103308
                                                                                                                                                                                                                                                                          103247 CCGCGCNNHNNNSGGCCCGACGCCGCCAVGACGGCCGCGCNNHNNNSCGGCCCGACGCCG 103188
                                                                                                                                                                                                                                                                                                          360
                                                                                                                                                                              240
                                                                                                                                181 TCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCG
                                                                                                                                                                                                                                                                                                          301 GGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGGCAGGGAGGTTCC
                                               GGCGCTGCGCACACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACT
                                                                                                               121 ACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCGCCACGGCGGCGCG
                                                                                                                                                                                                                                             241 CCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A DNA sequence (AAT10429) codes for the mature isoamylase (plus an N-terminal methionine) of Flavobacterium sp. (see also AAR92692). It was obtd. by amplification of the cloned isoamylase gene (AAT10428) using primers (AAT10423-33) designed to add a start codon to the beginning of the processed mature enzyme (Ala-33) and a stop codon adjacent to the endogenous TGA codon. The DNA sequence is used for the recombinant prodn. of isoamylase or can be expressed in transgenic plants, e.g. potato, cassava, sweet potato, corn, wheat, barley or rice, to alter the amylose:amylopectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated DNA encoding isoamylase - used to produce plants having a modified starch content, e.g. a higher ratio of amylose to
                                                                                                                                                                                                                                                                                                                                                                                                  103127 CGGCCCGACGCCGCCAVGACGCCCGCCNNHNNNSGCCCGGCCCG 103083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isoamylase; starch; amylose; amylopectin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                          361 TCGCCAGGGCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCCCG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 35-39; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT10429 standard; DNA; 2244 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krohn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US09323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0281902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barry GF, Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mature isoamylase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-117056/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flavobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR92693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fructose; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amylopectin
                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT10429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT10429
                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                    ŏ
                                                                                   g
                                                                                                                    ò
                                                                                                                                                 g
                                                                                                                                                                                   ò
                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                              ò
```

Query Match 9.2%; Score 52.8; DB 20; Length 114955; Best Local Similarity 35.6%; Pred. No. 0.24; Matches 144; Conservative 29; Mismatches 232; Indels 0;

ö

1996

330

```
1997 Aceechaceantrescentadescandescentations and anticommentation 2056
                                                                                271 GCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACCG
              151 CGGCCGGCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCGTCAAGGAGGAGTTCG
                                       1877 CGCCCAGCGACACCCAACGCCAACGTGATGGAGCAGTTGCGCTGGTTCAAGCCCGACGGCG
                                                                211 AGGAGGTCGACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCATGGTCACCACG
                                                                                                                                                                                                                                   Search completed: June 16, 2003, 02:09:39
Job time : 214.272 secs
                                                                                                                                                                                           2057 ececegicaec 2067
                                                                                                                                                                     331 GCGAGGTCCAC 341
                                                                                                                  ò
                                                                                                                                          g
                                     g
                                                               οχ
                                                                                   ద
                                                                                                                                                                     ò
                                                                                                                                                                                           g
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                     211 AGGAGGTCGACACGGTCTCACGCGCCGCCCAACCACCACCACCACCATGGTCACCACG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes the Flavobacterium isoamylase of the invention. The protein can be used to produce higher amylose starches, using genetically modified plants.
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                            ö
                                                 Ouery Match 9.0%; Score 51.8; DB 17; Length 2244; Best Local Similarity 54.5%; Pred. No. 0.25; Matches 104; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.0%; Score 51.8; DB 19; Length 2244;
Best Local Similarity 54.5%; Pred. No. 0.25;
Matches 104; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding for Flavobacterium isoamylase - for production of recombinant isoamylase or transgenic plants
                         Sequence 2244 BP; 427 A; 827 C; 704 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2244 BP; 427 A; 828 C; 703 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isoamylase; high amylose starch production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                              Flavobacterium isoamylase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Column 27-32; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..2241
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barry GF, Kishore GM, Krohn BM;
                                                                                                                                                                                                                                                                                                                                                 AAV23640 standard; DNA; 2244 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0476519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0476519.
94US-0281902.
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                          GCGAGGTCCAC 341
ratio of the starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-296898/26.
P-PSDB; AAW53886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flavobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
28-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5750876-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                           AAV23640;
                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                      AAV23640
                                                                                                                           셤
                                                                                                                                                                          g
                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                      ð
                                                                                                                                                                                                       à
                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                        ò
```

				.1
			- 1	
			4	
	•			
				2.0
1.				
			A)	
		4.		
*				
( <b>4</b> )				
	•			
	,		(*)	
	•		Ţ	
	•			*
		•		
			*	
ů.		16		
				•
	4			•
*	÷		÷	(A)
				[*
4,	·		÷-	
				•
	· · · · · · · · · · · · · · · · · · ·		4	
.7		•		•
•				
*	e a		h	**
				•
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\				•
				•
				4.2

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

ō

OM nucleic - nucleic	eic search, using sw model
Run on: J	June 15, 2003, 23:43:51; Search time 1684.35 Seconds (Without alignments) 9917.805 Million cell updates/sec
Title: US Perfect score: 57 Sequence: 1	US-10-090-035-3 574 1 acccacgcytccgcccacycaaaaaaaaaaaaaaa 574
Scoring table: II	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 20	2054640 seqs, 14551402878 residues
Total number of hi	hits satisfying chosen parameters: 4109280
Minimum DB seq len Maximum DB seq len	length: 0 length: 2000000000
Post-processing: M	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database ; G	GenEmb1:*
1:	9b_ba:*
• m	
9,	
: / 8	95_ph:* 95_pl:*
:6	
11	
12	: db_sy:*
11.	
15	
17	
19	
20	
. 22	-
23	
25	
26	-
28	-
29	_
30.33	em_htg_hum:* em_htg_hum:*
325	•
200	em_htg_mus:*
883	-
37:	
38:	
	em_htgo_hum:* em_htqo_mus:*
41:	em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Oryza	Oryza	oryz	Oryza	AJ2428U2 Sporobolu	מ מ	Streptom	Oryza	ALSYSB42 Streptomy	v18817 Ctanton	ADOMANA SELEPTOMYCE	ABOOAAS Organ	APON4873 Oruza cart	AF263463 Streptomy	AE005107 Halobacto	AP004088 Orvza sat	AC108759 Orvza sat	AP005412 Oryza sat	AP004765 Oryza sat	AL035206 Streptomy	AC128158 Rattus no	AL589164 Streptomy	Arubbasz Streptomy	ALLISTA STREPTOMY	ATTOCATO OFFICE OFF	AEOO6991 Mycobacto	vcobact	AP002485 Oryza sat	equence	AB040799 Homo sap1	edneuc	edne	ACTOSOS HOMO SEPT		AC130729 Original Sapt.	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	AP005182 Orvan ant	edine	equenc		tre	827 0
Ω	17.000	AF003415	h C	200	24.0	AP135147	75777	AC107225	10		50018817	AP003735	AP004045	AP004873	AF263463	AE005107	AP004088	AC108759	AP005412	AP004765	•	AC128158	SCARB	9 -	324	550	50	3	0248		שׁיַי	AA193930	1 4	7				18	59	R00	SU9012	4	AP003827
ery tch Length D	0 4 173600	0.4 174218	0.4 185095	0.4 185481	5.1 562	360	0.7 35100	7 150676	29080	1 18420	9.9 4851	9 150053	8 102688	8 138289	5 3164	5 13368	4 106050	4 146436	4 152263	4 187705	4 36368	4 1/4410	3 10512	3 41173	3 65547	3 120159	m	3 47852	2 136150	2 1128	2 1178	2 109519	2 163494	2 171297	2 190506	2 179198	1 41622	1 143676	0 2244	2334	2936	38532	0 149256
ore	174.6	174.6	174.6	174.6	143.8	62.6	61.4	61.4	58.2	57.8	57	56.8	56.2	56.2	54.6	54.4	54.2	54.2	54.2	2.4.2	40 cm	, c , c	53.0	53.4	53.4	53.4	53.2	53.2	5 23	8.7.9	0.00	22.8	52.8	52.8	52.8	52.6	25	52	51.8	51.8	27.8	. T. C	51.8
Result	:		υ υ	7	5	9	7		0		c 11	12	c 13	14	15	16	c 17		19	202	777	•	24	•	26	27	c 28		c 30	., .	, ,	34	c 35	36	c 37	m	39	40	41	24.	4 4	ָבָי בְּי	n e

## ALIGNMENTS

linear PLN 17-MAY-2002 genomic DNA, chromosome 1,	(cultivar:Nipponbare) DNA,	Embryophyta; Tracheophyta; a; Poales; Poaceae;
AP003416 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, AP003416 AP003416 AP003416.4 GI:20804922	Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0456E05. Oryza sativa (japonica cultivar-group)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
RESULT 1 AP003416/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SOURCE	REFERENCE

COMMENT

```
join(36977. .37082,37255. .37479,37607. .37701,37823. .38015,
38424. .38764,39169. .39399,39493. .39645)
/gene="P0456E05.6"
/note="contains ESTs D46801(S11706),AU095929(S11706)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .38015
RFLAATRPISVQGDLNLFPSLPYSCSLAAAGLVL"
join(18574. .18678,18821. .18984,20752. .21058,21870. .22177,
                                                                                                                                                           .21058,21870. .22177,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVVLKIKGKNERAGRWRRIWHWGIIVASSVLSVYTAAAVRLIVHNASVYHFFADM"
complement(join(40277. .40417,40717. .40773,40875. .41073,
41173. .41300,41399. .41504,41677. .41756,42145. .42242,
42324. .42437,42523. .42663,42757. .42841,43717. .44055))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OEISETSKRYEVDDESQLEVDREDYRSEADVSNGTFIGYKPHIEELEMLLEAYFVOL
DCTLNKLSHLREYVDDTEDYINIMLDDKONOLLOMGVMLSTATVVITAGVAVVGLFGM
NIGISLYADPTNEEERRASNMKFWFTIGTIAGCTVMYIVAMGWGKRSGLLO"
join (36977) 37082, 3755. 37479,37607. 37701,37823. 3801
38424. 38764,33169. 39399,39493. 39645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product."proline transport protein-like"
/product."proline transport protein-like"
/protein_id="BaB92607.1"
/db_xref="G1:20804928"
/db_xref="G1:20804928"
/tb_xref="G1:20804928"
/tb_x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTQAEKVFGAFGAIAAILVONTSGLLPEIQSTLRKPVVSNMRRALLLQYTAGAAVYYG
ISVAGYWAYGAAVSBYLPDQLSGPSWATVLINATAFLQSIVSQHLFTVPIHEALDTQM
QRLDEGMFSRYNLGRRLLARGLVFGANAFVTALFPFWGDFVNLFGSFVLFPLFFWFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="Bab92606.1"
/db_xref="G1:20804927"
/db_xref="G1:20804927"
/tanslation="MRPSAAAGGGGGGGGRRKAAAAAAAASREWLVVPASGQARVEEA
/translation="MRPSAAAGGGGGGGGGGRRKAAAAAASREWLVVPASGQARVEEA
GKHAVMARTGIPARDIRVLDPLLSYPSTILGRERAIVVNLERYKAVITAAEVLIPNSK
BAPAGSFVGLQARVIASSPOQAAERTPNBGEGSSATSPPFALTSTTPNBLEWTNNNS
NVVGGWTHSNAPTITAAARDGNIKVLPFEFALEVCLESAACRELEBETSTLEGGAAVR
LDBLTSKISTILNLERVRQIKSRLVALSGRVORVNDELEHLIDDEMDMARYLTERITR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAATGEVYFAFAYEVPTISAMRNWLATSAALTVAYDVALIVILIKDGKSNKQKDYNVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="meegvrragdaaaaavvvitssgrrripahstvlasaspvles
ilorrikkerdaaagggkvrravvlirgvtddaaafvrlltagssgdeeeideksaa
omlvlahayrvpwlkrrcegaigsrltaesvvdtwqlaalcdapolherctrllakef
kavekteawrfloendpwleldilorlhdaddrrkrrrraeggvyvelseawdcls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="WVKVATYFAMTFGAFLFWQSMDRVHVWIALHQDEKKERMEREQE
IKRWQAELMAQAKESES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HICTEGCTEVGPVGRAPAAAPCPAYATACRGLQLLIRHESRCHRTSCPRCQRMWQLLR
LHAALCDLPDGHCNTPLCMQFRRREEEKAAARKAKARAGDDDKWGLLVKKVRVARAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement join(26102. .26407,26766. .26901,27028. .27170,
27656. .27784.28154. .28402,28988. .29359))
/gene="P0456E05.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(26102 .26407,26766 .26901,27028 .27170,
27656 .27784,28154 .28402,28988 .29359))
/gene="P0456E05.5"
                                                                                                                                                                                                                                                                                            /note="contains EST AU070785(R10238)
similar to Arabidopsis thaliana chromosome 3, At3948360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(23558, .23638,24837. .24941))
/gene="P0456E05.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(23558, .23638,24837, .24941))
/gene="P0456E05.4"
                                                                                                                                                  jóin(18574. .18678,18821. .18984,20752.
22377. .22536)
/gene="P0456E05.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains EST AU162265(E30874)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   magnesium transporter-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0456E05.5"
/note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB92605.1"
/db_xref="G1:20804926"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAB92604.1"
/db_xref="G1:20804925"
                                                                             22377. .22536)
/gene="P0456E05.3"
                                                                                                                                                                                                                                                                                                                                                                                            unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLGKRRQMSCSQC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=]
                                                  oin(18574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                     clone: P0456E05

Published Only in Database (2001)

E 2 (bases 1 to 173699)

Sasaki, T. Matsumoto, T. and Yamamoto, K.

Direct Submission

My 15. 2002 this Sciences, Rice Genome Research Program: Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:isasaskienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, URL:http://rgp.dna.affrc.go.jp/, URL:http://rgp.dna.affrc.go.jp/, URL:http://rgp.dna.affrc.go.jp/, URL:http://rgp.dna.affrc.go.jp/, Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: Gotober 1998 version). The genomic sequence was searched against (ftp://noth.inlm.inl.gvv/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against the identified cDNA sequences using BLASTRY 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified as a moverland same name, 'unknown' protein any protein but with EST homology (covering significant homology to any protein but with EST homology (covering significant homology to any protein mare to indicate the homology to any protein but with sequence of P0456E05 clone has an overlap with p0470Al2 (DDBJ: Ap003436) at the position 130,058 to 173,699 of 3' end Detailed annotation of this entry is savallable at an information of this entry is available at an information of this entry is available at the homology than affreqo.jp/GenomeSeq.html.

Incation/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FCGDSSFAKSNQESLKNILIIFAKLAAGIRYVQGMNEILAPLEFYFRNDPDDKNANFA
EADSFPCFMELLSGFRDNFCQKLDNSAVGIQGTLSKLSQLVAKYDGELQRYLEITTEI
NPQFYAFRWITLLLTQEFNFADTIHIWDTLLSDPDGPQGRSIYRDGTGESMYTNIETS
VAHAYQSSRNSAVPVVEKLHRCRKATGAARLQFAAAPFLSPFRSPETTENAEAFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YWILSCSDQNOCYARRWRANASILIN"

YMILSCSDQNOCYARRWRANASILIN"

complement(join(11701. 11960,11998. .12076,12765. .12881, complement(join(11701. .13196),1360. .13758,14527. .14631, 15002. .15131,15421. .15487,17632. .17717,17924. .17952))
/gene="P0456E05.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB92602.1"
/db_xref="GI:20804923"
/translation="MCCLMPISTCACVCVERQQTQNADWLATPPAPAFAAAFALYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(11701. .11960,11998. .12076,12765. .12881,
13131. .13310,13459. .13587,13660. .13758,14527. .14631,
15002. .15131,15421. .15487,17632. .17717,17924. .17952))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGRENETVKNALLKHENFDGSLWYGELAQLSKKVIDLDELRMLAAQGVPDGAAVRPTV
WKLLLGYLPSDRALWEQELAKKRSQYAAFKEEFLSNPYSEIIEQIDRDYKRTHPDMHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MHEPLYRVHKKQQPVTAQHRPRLRGEATTLGSIRGRRRGSPHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="P0456E05.2"
/note="contains ESTs AU101913(S0657),AU101912(S0657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .173699
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0456E05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similar to rabGAP domains protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(9483. .9641,10723. .10785)
/gene="P0456E05.1"
join(9483. .9641,10723. .10785)
/gene="P0456E05.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB92603.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"GI:20804924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="P0456E05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

```
Update: 1 to 174218) .

Hahn, J.-H., Eun, M.Y. and Kim, H.-I.

Birect Submission
Submitted (27-MAR-2001) Rice Genome Sequencing Project, National
Institute of Agricultural Science and Technology(NIAST), RDA, 249
Seodun-dong, Suwon 441-707, Korea (E-mail:jhhahn@rda.go.kr,
Tel:82-31-290-0309, Fax:82-31-290-0308)

The PAC clone was provided by Japanese Rice Genome Research Program
                  Oryga sativa (japonica cultivar-group) chromosome 1 clone P0456E05, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridplantea; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (bases 1 to 174218)
Lee, J.-S., Hahn, J.-H., Yoon, U.-H., Lee, M.-C., Yun, D.-W., Kim, H.-I.
and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  **NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 53114 53213: contig of 53133 bp in length

* 53214 172404: contig of 53131 bp in length

* 172505 172504: gap of unknown length

* 172505 174218: contig of 1714 bp in length

* 172505 174218: contig of 1714 bp in length

* 172505 174218: contig of 1714 bp in length

//wariety="Nipponbare" //wariety="Nipponbare" //wariety="Laxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 TGAGGTCGGTGGCCC---CGGCCGGCTTCGGCCGCCGCGGCGGCGCGCCTCCAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 TCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCCCAACCACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 ACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 174218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                  Oryza sativa PAC P0456E05 genomic sequence
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 174.6; DB 2;
Pred. No. 5.4e-17;
0; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="P0456E05"
a 38377 c 37185 g 49417 t
                                                                    AC091071
AC091071.1 GI:13450004
HTG: HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.4%;
Best Local Similarity 72.8%;
Matches 257; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49037
                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                  JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/codon_start=1
/codon_start=1
/codon_start=1
/dw.xref="G1:20804930"."
/db_xref="G1:20804930"."
/db_xref="G1:20804930"."
/db_xref="G1:20804930"."
/translation="WAASRIARERIARKLPSLISKHORLISPEIDVEQAAESPASSSIPLD
/translation="WAASRIARERIARKLENLISPEIDVEDAAESPASSSIPLD
/translation="WAASRIARERIARKLENLISPTERPOPTODSIRACELLEPF
SUSPAFRPOHKLISLASRRADSFLASRRADSFLAEVERPOPTOSIRACELLEPF
RAALLAFAASGDIPAASLASRRADSFLAERENLISVIRTERPOPTODSIRACELLEPF
RAALLAFAASGDIPAASRASRADSFLAGENCEPRENTALRENTERPOTYRFYGE
ROCKEGIKVAREMIQLGFGLSVASMEININGLGROGEPREAAEVERIEFLUPGVVPEG
FOLLDLVESLCRYNVERAYEVVELILERNWYSCLGVPAGVTVLECLAKEGROADGFTYSINVG
FORGIRREGRAVLDEMLDAGYVPNIATYNRLLDGLHMGRRAQIAQACSHIRNAAN"
/GROM="PO456605.9"
/gene="P0456605.9"
/gene="P0456605.9"
/gene="P0456605.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157361
    complement(join(40277. .40417,40717. .40773,40875. .41073,
41173. .41300,41399. .41504,41677. .41756,42145. .42242,
42234. .42437,42523. .42663,42757. .42841,43717. .44055))
/gene="pod456E05.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 TCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCCCACCACCACC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 ACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATCAACACCTGCACCGGCGAGGTCCACGAGGGAGGGGAGAGCTTCCTCGCCAGGGCTA 372
                                                                          /note-"contains ESTs AU101665(R2414), D24709(R2594) similar to Arabidopsis thaliana chromosome 5, At5914420 unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGAGCCGCCCGGCGGCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 173699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein
similar to salt-inducible protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 174.6; DB Pred. No. 5.4e-17
                                                                                                                                                                                                                                                                                                                                                              51367. .52887
/gene="P0456E05.8"
51367. .52887
/gene="P0456E05.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ouery Match
Best Local Similarity 72.8'
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157300
                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
CDS
                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
```

a

ð

g

ö a ò g à q ò

ò

RESULT 2 AC091071

us-10-090-035-3\_1.rge

à

```
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL Submitted (21-Mark-2001) Takuji Sasaki, National Institute of Direct Submission

AL Submitted (21-Mark-2001) Takuji Sasaki, National Institute of Direct Submission

Submitted (21-Mark-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Race Genome Research Program; Rannondal 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

CE-mallitsasakifenias affic. 100-11, URL:http://rgp.dna.affic.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7446)

On Oct 17, 2001 this Sequence Varsion replaced gi:1343001.

Genes Ware predicted from the integrated results of the following: GRNSCANI.0, BLASTNZ.0 as well as SplicePredictor Genes Ware Protein Actabase, nr Replaced Tesults of the following: GRNSCANI.0, BLASTNZ.0 as well as SplicePredictor (Cotober 1998 Version. The genomic Sequence Was Searched against NoTEI NonRedundant Protein database, nr the CDNA Sequence database at (ftp://ncbi.nlm.nih.gov/blast/db) and the CDNA Sequence using BLASTN 2.0 with the corresponding DDNJ accession no. and KBC clone in A gene with identity or significant homology to any protein but with EST homology (covering significant homology to any protein but with a gene prediction protein almost the entire length of partial sequence) is classified as any hypothetical' protein.

The orientation of the sequence is from SP6 to 77 of the PAC clone. The orientation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.

Betailed information on overlap and assembly quality together with annotation of this entry is available assembly quality together with annotation of this entry is available assembly quality together with annotation (page 1907) procession and page 1907 procession 1907 proce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(10813. 11841,11094. 11205,11289. 11432,11817. 11921, 12046. 12129,12315. 12430,12535. 12636,12715. 12828, 12916. 12972,13222. 13288,13356. 13409,13798. 13872, 13956. 13991,14389. 14490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(10813. 10841,11094. .11205,11289. .11432,11817. .11921, 12046. .12129,12315. .12430,12535. .12636,12715. .12828, 12916. .12972,13222. .13288,13356. .13409,13798. .13872, 13956. .13991,14389. .14490)
                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0470Al2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryzayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0470A12.
                            /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0470A12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to Oryza sativa chromosome 5, P0574H01.5"
Published Only in Database (2001)
2 (bases 1 to 185095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar-"Nipponbare"
/db_xref="taxon:39947"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="P0470A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                       AP003436.2 GI:16197551
                                                                                                                                                                                RESULT 3
AP003436/c
                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
```

```
/produs_roll_id="bab90280.1"
/protein_id="bab90280.1"
/db_xref="G1:20161356"
/db_xref="G1:20161356"
/translation="MOSGTASPAGVAGDGAGGRGSVFRGDDAPKLLAALKEMKEGLD
L/Translation="MOSGTASPAGGIGYLEARHHILLSYCODIVYYLLERRAKGLSYBGHP
VYRGLVEIRLEFLER: TRP IDKKMEYQLQKLTNAADSGAAQEKEVDYCSEEVRSVTPTGG
PLGRGGVQQQHVVKETFQEIDRSGSGRHHHNNHGNDYLAWKETFVEEFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPASPPRSGREAGGEGGGGGRAPTINVTTRRSRKFWRDSSGGRRDHAASRHDSIHT
RERTINWNGAIKLRPTEVGTREFRCORFSLVYTPINAGILGGHUCVLARLLCLKOGNRN
RHAANHANRAELGVVVVLRHVPSPVAATMTRRKQCATGAALPRYEAHTIBYTIGE
GEBEHDVRQPPQGGIRTLRLHQOPRRYESTSCARIGGGSRAGEKHPTLNCQHQRHDRY
TDDQATVRWTTLKRKTTCMSVCHGRVQVWVQAPYQG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="magyysevdhcaeemnrpphaggenyavrresyeevdemaragr
ghhhgnggggghlgysgsrhgdahlgghreehlvhgdehrhghgggrqydscyfgyyg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEMSYHEDNAVOKMSSSFREEKYYEQQGGAGGDVQVCRNGGAAAGAVQKHTYEEKKEEE
VYEESNHGGGGGGCGCGYARQHGAGGGQKHATYQHEVIKGYESAGGGYAAARINGGAGA
GVKKOYSYEREEETDAGGYARINGGAVOKOYSSR RADBEEEDDAAAGGGYGRHHGAGG
AVKQHATYKQHQAIEGGYARYNGCGGGYNYNRHQAVAGGGGHHYGGATAAAYGHSANG
HFTAAAAGHHSSGGAHTOYHHQSYECEEEDSDEDDCEDDDDDESDDDDDGHCPPSRQC
SVHSYHQAAYQHEEKQHAGGRNHYHAVERHEEHGGGAQRYKYKYESSTQVGYAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Translation="MARRRVGGGTSEVGGGNGEARGRRRQRSGRREARGARRRLPRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(27239. .27499,30542. .30622,30720. .30899,
30998. .31165))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(27239. .27499,30542. .30622,30720. .30899,
                                                                                                                                                                                        DEDLSVQHENARATIKLVRKHGLETSOPGLEPDKGLTWQMTKRLGDOEVHKVTEERPG
WCTDPHLPPCAAFVETMATVFSRDAWRCVWHMIQNDLVHGWGLDFALRRCVEFAHEKI
GVVDSQWVIHQVIPSLGNQGTAENGRTPWEGVRARCRKEWGMFQKRLADAEKAYYLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BaB90277.1"
/db_xrefn="G1:20161353"
/translation="MAMARRGNGGYQYGAYSYGYGYSKPQVNYHSQSSESVTTVVTKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(19564. 19724,21382. .21688,22059. .22217,
22387. .22505,22923. .23035,23239. .23318))
/gene="P0470A12.3"
                                                                                                                          KGAEGLAPGIVVPETDLYLRRLWGEPSEDLTSOPRYLITFTVGYSOKANIDAAVKKFS
ENFTIMLFHYDGRINDWDEFEWSKRAIHVSVRRQTKWWYAKRFLHPDIVAPYDYIFIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .21688,22059. .22217,
/protein_id="BaB90276.1"
/db_xref="G1:20161352"
/tb_xralation="MSASSGLPRSNEGMRLLESAVIGYMLGYLFGISFPTVN
/translation="MSASSGLPRSSGLPRSNEGMRLLESAVIGYMLGYLFGISFPTVN
/TKLHFPSSIISYIEDFUSGIITYQTLLNHAWTSANSKKRNNSESNSDRIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(34470. .34734,34836. .34921,35025. .3511
35201. .35364,35440. .35601,35682. .35861,35978. .36414,
36513. .36568))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(19564..19724,21382..21688
22387..22505,22923..23035,23239...23318))
/gene="P0470A12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="P0470A12.5"
/note="contains EST AU070442(S15668)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="contains EST AU069076(C51993)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(23929. .24237)
/gene="P0470b12.4"
complement(23929. .24237)
/gene="P0470b12.4"
                                                                                                                                                                                                                                                                                                                                                                   /gene="P0470A12.2"
complement(15118. .16344)
/gene="P0470A12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB90279.1"
/db_xref="GI:20161355"
                                                                                                                                                                                                                                                                                                                                       complement(15118. .16344)
/qene="P0470A12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB90278.1"
/db_xref="G1:20161354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30998. .31165))
/gene="P0470A12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCVRGNAKPCFRIMA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
```

```
ACUSTUBER. I GILL3487944

S HTG; HTGS_PHASEZ.

Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group).

Spermatophyta; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Eukaryota; Viridiplantes; Oryza.

I (bases 1 to 18481)

RS Lee_J.-S., Hahn,J.-H., Yoon,U.-H., Lee,M.-C., Yun,D.-W., Kim,H.-I.

Oryza sativa PAC P0470A12 genomic sequence

L (bases 1 to 185481)

AL Unpullshed

I (bases 1 to 185481)

RS Hahn,J.-H., Eun,M.Y. and Kim,H.-I.

Direct Submission

AL Submitted (29 MAR-2001) Rice Genome Sequencing Project; National Institute of Agricultural Science and Technology(RIAST), RDA, 249

Secdun-dong, Suwon 441-707, Korea (E-mall:)hhahn@rda.go.kr,

Tel:82-31-290-0309, Fax:82-31-290-0308)

** NOTE: This sat working draft sequence. It currently consists of Agricultural Science and 10 the pieces

** Are represented as runs of N. The order of the pieces

** Tel:82-31-290-0309, Fax:82-31-290-0308)

** This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.

** This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.

** This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.

** This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.

** This sequence will be replaced

** by the finished sequence as soon for it is available and

** the accession number will be preserved.

** This sequence will be replaced

** the accession number will be preserved.

** This sequence will be replaced

** the accession number will be replaced

** the accession number will be replaced

** the accession number will be replaced

** the apple of unknown length

** 138784 138883: gap of unknown length

                                                27414 TCGTCAAGGAGGTTCCAGGAGATCGACA-------GGTCCGGCTCCGGCGCCACC 27364
                                                                                                                                                Oryza sativa (japonica cultivar-group) chromosome 1 clone P0470A12, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces. AC091088 AC091088 I GI:13487944
                                                                                                                                 312
                                                                                                                                                                                                                ä
                                                                                                                  253 ACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG
                      193 TCGTCAAGGAGAAGTTCGAGGAGGTCGACGGTCTCACGCGCGGGGGCGCCAACCACCAC
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                           373 ACTGAGCCGCCGGCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 185481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.4%; Score 174.6; DB 2; 72.8%; Pred. No. 5.3e-17; Live 0; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41522 c 41493 g 50653 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref-"taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /variety="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lone-"P0470A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.4
Best Local Similarity 72.8
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51439 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
AC091088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                  g
                                                                                                                  õ
                                                                                                                                                          셤
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                      /COCOL-SCALCE-BABBORRED 1"
//DOCKETID.1d="BABBORRED 1"
//DOCKETID.1d="BABBORRED 1"
//DOCKETID.1d="BABBORRED SATLLIN TAAVAVAPLASAVRPVSDAHRSAAAEL
FAASPDGSFGDLETTYEAVRTFQILGVEKOKGLIGKACKFAAKELASSSSSPAKDLEH
FAARISCVLKCSVDSGVYDDVATRIKAVIKDINSLIELTYSVGGLLS IKEGGHNVVLPD
ADNIFHAIKALSOSGGRWRYDTRIKAVIKDINSLIELTYSVSVGGLLS IKEGGHNVVLPD
RADIVKLETDIKSYDGGTFYPDEKHVDAAEKGAILELYSSVGGLSSTRANSGKLNI
RGEKILGLARFFLGIGLGSAKDCHONJEVVPLLSLPSKVFSLTSSDQLKVSTTTV
FGSAAPPLRVNLVQVLGSDSKVITTFFRELOFDLDNNVYYLDIAPLKIDVGKYSLTVF
ISLOGOBETITYATGGTNYDRIFVTGLIKVDKAETGISDNDAGTVESVQRIDLGKDTS
VSLSANHLORLRLSFQLSTPLGKTFKPHQVPLKKHDDESKVBHLKTVPGSRARGFKIVL
PFSKFGPKKEISHIFRSPBKRPPKELSFAFTGLILDIJVGFLIGLMRLGVNIKNFPSL
PAFAAFASLFHAGIGAVLLLYVLFWIKLDLEFTLKTLSFLGVFLUKNFFSL
PAFAAFASLFHAGIGAVLLLYVLFWIKLDLFTLKTLSFLGVFLUKNFFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(34470. .34734,34836. .34921,35025. .35117,
5201. .33364,35440. .35601,35682. .35861,35978. .36414,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(47978. .48061,48179. .48239,48314. .48378,48478. .48759,48837. .48911,49020. .49094,49242. .49289,552. .49625.49763. .49964,50111. .50213,50317. .50378,50507. .50561,50738. .50841,50926. .51048,51175. .51219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement join 47978. .48061,48179. .48239,48314. .48378,48478. .48759,48837. .48911,49020. .49094,49242. .4928. 49552. .49625,49763. .49964,50111. .50213,50317. .50378,50507. .50561,50738. .50841,50926. .51048,51175. .51219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36513. .36568))
/gene="P0470A12.6"
/note="contains ESTs AU058030(C61369),AU088621(C61369)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 185095;
                                                                                                                       /codon_start=1
/product="putative RNA helicase"
/protein_id="BAB90381.1"
/db_xref="GI:20161357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%; Score 174.6; DB 8 72.8%; Pred. No. 5.3e-17; ive 0; Mismatches 84
     complement(join(34470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local S
Matches 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
```

```
PAT 16-MAY-2001
                                                                                                                                  AAGAGGACATCAACATGCACCGGCGAGGTCCACGAGGCGCAGGGAGAGCTTCCTCGCCA 366
                                                                                                                                                 GGGCTAACTGAGCCGCCCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCCT 426
                                                                                                                                                                                                             344 GGGCTGACTGAGCAGCTTCGTGCTGCTGCACGTTTCGTATGTAACCTGTGTAAGG 403
                                                                                                                                                                                                                                        427 TATGTATGTCTGTGGTTGACTGGTTGT-----TCAGGGTCATCGTACTTGGCTATCGTAC 481
                                                                                                                                                                                                                                                      254 -----CCACCAIGGICACCACGGCGGCCACGGCIICGIGGIGGGGGGAGACCAGGGICG 306
106 CGATGCCCAAACCGGGCTTCGGCCGCCACGGCGGCGGCGTCCAGCAGTTCGTCGTCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 CGGTCTCACGCGCCGGCGCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACG
                                                                                                                                                                                                                                                                                            GTGCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTG----AATAAA
                                                                                                                                                                                                                                                                                                          226 GCCACCGCGGCAAACCAAGGCCACGCGCACTTCCAGGCGCGCGAACAAGTTG
                                        199 AGGAGAAGTICGAGGAGGICGACACGGICICACGCGCCGGCGCCCAACCACCACCA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 390)
Gold, L., Tuerk, C., Pribnow, D. and Smith, J. Drew.
Systematic polypeptide evolution by reverse translation
Patent: US 6194550-A 7 27-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                 538 ACTICITCGTAATACTAAAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62.6; DB 6;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCGCAGGGAGGCTTCCTCGCCAGGGCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ė
                                                                                                                                                                                                                                                                                                                                                                                                                                             390 bp
s 6194550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
126 c 133 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7 from patent US AR135147 GI:14124052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%;
52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.99
Best Local Similarity 52.09
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AR135147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343
                                                                                                                                                                                                                                                                                                    482
                                                                                                                                         307
                                                                                                                                                                   286
                                                                                                                                                                                              367
                                                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                   AR135147
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                   g
                                                                                                                                                                                              ò
                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                         õ
                                                            g
                                                                                                               a
                                                                                                                                         δ
                             δ
                                                                                        ŏ
           156932 ACTICAACACCGCAGCGCGAGTTCCGCGAGCGCAAGCAGAGAGTTCCTGCTCAAGTCG 156991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative glycine-rich protein"
/protein_id="CaB61838.1"
/db_xref="G1:6478144"
//tb_xref="G1:6478144"
//translation="MAHFKEWUDYEEVTSMAKPGFGRHGGGGVQOFVVKETFEEVEQV
/translation="MAHFKEWUDYEEVTSMAKPGFGRHGGRPCQG"
/ 113 c 154 g 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                      SST242802 562 bp mRNA linear PLN 27-NOV-1999 Sporobolus stapfianus mRNA for putative glycine-rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312
                                                                                                                    252
                                                                                                                                                                                                                        ACATCAACACCTGCACCGGGGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGCTA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 562)
Neale, A.D., Blomstedt, C.K., Bronson, P., Le, T.N., Guthridge, K.,
Neale, A.D., Gaff, D.F. and Hamill, J.D.
The isolation of lowly-transcribed genes which are induced during dessication of the resurrection grass Sporobolus stapfianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (27-MAY-1999) Neale A.D., Biological Sciences, Monash
University, Wellington Rd Clayton, Victoria, 3168, AUSTRALIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGTCAAGGAGAAGTTCGAGGAGGTCGACGGTCTCACGCGCGGGGGCGCAACCACCACC
                                                                                                                                                                      ACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                              TGAGGTCGGTGGCCC---CGGCCGGCTTCGGCCGCCACGGCGGCGCGTCCAGCACGACG
                                                                              373 ACTGAGCCGCCGGCGGCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sporobolus stapfianus.
Sporobolus stapfianus.
Sporobolus stapfianus
Sporobolus stapfianus
Sporobolus stapfianus
Sporobolus yiridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae,
clade; Chloridoideae; Eragrostideae; Sporobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sporobolus stapfianus"
/db_xref="taxon:56623"
/clone="SDG137c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 143.8; DE
Pred. No. 4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.1%;
nilarity 62.1%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                AJ242802.1 GI:6478143
                                                                                                                                                                                                                                                                                                                                                                                                                            glycine-rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 562)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases
Neale, A.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mac
Local Si.
321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                             253
                                                                                                                                                                                                                                 313
                                                                     136
                                                                                                                           193
                                                                                                                                                  156821
                                                                                                                                                                                                                                                                                                                                                  RESULT 5
SST242802
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     · Ş
                                                                                                                                                  g
                                                                                                                                                                            ò
                                                                                                                                                                                                     임
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                            g
                                                                                                                           ð
                                           g
                                                                       ò
                                                                                               g
                    ð
```

537

ö

162 168 222 228 282 288

```
/translation="McPSOTGRSPADTGTDPLGGBYLRTREVLPSRPATFLRORLI
/translation="McPSOTGRSPADTGTDPLGGBYLRTREVLPSRPATFLRORLI
/translation="McPSOTGRSPADTGTDPLGGBYLRTREVLPSRPATFLRORLI
/HUNGALRSPLTVVNGAAGAGKTLLTADWAAGLRVPTAWLTVETGDHPPGVFWAYVFE
SLRVGGRAGDTPGRAPDSGVGGRLLASLAAABLNALDSPVVLVLDGBYDRWTRPEIAE
GLOLPEYLHHAGGGLRLVLYRTFEPLLPLHTRYRASGELLEVRGSELSFTTEEAGALLRLH
KGRYGOEGDULLLKTRVSVLDRFCPDLADATTGRTDAGLLLAGLHRENAFIERLESVADFLLAGV
LKGRYGOEGDULLLALTWSVLDRFCPDLADATTGRTDAGLLLAGLHRENAFIERLESVADFLAGOLFAGNER
LHPLFREILRAHLRERLFGVEPELHLRAARNLRRSGFLPETLARBAAGGGAGLAGR
VDDLALGGLEFTGLRSDAALGEARLERTRARAGAGGETTVLLRYSESMGHLALLDYL
RNHLSDAGNSPGLAAARLSGALLEALAARLTGCPSRAEGAAATAEELRGELPDHLLDE
HPELSALLMTHVGSARLWEGREDDAAAKTRYAGAGGGTTYVLRYSESMGHLALLDYL
TGWLGRAERRALAAVSEABERGLERPRPGAGLGRLYLAAVANDRGELGRARVLLDETAR
LCHREHDPVPTAGRALAVSEABERGLERPRPGAGLGRLYLAAVANDRGELGRARVLLDETAR
LCHREHDPVPTAGRALAVSEABERGLERPRAAGIOVAAGRPRAAALLGAVRAGGRAGPA
VSGAALVRARLAGSGGDYVAACRLVARALLDARREHLRRRPFLAGAGDMIEPLLATAPL
TWSINYTHLKSKYRKLAVNRRGDAVRRARDLGLL
TWSINYTHLKSKYRKLAVNRRGDAVRRARDLGLL
TOMMATTER TATAPL
TOMMATTER TOMMATTER TOMMATTER TATAPL
TOMMATTER TATAPL
TOMMATTER TATAPL
TOMMA
                                                                                                                                                                                                                                                                                                                                                                     Complement(551. .3229)
/gene="SC3A7.02c"
/gene="SC3A7.02c"
/gene="SC3A7.02c, probable transcrittonal regulator, len:
892 as; similar to e.g. MALT_ECOLI MalT regulatory protein
(901 as), fasta scores; opt: 540 z-score: 495.9 E():
2.3e-20, 26.2% identity in 936 as overlap. Contains
PSO017 ATP /GTP-binding site motif A (P-loop).
helix-turn-helix motif from as 848 to 686 (Score 1229,
43.37 SD) and Pfam match to entry PF00196 GerE, Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSAATGSRCRPVRGRRPPSGARRSASRWVRRRPPCQSBCWAMTHRPQGRQPSGSSPSD
GLPRTAHTSRCCPPACAQSRGRTRWKRPACSRRGWPVGDPEDPANSGLEPNPPVPRS
STLSCACPASRKRSPEWARAEIAFLENFERAGLEALPVRWPGRLPGAILVPAAGRRLPR
FPGSRQILRPTTVARRSPPGGGVTWRCWSACSGVSVILSPVGAKVGALRTLGPDVPFI
HGLAVKTRLAVSKRRFRPEYADGPGSWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3235, .4149)
/gene="SC3A7.03c"
/note="SC3A7.03c, questionable ORF, len: 304 aa; this ORF is not predicted as coding by positional base preference"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MPPAEPVRIRVRRPRRYFFGTCPKASWTAVMWSDAVFEPALPGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 50.40, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SC3A7.02c" /Gene="SC3A7.02c" /Gene="SC3A7.02c" /Gene="PS00017 Arp/GTP-binding site motif A (P-loop)" /Gote="possible RBS upstream of SC3A7.02c" /Gene="SC3A7.02c" /Gene="SC3A7.03c" /Gene="SCGA7.03c" /Gote="SCGA7.03c"
                                                                                                              2. .103
/note="overlap with_cosmid 3A7 from 1 to 102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/product="putative transcriptional regulator"
/protein_id="cAA20065.1"
/db_xref="GI:336740"
/db_xref="SPTREMBL:086603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(211, .217)
/note="possible RBS upstream of SC3A7.01c"
complement(551, .3229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="possible RBS upstream of SC3A7.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"SPTREMBL:086604"
                                           /db_xref-"taxon:100226"
/clone-"cosmid 3A7"
                                                                                                                                                                                                                                                           /gene="SC3A7.02c"
/note="sc3A7.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(554. .745)
/gene="SC3A7.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                    RBS
                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Surrand).

Surrand).

Surrand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length Usually the highest socring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene specially developed Hidden Markov Model (Krogh et al., Nucleic of Bibb et al., Gene 30:157-66(1984) and the Frameplot program http://www.nih.go.jp/
Jun/Cqi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation ribosome binding site sequence (optimally 5-13bp before the most initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most initiation codon. If this cannot be identified we choose the most sequenced clone. It may be shorter because we arrange for a sequenced clone. It may be shorter because we arrange for a small overlap between neighbouring submissions. Cosmid 3A7 lies between 10H5 and 4A2 on the Asel-B genomic restriction fragment.
                                                                                                                                                                                                            BCT 12-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 35100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On May 9, 2002 this sequence version replaced g1:3367738.

Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC.

Betails of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC787.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                              3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase; ABC transporter; beta-galactosidase; exonuclease; IS3 type transposase; secreted amidase; secreted chitinase; two-component sensor/regulator. Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redenbach, M., Kleser, Kinashi, Denapaite, D., Elchner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 35100)
011ver. K. and Harris,D.
Unpublished
3 (bases 1 to 35100)
1 (bases 1 to 35100)
Parkhill,J. Barrell,B.G. and Rajandream,M.A.
Direct Submission
Submitted (30-JUL-1998) Streptomyces coelicolor sequencing projesner Centre, Relicome Trust Genome Campus, Hinxton, Cambridge CBIO 15A E-mail: barrell@sanger ac.uk Cosmids supplied by Professoid A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Streptomyces coelicolor A3(2)"
/strain-"A3(2)"
                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                            Streptomyces coelicolor cosmid 3A7. AL031155 AL645882
349 ACGACGACGACGACGCCATGGTT 377
                                                                                                                                                                                                    35100 bp
                                                                                                                                                                                                                                                                                                      AL031155.2 GI:20520754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
```

```
283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 13365 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. 150676
Organism="Oryza sativa"
/db_xref="taxon:4530"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig c
gap of u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
120987: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147035:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150676:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice Genomic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71713:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86874:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102999:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107622:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83673:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103000
                                                                                                                                                                                                                                                                                                                                                                             10069 TCG 10071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71714
                                                                                                                                                                                                                                                                                                                         403 CCG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC107225/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                              g
                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YOTLLEGOPDTSTRYUGGESTAYTHAYDKLYRPTTELLEDSDELVAAGAPAT
LOFEANYNLDGTCRAPRNPSADSPSRPSATUAPTTELLEDSDELVAAGAPAT
LOFEANYNLDGTCRAPRNPSADSPSRPSATUAPTTELTLEDSDELVAAGAPAT
LOFEANYNLDGTCRAPRNPSADSPSRPSATUAPTTELGLFODGHRLSCGGGGRS"
RRTTOTATAAAGATTTTVRYREEGOPPALTELGLFODGHRLSCGGGGRS"
complement(5244. 6176)
/gene="SCG3A7.05c"
/note="SCG3A7.05c"
/note="SCG3A7.05c"
/note="SCG3A7.05c"
/note="SCGAA7.05c"
/note="S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9829 écGAGCIGCCGACIGCGATCIGCIGCGCICGCAGGCGCIGCGGAGGGGGTCAGGC 9888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGSIRNTAPTGSARVTAELKOSCRRVNHKRGERVARKFHTVGLHIKKKVRTTIPEPS
ATPVPDILQRGIAAQMENTKRVGDITCLPVGRGERVARKFHTVGLHIKKKVRTTIPEPS
ATPVPDILQRGIAAQMENTKRVGDITCLPVGRGGFLYLATVLDLCSKRLTGWSIADHM
PTSLYTDVLRAAARARGGDGLRGAISHSGNGAQYVSKEFAQVCSELGYTRSRGAVGTS
NGAAAESINTTMKRGTLGGRKRWNGASEARLAVFRWATRYNTRRTPASARSARSPT
NGOQLRWPPPHDNRCPRSQGRPSSVRAGGWPSFS"

/gene="SC3A7.06c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MTPSASSGCAGYSRSRGPASTGGWPARTRGPAGRGRTPSSPNAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6207. .6494)
/gene="SC3A7.06c"
/note="SC3A7.06c, probable transposase, len: 95 aa;
/note="SC3A7.06c, probable transposase, len: 95 aa;
imilar to transposase ORF: s from many IS3 type insertion
sequences e.g. Corynebacterium glutamicum TR:046069
(EMBL:X69104) IS3 related insertion element ORF1 (97 aa),
fasts accores; opt: 244 z-score: 381.2 E/; 4.3a-14, 46.28
identity in 93 aa overlap. Contains probable coiled-coil
from 55 to 93 and helix-turn-helix motif from aa 25-46
(Score 1789, +5.28 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .223 CGGTCTCACGCGCCGCGCGCCCACCACCACCACCATGGTCACCACGGCGGCCACGGCT 282
                                                                                                                                                                                                                                                                                                                                                                                      /translation-*mlfysigmyiteaihsrelqypasawtpaaeydgeirdaawave
1Tgdyqryqrlahsqgdgparglrpepgrrqqrrggaersqqrsrsrarpaepsstpaa
                                                                                                                                                                                                                                                                                                                                                                                                                                              GIPRVRGHQPRRPPVRRHNGHQPVHLHNLPVHTGRPADPSHRPRRLPVDIRVRPVRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQRGRPRQGPDPPVLRPTGPTHPDHRLPRHITPYDALNRITGTWAGSKTEANQLTAFT
                                                                                                                                                                   /note="SC3A7.04, questionable ORF, len: 384 aa; this ORF
is not predicted as coding by positional base preference"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 GCCGCCACGCCGCCGCCGTCCAGCACCTCGTCAAGGAGAAGTTCGAGGAGGTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 35100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                          /product="hypothetical protein SC3A7.04"
/protein_id="CaA20067.1"
/db_xref="GI:3367742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61.4; DB 1;
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="putative transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative transposase"
/protein_id="CAA20068.1"
/db_xref="GI:3367743"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"SPTREMBL:086606"
                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:086605"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'transl_table=11
                                                                                                                     4186. .5340
/gene="SC3A7.04"
                                                                                                                                                                                                                                                           L_table=11
                                                                'gene="SC3A7.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                          note="SC06336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
nilarity 50.2%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "codon_start=
                                                                                                                                                                                                                                                                    /transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 152; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
Oryza sativa chromosome 3 clone OsJNBa0026H19, *** SEQUENCING IN PROGRESS ***, 10 ordered pleces. AC107225 AC107225 AC107225 AC107225 AC107225 AC107225 AC107225 AC107225 AC10725 AC10
                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

I (basea: Oryzeae; Oryza.
I (basea: Lto 150676)
Wing, R.A., Yu,Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T., Saski, C., Henry, D., Oates, R. and Simmons, J.
402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E 2 (bases I to 150676)

Saski,C., Henry,D., Oates,R. and Simmons,J.
Saski,C., Henry,D., Oates,R. and Simmons,J.
Direct Submissaion
Direct (17-JAN-2002) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
* NOTE: This is a "working draft, sequence. It currently
* consists of 10 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* are represented to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
      343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGGCGGCGGCATCCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen, M., Kim, H.-R., Rambo, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          provided by the summittee.

This sequence will be replaced by the finished sequence as soon as it is available and the finished sequence as soon as it is available and the accession number will be preserved.

I 11363: contig of 11363 bp in length gap of unknown length gap of unknown length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of unknown length
contig of 31816 bp in length
gap of unknown length
contig of 11960 bp in length
gap of unknown length
gap of unknown length
contig of 3201 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 16125 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26048 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown length contig of 3641 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 4623 bp in length
```

8 à

à a õ a ð g ð g

```
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Jun/Cgl-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Here possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream initiation codon.

IMPORTANT: This sequence (optimally 5-13bp before the upstream initiation codon. If this cannot be identified we choose the most language sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid StBAC28G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2. .94
/note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGIGEPTGGILLAHFWGSVLLYNVPPLAGGLVAVILVYPETRGTAGRRVDDAGLLLS
TGAVVPLVYATIEAGRSGGYTRPAVAAAGLAGLGLLVFLWHERRTPEPSLELGFFRM
KAFSTAVAAVGAIEAGRSGGYTRPAVAAGLAGLGLLIVFLWHERRTPEPSLELGFFRM
VLYRSIGPRAVAAAGHLFFSAFYLOSVRGTYPLOAGCGTVALANANVCGPLST
VLYRSIGPRAVCAAGHLAYTAGLGYTCOYTFVTOHAPVMLILLVLFAGAGVACWHTAAN
SIMNAIPREKAGVASAMNNTVROLGGALGYAVLGSLMGAAYRRGIEDELAVLPPSARH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:053903"
/translation="MTANPGRPGGPADOGHPRRWAILGVLVLSLVGIILDNTVLNVTL
RTLTDPEQGLGASHSQVEWVLSAYTLAFAATLFTWGVLGDRLGRRRVLLLGLGLFGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLAGAYAĞSPEQLIAARACMGVSGAAVLPSTLATIAAVFPLRERPKALGIWAASVGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OAGESLDATILAATRLGESGLVGPARQAFLDAMHLAAGAAAAVALVGALAVLRWLPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // S02. .2103
/gene="SCBAC28G1.02"
/note="SCBAC28G1.02, actVA1, probable integral membrane
protein, len: 533 aa; identical to previoualy sequenced
TR:053903 (BMBL:X58833) Streptomyces coelicolor 6 ActVA
region genes of the actinorhodin biosynthetic gene
cluster, ActVA1, 533 aa. Contains possible hydrophobic
membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="previously sequenced DNA fragment. EMBL:X58833.1
S.coelicolor 6 actVA region genes of the actinorhodin
biosynthetic gene cluster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .73
note="PS01162 Quinone oxidoreductase / zeta-crystallin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2. :518
Chote*Previously sequenced DNA fragment. EMBL:X62373
S.coelicolor genes for hydroxyacyl-CoA dehydrogenase*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
/product="integral membrane protein"
/protein_id="CAG44189_1"
/db_xref="GI:14717083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTTPTPPAGAVPGREHSDHLKVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCBAC28G1.02"
/note="SCO5076; actVA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone-"cosmid BAC28G1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2093. .2097
/gene="SCBAC28G1.02"
2105. .2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCBAC20F6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84. .5883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RBS
                                                                                                                                                                                                                                                                55347 GGAGGTGTGTACCGCAAGGCGCAGATGGTCGACCCGGACGCCAACAAGGCCTGCAACCT 55288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55168
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL593842.2 GI:20520872
actII-1; actII-2; actII-3; actII-4; actIII; actIORF1; actIORF2;
actIORF3; actVA; actVA2; actVA4; actVA5; actVA6;
actIVB; actIV; actIV; protein; gntR-family regulatory protein;
integral membrane protein; LySR-family transcriptional regulatory protein; methyltransferase; mini-circle protein; mutT-like protein;
streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
                                                                                                                                                                                                            229
                                                                                                                                                                                                                                                                                                                                                                                                                                                   289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCT 12-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 GCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGGGCAG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-JUL.2001) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: Barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinobacteridae; Actinobacteridae; Actinobacteridae; Actinobacteridae; Streptomycetales; Streptomycescaes; Streptomyces. 1 (Dases 1 to 29080)
Redenbach,M., Kleser,H.M., Denapaite,D., Eichner,A., Cullum,J., Ridashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are
numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 CGGCGGCGGCGTCCAGCAGCACGTCGTCAAGGAGGATCGAGGAGGTCGACGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                            230 ACGCGCCGGCCCAACCACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 29080)
Cerdeno,A.M., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
                                                                                                                    Length 150676;
                                                                                                                                                                          ö
                                    4 others
                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55107 CAACAGCGGCGGCAGCAGCAGCACGACGACGACGCG 55069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 GGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGGGG 388
                                                                                             Ouery Match 10.7%; Score 61.4; DB 2; Best Local Similarity 51.3%; Pred. No. 2.8; Matches 143; Conservative 0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor cosmid BAC28G1. ALS98042 AL645882
/clone="OSJNBa0026H19"
35084 c 34425 g 40132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 29080)
Warren, T. and Harris, D.
Unpublished
                         41031 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCBAC28G1/c
                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
```

COCUS

ö

CDS

```
SCC30
Streptomyces coelicolor cosmid C30.
AL352972. AL645882
AL552972. G1:20520831
ACTIONICCALES. Streptomycineae; Streptomycescee; Streptomycescentic Actinobacteridae; Actinobacterida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "(bases 1 to 18420) "Technology A. M., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission Submission Streptomyces coelicolor sequencing project, Submitted (14-APR-2000) Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 12-MAY-2002
(EMBL:X58833) Streptomyces coelicolor 6 ActVA region genes of the actinorhodin biosynthetic gene cluster, ActVA5, 381 as and similar to TR:09F013 (EMBL:AF128066) Streptomyces arenae hydrolase NorH, 405 as; fasta scores: opt: 1391 a. Score: 1231.5 bits: 290.3 E(): 3.9e-77; 56.522% identity in 368 as overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 CACGCGCCGGCGCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 TGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 ACGCCGCCGCCGCCACCACCACGTCCTCAAGGAGAAGTTCGAGGAGGTCCACACGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 29080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 10;
0; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                     /product="putative hydrolase"
/protein_id="CAC44193.1"
/db_xref="GI:14717087"
/db_xref="SPTREMBL:053907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58.2;
Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seeger, K.J. and Harris, D. Unpublished
                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%;
nilarity 49.5%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 18420)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
150; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17686 GCG 17684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 GTG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97000351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8843436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
SCC30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="conserved hypothetical protein"
/protein_id="cAo44192.1"
/db_xref="G1:14717086"
/db_xref="SPTRABL:Q53906"
/translation="WPDENKFVLVCATGKQGGSAARYLLERGWTVRAFVRDFGAPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KELRELGASIHTGDLEDAGSVRAAMKGAYGYFSIQTPMTPAGVEGEERQGKICADAAR
DLGYQHYVHSSYGGAERPEGVNWRLSKLAIEQRIQENALRFTFLRPSYFMENLNHDMS
PLVWEDGVLTFRRGLGPANTLQMISGPDIGYFRADAFDDPDTFGGARIELAGDELTGE
QIAAAFGRHTGLPARFVSVPIPELHRTGFEWQAISYTWLNGIGYHADIPTLRARFPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTERMEL:093122"
//db_xref="SPTERMEL:093122"
//translation="MSTEIFHEEFAGGLVTEGPGAPWRLRPVDGLEAGDGIVRGGPDG
//translation="MSTEIFHEEFAGGLVTHLRWFTTGGTAGARAAFTAVPGE
ILVVRSAAHGCTRRAFFTERVEDDTFEDAHLRAGGLISVDLESGIIFDFFLTHSRLY
AVYERLALRPDAEFAFTYCVPVADRTPGTLHRLEVGYDVAAGTAHWTADGGEVLSVD
RIGFRALDARWLRRDNGGREEAVRPRGLSFGLGLFLERHFGGGVRLSVRLSVLTSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2582. .2586
./gene="SCBAC28G1.04"
/pene="SCBAC28G1.04"
/note="SCBAC28G1.04"
/gene="SCBAC28G1.04"
/gene="SCBAC28G1.04"
/note="SCBAC28G1.04"
/note="SCBAC28G1.
                                                                                                                                                                                                                                                                                                                                                                                                        /note="SCBAC28G1.03, actVA2, hypothetical protein, len:
131 aa; identical to previously sequenced TR:053904
(EMBL:X58833) Streptomyces coelicolor 6 ActVA region genes
of the actinorhodin biosynthetic gene cluster, ActVA2, 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SCBAC28G1.06"
/note="SCBAC28G1.06, actVA5, possible hydrolase, len: 381
aa; identical to previously sequenced TR:Q53907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCBAC28G1.05, actVA4, conserved hypothetical protein, len: 294 as; identical to previously sequenced TR:0259G6 (EMBL:X58833) Streptomyces coelloolor 6 ActVA region genes of the actinorhodin biosynthetic gene cluster, ActVA4, 294 as"
                                                                                                                                                                           protein, len:
TR:Q53904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="CAC44191.1"
/db_xref="GI:14/17050;";"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3465. .4349
/gene="SCBAC28G1.05"
/note="SCO5079; actVA4"
3465. .4349
/gene="SCBAC28G1.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCO5080; actVA5"
                                                     /note="SCO5077; actVA2"
2105. .2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4346. .5491
/qene="SCBAC28G1.06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="SCBAC28G1.05"
                                                                                                                  2105. .2500
/gene="SCBAC28G1.03"
                                                 'gene="SCBAC28G1.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTLDQWLARTGWTPRDPA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .3457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSRDS"
```

gene

RBS

CDS

CDS

gene

Sas

RBS

COMMENT

```
complement(1681.

complement(1681.

/gene="SCC30.02c"

/note="SCC30.02c, probable arac-family regulatory protein,

len: 278 aa; similar to SW:ARAc_SALY (EMBL:J01797)

len: 278 aa; similar to SW:ARAc_SALY (EMBL:J01797)

Salmonella typhimurium arabinose operon regulatory protein

Arac, 281 aa; fasta scores: opt: 232 z-score: 270.4 E():

1.3e-07; 26.7% identity in 270 as overlap and to various

Streptomyces coelicolor putative arac-family

transcriptional regulators, e.g. TR:O50480 (EMBL:AL031031)

S. coelicolor putative transcriptional regulator SC707.17

(SC4H8.01), 288 aa; fasta scores: opt: 638 z-score: 605.1

E(): 3.3e-28; 43.8% identity in 292 as overlap. Contains

Pfam match to entry PF00165 HHL Arac, Bacterial regulatory

helix-turn-helix proteins, arac family and possible

helix-turn-helix motif at residues 189. .210 (+3.81 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
/product="putative araC-family regulatory protein"
/product="putative araC-family regulatory protein"
/product="cf:7619749"
/db_xref="cf:7619749"
/db_xref="SPTREMBL:09L019"
/translation-"MAGAREQARMSRARIGRGEPLDLLTARFDRHVYAPHAHDEYTV
YVVGGLEVAYARGHHHSGPGSINVLEPGEWHTGGPAPPGYSYRALYAAPNLLTDG
TRTDTVLPHFREPVLDDPELAALRAHTDLLARCHSGRAPRITAGRRHSGTA
RAADDTVPGAGRAVARVRRIADBELAAPPSIAALAADLGLSRYQLLARFRITSTGMPP
AMLAQHRVARARGLLDAGLRPAEVAALVGFADQAHLTRWFRRVLGVTPAAAYRUSVGDR
                                                                                                                                                                                                                                                              /note-"Pfam match to entry PF00892 DUF6, Integral membrane protein, score 38.50, E-value 1.6e-07" complement(1681. 2517)
                                                                                                                         /note="Pfam match to entry PF00892 DUF6, Integral membrane protein, score 51.40, E-value 1.9e-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2628. 3389

Agene="SCC30.03"

Anote="SCC30.03"

Anote="SCC30.03"

N-terminal region similar to TR:CAB52842 (EMBL.AL109848)

Streptomyces coelicolor putative transcriptional regulator SCI51.18, 548 as, fasta scores; opt: 114 z score: 134.1

E(): 5, 30.68 dentity in 196 as overlap. Contains possible coiled-coil region at aprox residues 76. .93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:09L018"
/translation="MRIGELADTVGVTTRTVRHYHHQCLLPEPERLANGYRTYTLRHV
VVLARIRRITELGIGLAEVRDVLADDAGKDLAEVLEELDSDLARQEAAIRERRTRLRA
LLGTEGGVPPEGPVSPELAELFAGIGDVSGSPWALRDREMLVLLESTVAPEERAGLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMRGALGSPEAAARARRTYELLDELADAGADDPRVAEAARVLADCMPAELLPEEGFDL
DPGHGLLRALYADFAPQAEAVRRAME1AARGRRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SCC30.04, possible integral membrane protein, len: 204 aa; similar to TR:AAF12504 (EMBL:AE001863) Deinococcus radiodurans hypothetical 32.0 kD protein, 289 aa; fasta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF00165 HTH_AraC, Bacterial regulatory helix-turn-helix proteins, araC family, score 59.80, E-value 5.8e-14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein SCC30.03"
/protein_id="CAB88173.1"
/db_xref="G1:7619750"
                                                                                                                                                                                                   complement(1212, .1622)
/gene="SCC30,01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1699. .1956)
/gene="SCC30.02c"
                                                                                                                 /note="Pfam match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCC30.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCC30.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SCC30.04"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"SC02294"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-"SC02295"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SC02296"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rg.
                                              misc_feature
                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al. codons using a Acids Research, 22(22):4768-4778(1994)) and the Frameplot program http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid C30 overlaps cosmid C75 on the Asel-c genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement(681. 1661)

/gene="SCC30.01c"

/note="SCC30.01c"

326 as: similar to TR:BAA87714 (EMB:AB016260)

#### Agrobacterium tumefaciens TIORF89 protein, 306 as; fasta scores: opt: 396 a. score: 465.4 E(): 1.88-18; 28.78

identity in 286 as overlap. Contains 2x Pfam match to entry PF00892 DUF6, integral membrane protein and possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREME.jou."
/db_xref="SPTREME.jou."
/translation="WTARGWFLFSLMGVVWGVPYLMIKVAVDEVSESGVVFARCALGA
/translation="WTARGWFLFSLMGVVWGVPYLMIKVAVDEVSESGVVFARCALGA
/translation="WTARGWFLFGAERAVATIOTYOPHICGOBARELENEUTYVUGY
ATAPLIAARHIKDVPTLQLITPCLTLAAVYAPAAFLTRPATLPSGBALAALAGLGUV
CTAIAFVAFLELIKEVGPTRAGVITYVNPAVANAGALLDEELIGGIGVAFTLIAG
SVLATAAAGFGREARRYPWSTRQTSRAGGRVESLITGLFEERPGSTGGGGG"
                                                                                                                                                                                                                                                                                             Details of S. Coelicolor sequencing at the Sanger Centre are available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                   Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4, 7UH, UK ON May 9, 2002 this sequence version replaced gi:7619747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"probable ribonuclease P RNA, (rnpB) (positions taken from Streptomyces lividans EMBL:SLXLNB)" complement(681. .1661) /gene-"SC0210.01c" /note-"SC02293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative integral membrane protein"
/protein_id="CAB88171.1"
/db_xref="GI:7619748"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 18420

7. Organism-Streptomyces coelicolor A3(2)"

/strain-A3(2)"

/db_xref-"taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="cosmid C30"
complement(346. .771)
/gene="rnpB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(346. .771)
/gene="rnpB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
```

gene

FEATURES

gene CDS

```
/product="hypothetical protein"
/protein_id="CAB51134.1"
/protein_id="CAB51134.1"
/protein_id="CAB51134.1"
/d=xxef="G1:554192"
/translation="MARATDYLDAVGPRIRTIRRERGITIAHLSAATGVSESTLSRL
ESGORRATLELLIPLARIYDYPLDDIVGAPRTGDPRIHLKFVRRFGAVFYPLSRRFOG
FOAFKMITPSRRAPLEPFPGTHEGSEWLYVLSGRLRLLVGERDLTLSPGEAAEFDTSL
PHWLGSANGGAVELIVLFGLQGVRAHVHSG"
complement(2168. .3091)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /LTTAINSTANTON-WITDOWNEDVRY FATVAEELHFTRAAELLYVSOPALSKOIRALE
ROLGAELHRGPRGYLIFBAGTALLPHARRMIADWTEGAAAVEAARAARRDTLVVGMS
TSPGRGGLLPAIRSRETAAHPEAVLOLROMSWEDPTRALADGATADVAYVWLFLDBADR
TSPGRGGLLPAIRSRETAAHPEAVLOLROMSWEDPPTRALADGATADVAYVWLFLDBARR
ALDGPAARPPRVGAELSGTEETYEALVAGLGGTCLVATGNAPLITLGGVVTRPVRGLSF
SRYALARREEDGRALVRGYVEACRRVTDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative methyltransferase"
/product="putative methyltransferase"
/protein_id="CAB51133.1"
/db_xref="GI:5541919"
/db_xref="GI:55419"
/db_xref="GI:55419"
/db_xref="GI:55419"
/db_xref="GI:55419"
/db_xref="GI:55419"
/db_xref="GI:55419"
/db_xref="GI:55419"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MPTTPRTHRRDTPPPRRGGGRAETLRGFLDYLRTSIAGKVEDAP
EPOYRTAAVASGTNLLGLLNHLTHVBRAVFLGEEVRSWPATFRAASQDGVADVVARYR
EAVERANRVLDACTDLGAPLPRPRPGRPAPSVRWALTHWVEETGRHAGHADILRELID
                                                            Direct Submission
Submitted (01-MAR-1999) F. Malpartida, Centro Nacional de
Submitted (01-MAR-1999) F. Malpartida, Centro Nacional de
Biotecnologia, Microbiologia, Campus de la UAM 28049 Canto Blanco,
Madrid, 28049, SPAIN
Location/Qualifiers
1. 4851
/organism="Streptomyces coelicolor A3(2)"
/strain="J501"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
/product="transcriptional regulator of LysR family"
/protein_id="CAB51135.1"
/db_xref="G1:5541921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="oxidoreductase of short-chain"
/protein_id="CAB51136.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
/product="putative mini-circle protein"
/protein_id="CAB51132.1"
/db_xref="GI:5541918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1215. .1221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(583. .1209)
/gene="ORF8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(583. .1209)
/gene="ORF8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(539. .543)
/note="ORF7"
                                                                                                                                                                                                                                                                                                                                complement(32..529)
/gene="ORF7"
                                                                                                                                                                                                                                                                                                                                                                                               complement(32. .529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3180. .3186
/note="ORF11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1344. .1916
/gene="ORF9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1344. .1916
/gene="ORF9"
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ORF7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="ORF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGR"
                                      Malpartida, F
                                                                                                                                                                                                                             source
                                      AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCO18817 4851 bp DNA linear BCT 19-JUL-1999 Streptomyces coelicolor A3(2) transcriptional regulator and actinorhodin biosynthetic genes, strain J1501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6841 GCCCGGGTACTCGGCCACGTTGTTCGTCACGACGCCGAGGTACTCGGCGGCGTCCACCAC 6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="possible integral membrane protein"
/protein_d="CAB88174 1."
/brotein_d="CAB88174 1."
/db_xref="G1:7619751"
/db_xref="SPTEMBL:091017"
/db_xref="SPTEMBL:091017"
/translation="MRATCPARPYZILARHELRIMASIMINMARRTHDSAAGGAAFGY
ARGGGAMMEGLAFVCVVESVTMSVLLRDWPAAHHVVLVLDVYTVVWWYGLHAASVVRP
HVLDAAAGTLRVRAAHVDR.PLERTASVRREIRTTHTPADGELDLAVGSGTSVTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcriptional regulator.
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycineae; I (bases 1 to 4851).
Martinez-Costa,O.H., Martin-Triana,A.J., Martinez,E.,
Fernandez-Moreno,M.A. and Malpartida,F..
An additional regulatory gene for actinorhodin production in
Streptomyces lividans involves a LysR-type transcriptional
scores: opt: 178 z-score: 231.0 E(): 2e-05; 29.8% identity in 161 aa overlap. Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"SCC30.05, hypothetical protein, len: 260 aa; similar to SW:YHI3_CAMJE (EMBL:236940) Campylobacter jejuni hypothetical 28.7 kD protein in HipO 3'region, 246 as; fastas scores: opt: 245 z-score: 295.9 E(): 4.9e-09; 28.1% identity in 210 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 GAGGACATCAACACCTGCACGGCGAGGTCCACGAGCGCAGGGAGAGTTCCTCGCCAGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCGCCGCGGCGCGCGTCCAGCAG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 CACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y18817.1 G1:5541917
methyltransferase; mini-circle protein; oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 181 (14), 4353-4364 (1999)
99328982
10400594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57.8; DB 1;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7021 CACCGGACCGCCCTACAGCCCGGAGTC 7049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 GCTAACTGAGCCGCCGGCGGCGGCATC 397
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCC30.05"
/note="SC02297"
/note="SC02297"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4040. .4822
/gene="SCC30.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity 50.9
137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S:
Matches 137,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
SC018817/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                               RBS
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail-tsasakidalas-affrc-go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7469.

Tel:81-298-38-7441, Fax:81-298-38-7469.
Tel:81-2002 this sequence version replaced gi:16904696.
Genes were predicted from the integrated results of the following:
GRNSCANI.0, ELASTNI.0, BLASTNI.0 as well as Splicepredictor
(October 1998 version). The genomic sequence was searched against
NCBI NonRedundant Protein database, nr
(ftp://ncbi.nlm.nin.gov/blast/db) and the cDNA sequence database at
(REP. Protein homologies of the coding regions were searched against
(REP. Protein homologies of the coding regions were searched against
NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent
the identified CDNA sequences using BLASTN 2.0 with the
corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology lovel
such as same name, 'putative-' and '-11ke protein'. A gene without
slighticant homology to any protein name to indicate the homology covering
such as same name, 'putative-' and '-11ke protein'. A gene without
slighticant homology to any protein name to indicate the homology covering
unknow' 'protein. A gene predicted with a gene prediction program
is classified as a 'hypothetical' protein.
The orientation of the sequence is from Milysev to -21Mi3 of the BAC
Clone. This sequence of Bl147A04 clone has an overlap with P0431G06
(DDBJ: AP003683) clone at the position 141,300 to 142,730 of
end. The sequence of this clone ends at the position by 754 of
P0431G06. Detailed information on overlap and assembly quality
together with annotation of this entry is available at
theth://rgp.daa.affrc.go.jp/cenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cocolistal.c=naba6187.1"
/protein_id="BAB86187.1"
/db_xref="GI:19386809"
/translation="MIKYHKEKLKATRIVLERFLILLPVEAGOISVCSCMPASGLOHS
LFYNYSVOLYTSCTVLTPVATAARCAPARALA-
Complement(join(2478..2681,2738..2961,4410..4618,
4632..4750,4830..5006,5081..5155))
/gene="B1147A04.2"
complement(join(2478..2681,2738..2961,4410..4618,
4632..4750,4830..5006,5081..5155))
/gene="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="WCGRGIDPRIDPLAPGSPLVPVGSDRNPYVDLYGMTTKRRROTS
GTTYALCVSSAGRRRYMINAIIISSICVRTPCRAAARVFVLPGWGSSIIOSVVNCPAA
VOQNRCHSQAATYYASHLLHCCYACTAWQROPISIDRSGQAKPARALAVASHALAAS
ALIDROPSPRITAPAYVGGGYTLYSTHYASTANAPSPIEH
ADDQAPNGTDQDRTWHACSYPSRRKSMPGBNRMSSFAIDPLGIGDRSTOTTYRACOS
RSFSNVYAPFRGMSVPRKAHTVLAELAVKFQCGITRTLARHYVVLHRTYKDPFNAITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id-"Bab86189.1"
/db_xref="G1:19986811"
/db_xref="G1:19986811"
/tcanslation="mempicropavademenshriridolvvvararppishcaarti
TCPAACVSREVNLY FROKSCCLEYLDRERHLTYSCRGKTSIDRSIDOPTLFTTPSTHPP
GTAHATKRLDDLSHPIAAAVVKTYYVOMRRHIAHCVVTSCMOAAPRAMDRWSTLLRWA
LIVMSTLLTFCRRGFLSRLVSSPARRYNDDARRNCISTTRYNAAMPGFSTTSRAREAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8779)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="B1147A04.3"

Join (7327. .7477,8191. .8507,8585.

/gene="B1147A04.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7477,8191. .8507,8585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB86188.1"
/db_xref="GI:19386810"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1278. .1520
/gene="B1147A04.1"
1278. .1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1278. .1520
/gene="B1147A04.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="B1147A04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
     /translation="mnkvwlittgassgfgralaeaaladgdvvvgaarrpealdduva
Arddomalaedadaavrdvvarhgrvdvuvnagrthvgaleetgedelra
Ledvhvegpaaltravleprmerrsgalvdmsgragdomsfrebsaysgrafelemse
Gladbyrdgravivregsrrtgleragnagistadsgvyakvgetremiaagdgs
GDPARNAAVIRAALAAEHTPLRLPLGDDGVTAVLGHLDRVREEVETWEKQTRATAFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLSSLKAVNLLVMFLLELAVYTAVVLWGVAVGGTWPVEVALGVG
APVVWMAANALEGSPRARRFARGAGREVLEVLWFGAGAAALAASGRPWWAAALAGVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150053 bp DNA linear PLN 13-MAR-2002
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
AP003735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 CACGCGCCCGCCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 TGCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACCGGCGAGGTCCACGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:Bild/A04.

Oryza sativa (japonica cultivar-group)

Eukaryota: Vildiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Nagnollophyta; Liliopsida; Poales; Poaceae; hinartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Only in Database (2001)
2 (bases 1 to 150053)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
Submitted (13-JUN-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 ACGGCGGCGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:B1147A04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 1; Length 485
Pred. No. 20;
0; Mismatches 145; Indels.
                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="CAB51137.1"
/db_xref="GI:5541923"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     622 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.9%; Score 57;
49.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1893 д
                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                  /note="ORF12"
4203.
                                                                                                                                                                                                                     1203. .4544
/gene="ORF12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AP003735.4 GI:19386808
                                                                                                                                                                                                                                                                      4203. .4544
/gene="ORF12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNAVLRRLWKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1777 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.9
Best Local Similarity 49.8
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
AP003735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                             RBS
                                                                                                                                                                                                                                                                 cos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
54591 GAGGAGCTCCGCGGGCGTCATCGTCGCCATCCTCGGCGGCGACGGCGACGGCTGCAGCCTC 54650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group) chromosome 2 clone OJ1135_F06, *** SEQUENCING IN PROGRESS ***, in ordered pieces. AP004045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54530
                                                                                                                                                                                                                                                                             /translation="MSSGGGGGSLGAGLLYHKFVSFALEETRLRTTLTPHPSQEKFK
SIKPNDDNTVFNALSFSAPKIRLLRSLTIEKKNSYQVLDFAAFSBEEYDLPIFCANVF
SIKPNDDNTVFNALDSFSAPKIRLLRSLTIEKKNSYQVLDFAAFSBEEYDLPIFCANVF
THAQSTVYDDNHPYHKDYKRSTRSIMPLYHKYNEVWLELMDQAIKENNKAT
TARNQEEQHYLTMHAEKDLYMEFLFEGVNTLGTKSFLDYFPEYARDDGSVNKKRSMI
GKSFETRPWDANGETIGDAEAQ"

GCOMPLAMENT (62266 ..62823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /prodes.ac.id="Babb6193.1"
/protesin_id="Babb615"
/db_xref="G1:19386815"
/translation="MVKIKMPALFRRRSGSKSPPLPQADPASGGGSPAPTPEEMERV
FRKPANGDGRISRESIGALEFSEIGHATDDELARMAAEADADGDGFISLDEFAALNA
TASGDAAAVEEDLRHAFRVFDADGNGTISAAELARVLHGLGEKATVQQCRRMIEGVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGGTTCCTCGCCAGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
ISRSEASSFASASSESESSSDDALMARSTPRSVLPAEISRRELEAVLRRLGHGEPDDE
                                DDCRRNIGGVDADGGGTVGFQDFARMAMAATATATATATAGGFRSW

complement(join(58262.58450,58741.58845,59228.59321,

59432.59432.5956,59597.60076,60648.60767),

/gene="B1147Ad4.9"

complement(join(58262.58450,58741.58845,59228.59321,

59432.59556,59597.60076,60648.60767)),

/gene="B1147Ad4.9"

/note="hypothetical protein

similar to Arabidopsis thallana chromosome 3, F3124.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sat<u>i</u>va (japonica cultivar-group) (cultivar:Nipponbare) DNA.
clone:OJ1135_F06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 GAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGGCGGCGGCGCGTCCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 CACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 150053;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.9%; Score 56.8; DB 8; Length 1
Best Local Similarity 50.4%; Pred. No. 13;
Matches 139; Conservative 0; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 GCTAACTGAGCCGCCCGGCGGCCGGCATCCACGCCC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGDGLISFEEFKVMMAGGGSFAKIA
                                                                                                                                                                                                                                               /protein_id="BAB86192.1"
/db_xref="GI:19386814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AP004045.1 GI:15208413
HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
AP004045/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
protein_id="mass6191.1"
/db_xref="G1:19386813"
/translation="MKLSIQSFARKLSLPSPKRTWSSGGGSSKRDGGWSKNGSGVKRA
                                                                                                                                                                                                                                                                                                                                                                                                                 VSGYRNEYDEN LINEARDOVARPODMYDNRPOCKKIGS INAKYPDFKINNSKEALMIDTAR
KAVLEKLIDDLVFSSDFSAAKKYRPFGGDKGNGELMQDLVDNPGKWWDNRSDKLLFSVF
NRKGALFFRANLEQPESCAILLSLEMDGIDNPDVHLSTYCKEDDLCYYLLADGROCLIH
FADRCTILSFWGECSIGASTLIQRHRILCNIAYYSLDKFKELYRFYLATYMSKYWQLT
DGVFTNSYMINSLLIGISAAMDGYRLAFYMIELEMSEPMYGRVLNRGATYMSYSLRI
LSTAHVRRSTWWCMGAVASRHVQHRTPTSRTVARVRGACGWLELFVVSSSQCAVLIVL
                       PAAVEGEGEEERGPGWQREKLPAEIPRPSTIAFQPRVANAVRLVGTVGAPVQLORLPD
GRESAVSVLVQDRHADYPKFWIPIIFQDDLAQVAASHLQEKDHIYVSGQLTGDIPPTK
LMDGQANIQVLAQMLSFVGGKAVQADSMVDEEEGFWQIVEAEKKVETKKFIPKYPPRT
                                                                                                                                                                                                                                                                                                  /protein_id="BAB86190.1"
/db_xref="GI:19386812"
/translation="MRHLARLLNNRILLPASSSPAAAFSKRTYARRTKPAPPTADAAA
                                                                                                                                                                                                                                        /note="hypothetical protein
similar to Arabidopsis thaliana chromosome 4, At4g20010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54171. .54785
/gene="B1147A04.8"
54171. .54785
/gene="B147A04.8"
/note="contains_ESTS_AU057399(S21412),AU057400(S21412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(36287. .43479)
/gene="Bl147A04.7"
complement(36287. .43479)
/gene="Bl147A04.7"
/note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement(44492. .45414)
/gene="Bl147A04.6"
complement(44492. .45414)
/gene="Bl147A04.6"
/note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(32547. .34495)
gene="B1147A04.6"
/note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to Oryza sativa chromosome 1, P0492F05.19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to Oryza sativa chromosome 1, P0492F05.19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oseudogene
similar to Oryza sativa chromosome 1, P0684B02.19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(32547. .34495)
/gene="B1147A04.6"
complement(32547. .34495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pseudogene
similar to polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24705. .25674
/note="5' LTR"
25762. .31913
/gene="B1147A04.5"
25762. .31913
/gene="B1147A04.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="3' LTR"
54171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3' LTR"
.54785
                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVVAVPVASWSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /pseudo
45943. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /bsendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIR
                                              gene
                                                                                                                                               CDS
```

ö

```
38862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
AF263463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

**Matsumoto, T. and Yamamoto, K.

Submitted (15-MG-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai

**Agrobiological Resources, Rice Genome Research Program; Kannondai

**E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

Tel:81-298-38-7444, Fax:81-298-38-7468)

Tel:81-298-38-7444, Fax:81-298-38-7468)

Tel:81-298-38-7444, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by
Combining Monsanto and RGP-Japan Sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

** This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.

** Cocation/Quallifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38485 écGGCGTCCTCCTGGACCACGCCACGGGTGGTCATCGGCGAGACCGCCGTCGTCGCGG 38426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38365 GCCACCCAAGGTCGGCGACGGCGTCCATCGGCGCCGGCGCGACCATCCTCGGGAACG 38306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 GCGCCGCGCCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP004873

138289 bp DNA linear HTG 31-MAY-2002
Oryza sativa (japonica cultivar-group) chromosome 2 clone P0453G09,
*** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 GCGGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCAC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38305 TCAGGATCGGCGGCGCGCGAAGATCGGGGCCGGGTCGCTGGTGGTCGCTGGCGACGTGC 38249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0453G09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 AGAGCTICCICGCCAGGGCIAACIGAGCCGCCGGCGGCGGCAICCACGCCCGIIC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasak1,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0453G09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 102688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 9.8%; Score 56.2; DB 2; Length 19
Best Local Similarity 52.3%; Pred. No. 17;
Matches 124; Conservative 0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="OJ1135_F06"
22012 c 21866 g 27986 t
                                                               Published Only in Database (2001)
2 (bases 1 to 102688)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP004873.2 GI:21280398
HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AP004873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                            TITLE
JOURNAL
                                                             JOURNAL
                                                                                REFERENCE
                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14'
AP004873
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptonyces olivaceus Tcm B2 oxygenase (elmG), Tcm F1 monooxygenase (elmI), Tcm F2 cyclase (elmI), and ElmJ (elmJ) genes, AF263463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 GCGGCGGCGTCCAGCAGCACGTCGTCAAGGAGATTCGAGGAGGTCGACACGGTCTCAC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces olivaceus.
Streptomyces olivaceus.
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomychaee; Streptomycetacea; Streptomyces.

(bases 1 to 3164)
Rafanan, E. R. Jr., Le, L., Zhao, L., Decker, H. and Shen, B.
Cloning, sequencing, and heterologous expression of the elmGHIJ genes involved in the blosynthesis of the polyketide antibiotic elloramycin from Streptomyces olivaceus Tu2353
J. Nat. Prod. 64 (4), 444-449 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 AGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGGCGGCCGCATCCACGCCCGTTC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 GCGCCGGCGCCAACCACCACCACCATGGTCACCACGGCGGCGACGGCTTCGTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 GCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 138289;
                                                                                                                                                                                                                                                                                                                                                                                                                                        50 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56.2; DB 2; )
Pred. No. 16;
0; Mismatches 113;
                             Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                      28968 g 42315 t
olished Only in Database (2002) (bases 1 to 138289)
                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="P0453G09"
                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces olivaceus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:8118600
                                                                                                                                                                                                                                                                                                                                                                                                                                     28094 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF263463.1
```

2 (bases 1 to 3164)

```
/translation="mraqrpppvigyddyrpstrogggrtrallrptsagatggflgtl
Dlgpgerisbhyrptsdkylvavagsvvvevdgheftlgtdghllvtrgmrhrphnrt
EaparlygisplaaprpdlghvdfepvprpQdapptvggvr"
1236 c 1003 g 437 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Procein_id="AAP73052.1"
(db_xref='G1:8118603"
(translation='MYYRALMYLRMDPADAERVAAAFEDHDTTGLPEEIGLTRRTLFR
'HDLYRHLIEADDDVLPKILEARDDPRFRKVNEEVGRYLTPYASDWSRLTDSKAEVIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLGIPDIPLDVQLVQPWEMSHHVADSYRSGRVFLAGDAAHVHPPAGAFGANGGIQDAH
NLAWKLASVLHGRASDALLDTYHQBRHPVGTFIABGAWTRHTYRLDGDDELGRRLVDT
YRVAAGYRTYSSAVLGAATPAIPHELALIGLPGQRVPHVWLDHDGRRVSTVDLAVDF
FVILARADGTPWADARRLAATGIPLTAHVGKTLTDPADALAAATGLGEAGALLLR
PDGFVAWRSDISADDPEAVLDGVLARILART"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_id="AaF73051.1"
db_xxef="d1:811860"
/translation="#RRLSPDAAYTLVNVFTVSPDDQEKLYRHLVDVTERTIRHLPG
vvSaTFHLGNNGRHVVNYAQWESEETFRSMHALPELQEHFAFGRGIATPLSVPCAVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                      Translation "MDRIEIPVLVVGGGLTGLAAAVFLRQQGVDCLLVERHRSTTFLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERAVIVEEBSLDVADVSPTRAQWCGQDKLEPILRDEAVRRGADIRFHTRLDSFAQDAD
GVDAVIVDRGTGARTAVRSRYLIAADGVRSTVRQALGVTGTGHGSLGRAMSVLFQADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPVLHGRRFVITYMANPQAPGVLQTFDENRWIFGFFCDAYGGGDAAFDTGRCADIVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                RASGINARTMELLRNAGLEETVIDRSLHLIEGKRWRELGQPADRIPWVVLRARDLADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="may effect polyketide antibiotic elloramycin A biosynthesis"
Rafanan, E.R. Jr., Le, L., Zhao, L., Decker, H. and Shen, B. Direct Submission
Submitted (03-MAY-2000) Chemistry, University of California Davis, One Shields Ave., Davis, CA 95616, USA
Location/Qualifiers
1. 3164
/organism="Streptomyces olivaceus"
/strain="Tu 2353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'transl_table=11
product="Tcm F1 monooxygenase"
protein_id="AAF73051.1"
                                                                                                                                                                                                                                                                                                                        /codon_start=1
transl_table=11
product="Tcm B2 oxygenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAF73053.1"
/db_xref="G1:8118604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product-"Tcm F2 cyclase'
                                                                                                                                                                               /db_xref="taxon:47716"
339. 1958
/gene="elmG"
339. 1958
                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAF73050
/db_xref="GI:8118601"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="ElmJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="elmJ"
2648. .3079 '
/gene="elmJ"
                                                                                                                                                                                                                                                       339. .1958
/gene="elmG"
/note="ElmG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2316. .2636
/gene="elmI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1990. .2319
/gene="elmH"
1990. .2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1990. .2319
/gene="elmH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .3079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316. .2636
'gene="elmI'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="ElmI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"ElmH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEEAAG
                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                            SGO
                                                                                                        FEATURES
```

Length 3164;

9.5%; Score 54.6; DB 1;

Query Match

487

BASE COUNT ORIGIN

```
2495 gccdaagarccrcdaagcccgcacacaccccccccrrccgaagcrcaacaagaagrcgg 2554
        ö
                                                                                                          2315 GATGACGTACCGGGCCCTGATGGTGCTGCGGATGGACCGGCCGACGCCGAACGGGTGGC 2374
                                                                                                                                                292
                                                                                                                                                                                                     293 CGAGACCAGGGTCGAAGAGAACATCAACACCTGCACGGCGAGGTCCACGAGGCAGGGA 352
                                                                                          173 CGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACG
                                                                                                                                                233 CGCCGGCGCCAACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCG
          ö
           Indels
           0; Mismatches 124;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                 Search completed: June 16, 2003, 03:10:51 Job time : 1694.35 secs
 51.0%;
                                                                                                                                                                                                                                                                                  111 ||| || 1255 CCGCTACCTCACC 2567
                                                                                                                                                                                                                                                                  353 GAGCTTCCTCGCC 365
Best Local Similarity 51.0 Matches 129; Conservative
                                                                                                                                                                                                                                         엄
                                                                         g
                                                                                                    δ
                                                                                                                              g
                                                                                                                                                          ò
                                                                                                                                                                                    g
                                                                                                                                                                                                                ă
                                                                                                                                                                                                                                                                      ŏ
```

```
BE129644 945027E06
BE129644 945027E06
BE519299 945007B05
BE519299 945007B05
BE519299 945007B05
BE519299 945007B05
BE519299 945007B05
BE519318 RNOSEGÉED
BE619318 RNOSEGÉED
AT104409 ZEB MASTALTA-HI
ANGESTÓEN AT126HI
ANGESTÓEN AT126HI
ANGESTÓEN AT126HI
ANGESTÓEN AT126HI
ANGESTÓEN AT126HI
ANGESTÓEN AT126HI
BEE12510 DGILJOGE
BEE12510 DGILJOGE
BEE12510 DGILSEE
BE597738 PILLBSEG
BE597738 PILLBSEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM501439 417 bp mRNA 11near EST 14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
Zea mays
Zea mays
Sea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 417)
Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Jung R
Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jung,R.
Maize opaque endosperm mutations create extensive changes
patterns of gene expression
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                              AW787314
BQ619167
BQ619315
BQ619318
BQ619337
BQ619383
                                                                                                                                  AY104409
BE225008
AI372183
BG840383
10 AW787315
10 BE025303
10 BE025303
10 BE52929
10 BE52929
10 AW787314
14 BO619315
14 BO619318
14 BO619318
14 BO619318
14 BO619318
14 BO619318
16 BE25008
10 BE25008
10 BE25008
10 AW289056
10 AW289056
11 AW289056
                                                                                                                                                                                                                                                                               AW679347
BE125310
                                                                                                                                                                                                                                                                                                                                  BE597738
BE599123
                                                                                                                                                                                                                                                                                                                                                      BQ280894
BQ280709
BE364814
                                                                                                                                                                                               A1964534
A1964458
A1855425
T12683
AA051890
T18841
                                                                                                                                                                                                                                                                                                                                                                                   AW680016
AW679969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rudolf.jung@pioneer.com
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM501439.1 GI:1866j517
                                                                                                                                           RESULT 1
BM501439
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
TITLE
                                                                                                                                                                                              000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM501439 PACC00000
AW788732 94500260
AW787732 94500260
BEL129897 945032C12
AW331212 707049E04
BE025302 945028B09
                                                        June 16, 2003, 05:14:00 ; Search time 1163.61 Seconds (without alignments) 7989.092 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      Description
                                                                                                                                                                                                                      32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                        16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                     parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                        nucleic search, using sw model
                                                                                                                                                                                                                                                                       summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM501439
AW288876
AW787732
BE129897
AW331212
BE025302
                                                                                                                                          OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                             Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_gss_mus:*
em_gss_other:*
em_gss_pro:*
em_gss_rod:*
                                                                                                                                                                                                                                                                 Post-processing: Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss:*
em_gss_hum:*
em_gss_inv:*
                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                em_estba:*
em_esthum:*
em_esthum:*
em_esthu:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
gb_est2:*
gb_est2:*
gb_est3:*
gb_est4:*
gb_est4:*
em_estpu:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_gss_vrt:*
em_gss_fun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_gss_mam:*
                                                                                                    US-10-090-035-3
574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417.
524
500
523
5523
                                                                                                                                                                                                                                                                                        EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %
Query
Match I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.6
67.9
67.4
63.2
59.2
                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                           Perfect score:
                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
390
387
363
340
315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                        nucleic -
                                                                                                                                                                                            Word size :
```

Database :

Sequence:

Run on:

Searched:

/organism="Zea mays" /db\_xref="taxon:4577"

source

FEATURES

Result

ö

Gaps

ö

Indels

5;

Length 524;

175

152

```
adult tissues from Walbot lab, same as 707 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCAGGGTCGAAGAGGACATCAACACCTGCACGGCGAGGTCCACGAGGCGCAGGGAGAG 355
                                                                                                                                                                                                                                                    /note="Organ: tassel, kernel, silk, husk, root, leaf; /note="Organ: tassel, kernel, cDNA library from fully vector: pGAD: Site_1: ECORI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."
                                                                                                                                                                                                                                                                                                                                                                                                       273 GACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGTTCCACGAGGCAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGCGTGCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 ACACGGGCGCTGCGCACAGACACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize ESTs from various cDNA libraries
                                                                                                       Score 390; DB Pred. No. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              945002E06.X3 945 - Mixed (SK) Zea mays cDNA, mRNA AW787732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW787732.1 GI:7844510
                                                                                                          67.98;
99.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACTICITCGT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACTTCTTCGT
                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW787732
                                                                       107
                                                                                                                                     490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536
                                                                                                                                                                                                                                                                                                                                                             296
                                                                                                              Query Match
                                                                                                                          Best_Local
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                    ద
                                                                                                                                                                                                               δ
                                                                                                                                                                                                                               . 엽
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW288876 524 bp mRNA linear EST 16-JAN-2000 707009E07.x4 707 - Mixed adult tissues from Walbot lab (SK) Zea mays cDNA, mRNA sequence.
AW288876.1 GI:6695663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SK
                                                                                                                                                                                                                                                                              241 CACCACCATGGTCACCACGCCGCCACGCTTCGTGGTGCGCGGACCACGGTCGAAGAG 300
                                                                                                                                                                                                                                                                                                                                                                GACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371
                                                                                                                                                                                                                                                                                                                                                                               GTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGCGGCGCCAACCACCAC
                                                                                                                                                                                                                                                                                                                252 CACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGGGGACCAGGGTCGAAGAG 311
                                                                                                                                       9
                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                 from Walbot lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
                                                                                                                              CGCCCACGCGTCCGCACAGCAATCCACACAAGCACTTCGACGTCACACGGGCGCTGCGCA
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at Stanford
   /clone_lib="Pioneer AF-1 array"
/note="Vector: pSport1; Site_1: Sal1; Site_2: NotI"
/ 150 c 133 g 53 t
                                                                                         ;
                                                                 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sedneuced
                                                                                          Indels
                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Walbot V
Department of Biological Sciences
Standord University
855 California Ave, Palo Alto, CA 94304, US
Tel: 650 723 227
Fax: 650 725 8221
Fmai: walbot@stanford.edu
Plate: 707009 row: E column: 07.
                                                                                          ö
                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize ESTs from various cDNA libraries
                                                                  72.6%; Score 417; DB 100.0%; Pred. No. 0; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University
Unpublished (1999)
                                                                                           417; Conservative
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
Zea mays
                                 ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                                                                                                         312
                                                                                                                                                                                                                                                                                                                                                                                                                         372
                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                       192
                                                                                                                      12
                                                                                                                                                                      72
                                                                                                                                                                                               61
                                                                                                                                                                                                                        132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
AW288876
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL COMMENT
                                 BASE COUNT
ORIGIN
                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
```

Dp ò 셤

g

셤 ŏ 셤 ò

ò

g õ 셤 ò

ò

415 392

332

295 272 475

at Stanford

sedneuced

m

us-10-090-035-3.rst

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 465)

2 Maloct, V.

Maloct ESTs from various cDNA libraries sequenced at Stanford University

2 Unpublished (1999)

3 Contact: Walbot V

4 Department of Biological Sciences

5 Stanford University allory various and various of Biological Sciences

5 Stanford University allory various have, Palo Alto, CA 94304, USA

Tel: 650 723 2227
                                                                                                                                                                                                                                                                                                                                                              /note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACGGGCGCTGCGCACAGACACAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGGCGGC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCGTGCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTAT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"/dev_stage="fully-grown"
/lab_host="bH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 GGCGCCAACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAGGGTCGAAGAGGACATCAACACCTGCACGGCGAGGTCCACGAGGGGAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11arity 99.6%; Score 363; DB Conservative 0; Mismatches
                                                                                                                                                                                               Email: walbot@stanford.edu
Plate: 945032 row: C column: 12.
Location/Qualifiers
                                                                                                                                                                                                                                         1. .465
/organism="Zea mays"
/cultivar="W23"
           Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 463; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
                                                              AUTHORS
TITLE
                                                                                                     JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                   REFERENCE
                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                 // Corganism="Zea mays"
// Organism="Zea mays"
// Cultiva="wu2"
// Cultiva="wu2"
// Clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
// Save_type="tassel, kernal, silk, husk, root, leaf"
// Libb_host="DHIOB"
// Abb_host="DHIOB"
// Note="Organ: tassel, kernal, silk, husk, root, leaf;
// Note="Organ: tassel, kernal, silk, husk, root, leaf;
// Cotcor: pGADIO: Sile_l: ECORI: cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 bp mRNA linear EST 21-JUN-2000 adult tissues from Walbot lab, same as 707 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCTGCCCACAGACACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTA
                                                                                                                                                                                                                                                                                                                                                                                                        122 CTGCTCGGAGGAGGTGAGGTCGGTGGCCCGGCTTCGGCCGCCACGGCGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                     Length 500
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                              cch 67.4%; Score 387; DB 10; 21 Similarity 99.6%; Pred. No. 0; 487; Conservative 0; Mismatches 2;
                                90
Fax: 650 725 52.2
Email: walbot@stanford.edu
Plate: 945002 row: E column:
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SK) Zea mays cDNA, mRNA s
BE129897
BE129897.1 GI:8577705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [][]]]]
CTTCGTAAT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCGTAAT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
Zea mays
                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542
                                                       source
                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE129897
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                         ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

ö

120

236 180 296 240 356

300

```
Zea mays.
                                                                                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                    RESULT 6
BE025302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                              g
                                                                                             δŏ
                                  ŏ
523 bp mRNA linear EST 31-JAN-2000 707049E04.x1 707 - Mixed adult tissues from Walbot lab (SK) Zea mays CDNA, mRNA sequence. AW331212. AW331212.1 GI:6827569 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCAGGGCTAACTGAGCCGCCCGGCGGCGTCCACGCCCGTTCGTGCTTGCCTGCGT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTATCGTAGG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/dab_host="bhl0b"
/note="organ: tassel, kernel, silk, husk, root, leaf;
/note="organ: tassel, kernel, cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
plant, root, leaf). Unidirectionally cloned."
a 158 c 149 g lt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCCC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 AACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGAGACCAGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AACCACCACCACCACCACGACGACGACGACGACGCTTCGTGGTGGCGAGACCAGG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 CGCTGCGCACAGACACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTAC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGCGGCGCC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SK
                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; 2ea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .523
/organism="Zea mays"
/cultiva="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                       1 (bases 1 to 523)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                             Contract: Walbot V
Department of Biological Sciences
Stanford University
85.California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Eax: 650 725 8221
Email: walbotestanford.edu
Plate: 707049 row: E column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 59.2%; Score 340; DB sal Similarity 99.4%; Pred. No. 0; 490; Conservative 0; Mismatches
                                                                                                                                                                                                                                     University
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ಥ
                                                                                                                  Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                           DEFINITION
                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                   JOURNAL
                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
               AW331212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

T

```
552 bp mRNA linear EST 07-JUN-2000 945028B09.Y1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence. BE025302 BE025302.1 GI:8318737 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ:.tassel, kernal, silk, husk, root, leaf;
Vector: pGADIO; Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 CGACGTCACACGGCCCTGCGCACAGACACAACAACGTCGGCACCAATGCTTACTACC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 CACGCGCCGGCCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                362 GCCTTATGTATGTCTATGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 552
/organism="Zea mays"
/oultivar="Wi3"
/db_xref="Fiaxon:4577"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 cGACGTCACACGGGCGCTGCGCACAGACACCAAGGGTCGGCACCAATGGCTTACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University
Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tex: 650 725 8221
Fax: 650 725 8221
Email: walbotdestanford.edu
Plate: 945028 row: B column: 09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.9%; Score 315; DB Best Local Similarity 99.2%; Pred. No. 0; Matches 515; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                  543 TTCGTAATACTAA 555
                                                                                                                                                                                                                                                                                                              482 TTCGTAATACTAA 494
```

S

```
Zea mays.
      115
                         н
                                               175
                                                                  61
                                                                                                                                295
                                                                                                                                                                          355
                                                                                                                                                                                                                       415
                                                                                                                                                                                                                                                               475
                                                                                                                                                                                                                                                                                                          535
                                                                                                                                                                                                                                                                                                                            421
                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                             RESULT 8
BE025303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                     g
                                             à
                                                               셤
                                                                                                       셤
                                                                                                                                ò
                                                                                                                                                   a
                                                                                                                                                                       ò
                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                  g
                                                                                     ç
                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                    436 bp mRNA linear EST 16-MAY-2000 945002E06.X2 945 - Mixed adult tissues from Walbot lab, same as 707 6XK) &ea mays cDNA, mRNA sequence. AW787315 AN787315.1 GI:7844112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                               Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Palicoideae; Andropogoneae; Zea.

1 (bases 1 to 436)
Walbot,V.

Malbot,V.

Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                    408
                                                                                                                  GTGCTTGCCTGCGTGCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTAC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.3%; Score 283; DB 10; Length 436; 99;3%; Pred. No. 0; 1.ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 728 221
Email: walbotéstanford.edu
Plate: 945002 row: E column: 06.
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 433; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                Zea mays.
                                                                                                                                                                                                                                                                                                                                     EST
           181
                                                                                                                  409
                                                                                                                                                                                                                                                          RESULT 7
AW787315
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                          g
                                                                                                                                                                               윱
                                                   g
                                                                      à
                                                                                                                                  a
                                                                                                                                                                                                                       g
                              ò
                                                                                                                  à
                                                                                                                                                            ç
                                                                                                                                                                                                      ò
```

```
mRNA linear EST 07-JUN-2000 tissues from Walbot lab, same as 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGADIO; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
                                                                                                                         120
                                                                                                                                                                      294
                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                        354
                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                           414
                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 ATCGTACGTGCACCCACTCACCTGTACGACTACGACAATAAGCTCGTGACCTGGAAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
Zea mays
Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viidiplantae; Streptophyta; Euliopsida; Poales; Poaceae; PACC
Clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 326)
Walbot, V.
                                                                                 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534
174
                                        9
                                                                                                                                                                181 AGACCAGGTCGAAGAGACATCAACACCTGCACCGCGCGAGTTCCACGAGCGCAGGAGA
                                                                                                                                                                                                                                                                                                                                                               GCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCG
                                                                                                     AGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                              GCCTGCGTGCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCGTACGTGCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="W23" "M.75" /db_xref="taxon:4577" /db_xref="taxon:4577" /clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)" /tissue_typ="tassel, kernal, silk, husk, root, leaf" /dev_stage="fully-grown" /lab_host="DH10B"
GCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGGCGCCGCCACGCCCGTTCGTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unjublished (1999)
Contact: walbor (1999)
Contact: walbor (1999)
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Fax: 650 725 8221
Fax: 650 725 8221
Carillo California Ave, B column: 09.
Plate: 945028 row: B column: 09.
Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 bp
945028B09.y2 945 - Mixed adult tis
(SK) Zea mays CDNA, mRNA sequence.
BE025303
BE025303.1 GI:8318738

    .326
    /organism="Zea mays"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAACTTCTTCGTAAT 550
```

ð 셤 g ò 유 ö g ŏ a

ò

```
/organism="Zea mays"
/cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW288875.1 GI:6695662
                                                                                 Query Match
Best Local Similarity 99.4%;
Matches 351; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University
Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
AW288875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                        셤
                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-2000
same as 707
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (243) Walbot, V.
root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
                                                                                                                                                                                       235
                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                     296 GACCAGGGTCGAAGAGGACATCAACACCTGCACGGCGAGGTCCACGAGGGCAGGGAGAG 355
                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="laxon:4577"
/db_xref="laxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf" /dev_stage="fully-grown"
/lab_host="DH108"
                                                                                                                                                                                                     CGGCGCCAACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGA
                                                                                                                                                                                       CGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGC
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE129644 11near EST 945027E06.X2 945 - Mixed adult tissues from Walbot lab, (SK) zea mays cDNA, mRNA sequence.
                                                                                                   ö
                                                                        Length 326;
                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Statifornia Ave, Palo Alto, CA 94304, USA Tel: 650 723 227
Fax: 650 725 8221
Email: walbotestanford.edu
Plate: 945027 row: E column: 06.
                                                                         DB 10;
                                                                      Score 254; DB
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Biological Sciences Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'cultivar="W23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE129644
BE129644.1 GI:8577007
                                                                      Query Match
Best Local Similarity 99.7%;
Matches 304; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||
| CCTGC 326
                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays
                               23
                                                                                                                                                                                                                                                                          142
                                                                                                                                                                                                                                                                                                                                                              356
                                                                                                                                                                                                                                                                                                                                                                                        262
                                                                                                                                 116
                                                                                                                                                            22
                                                                                                                                                                                         176
                                                                                                                                                                                                                                               236
                                                                                                                                                                                                                                                                                                                                                                                                                      416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
BE129644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
```

à

a

FEATURES

COMMENT

```
AW288875 . 274 bp mRNA linear EST 16-JAN-2000 707009E07.x3 707 - Mixed adult tissues from Walbot lab (SK) Zea mays cDNA, mRNA sequence.
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade; Pantcoideae; Andropogoneae, Zea.

1 (bases 1 to 274)
Walbot,V.
                                                                                                                                                                                                                                                                                                      162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
                                                                                                                                                                                           160
                                                                                                                                                                                                                             102
                                                                                                                                                                                                                                                                  220
                                                                                                                                                                                                                                                                                                                                          280
                                                                                                                                                                                                                                                                                                                                                                               222
                                                                                                                                                                                                                                                                                                                                                                                                                     340
                                                                                                                                                                                                                                                                                                                                                                                                                                                          282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
                                                                                                                                                                                                                                                                CITCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                        223 CITCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGITCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 CGAGCGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCCGGCGGCGCGCATCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                               Maize ESTs from various cDNA libraries sequenced at Stanford
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, root, leaf). Unidirectionally cloned. New library given to library 707 for additional sequencing." 144 c 148 g 73 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                  DB 10; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biological Sciences Stanford University B55 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot/estanford.edu
Plate: 707009 row: E column: 07.
                                                                                                                                                          5
                                                                                                                Score 251; DB
Pred. No. 0;
0; Mismatches
```

```
Similarity
                                                                                                                                                                                         158
                  Best Local
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
BF729420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                      ద
                                                                                                                                                                                       õ
                                                                                                                                                                                                                                   쉽
                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 bp mRNA linear EST 08-AUG-2000 945007805.x1 945 - Mixed adult tissues from Walbot lab, same as 707 BE519299 BE519299.1 GI:9743151
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
Vector at loss of the control of
                                                                                                                                                                                                                                                                                                                                               160 TCGGCCGCCACGGCGCGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; permatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."
                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                CAAGCACTTCGACGTCACAGGGCGCTGCGCACAGACACACAAGCGTCGGCACCAATGG
                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
/clone_llb="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA libraries sequenced at Stanford
                                                                                                                                                                                                            ö
                                                                                                                                                        DB 10; Length 274;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                      ó,
                                                                                                                                                38.9%; Score 223; DB
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: walbot@stanford.edu
Plate: 945007 row: B column: 05.
Locatlon/Qualifilers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Biological Sciences
Stanford University

    476
    /organism="Zea mays"
    /cultivar="W23"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize ESTs from various
                                                                                                                                                                       Best Local Similarity 100. Matches 223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University
Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Walbot, V
                                                                          57
                                                                                                                                                                                                                                                  40
                                                                                                                                                   Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
BE519299
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Source
                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                    윱
                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

10; Length 476;

B

Score 210;

36.68;

Query Match

```
/organism="Zea mays"
/db_xref="dbEST:945032C12.Yl"
/db_xref="taxon:4577"
/clone_lib="loud" - Unique I from Maize Genome Project"
/clone_lib="This library represents the unique ESTs found in the first round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 466, 487, 487, 603, 605, 605, 604, 618, 660, 687, 707, and 945. Contigs were assembled using TIGR's
                       ö
                                                       157
                                                                                                                          217
                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 09-JAN-2001
                                                                                                                                                                                           277
                                                                                                                                                                                                           337
                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                397
                                                                                                                                                                                                                                                                                                                                                                311
                                                                                                                                                                                                                                                                                                                                                                                             398 CACGCCCGTTCGTGCTTGCCTGCGTGCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAG 457
                                                                                                                                                                                                                                                                                                                                                                                                               458 GGTCATCGTACTTGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATTACGACAAT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryóta; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Permatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea. (bases 1 to 311)
                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Maize Genome Project 2ea mays
                                                                                                                                                                                                                                                                                                                        CITCGGCCGCCACGCGCGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGT
                                                                                                                                        218 GGACACGGTCTCACGCGCGGCGCCAACCACCACCACCATGGTCACCACGGCGGCCA
                                                                                                                                                                                                                                                          278 CGCCTTCGTGCTGCGCGAGCCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGT
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Walbot,v. Malze ESTs from various cDNA libraries sequenced at Stanford
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518 AAGCTCGTGACCTGAATAAAACTTCTTCGTAATACTAAAAAAA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                   .
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                855 California Ave, Palo Alto, CA 94304, Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 1000077 row: C column: 04.
 Pred. No. 0;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Walbot V'
Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 bp
1000077C04.x2 1000 - Unigene I
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:12047281
98.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA, mRNA sequence.
BF729420
BF729420.1 GI:12047
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
```

90

Б 153

Ö

g ò g ð a g à

ð

```
156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ619167
BQ619167.1
   ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                          549 AT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS TITLE JOURNAL COMMENT
 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
BQ619167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                         셤
                                                                                                                                                                          δ
                                                                                                                                                                                                      g
                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
/organism="W23"
/db_xref="taxon:4577"
/dlone_lib="945 - Mixed adult tissues from Walbot lab,
/same as 707 (SK)"
/fissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10P"
/nb_host="DH10P"
/nb_host="OH10P"
/nb_host="OH10P"
/nb_host="OH10P"
/nb_host="OH10P"
/nb_host="fill:1:" (fassel, kernal, silk, husk, root, leaf)
/orctor: pGAD10; Site_1: ECORI; cDNA library from fully
/nisme ratio as 4:2::1::1::1 (fassel, kernel, silk, husk, root, leaf). Unddirectionally cloned. New library number given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 496)
Walbot,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA linear EST 16-MAY-2000 tissues from Walbot lab, same as 707
                                                                                                                             ö
                                                                                                                                                                                                                   54 CAGCAGCACGTCGTCGAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGCCGCCGC 113
                                                                                                                                                                                                                                                                                  GTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGGCGCAGGGAGAGCTTCCTC 362
                                                                                                                                                                                                                                                                                                                                                 422
 CAP program and a representative EST from each contig was selected for the Unigene set. All singlets were also selected." 107 g 46\ \rm t
                                                                                                                                                                                                                                                                                                                                                 183 CAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCC
                                                                                                                               Gaps
                                                                                                                             ö
                                                                                              Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at
                                                                                                                          0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize ESTs from various cDNA libraries sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 728 821
Email: walbot@stanford.edu
Plate: 945002 row: E column: 06.
                                                                                                 DB 12;
                                                                                                Score 207; I
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW787314 496 bp
945002E06.X1 945 - Mixed adult tis
(SK) Zea mays cDNA, mRNA sequence.
AW787314
                                                                                                                                                                                                                                                                                                                                                                                                                  423 GCCTTATGTATGTCTGTG 440
                                                                                                                                                                                                                                                                                                                                                                                                                                    294 GCCTTATGTATGTCTGTG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW787314.1 GI:7844111
                                                                                                36.1%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                 257; Conservative
                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST.
                                                                                                                                                                                                                                                                                       303
                                                                                                   Query Match
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                    BASE COUNT
ORIGIN
                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
AW787314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
```

```
BQ619167 EST 27-JUN-2002 RNOSEQ4E05_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases I to 648)

1 (and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
                               ô
                                                                                                                                                                                                                                                                                                                               302
                                                                                                                                                                                                                                                                                                 422
                                                               249 CACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGGGGAGACCAGGGTCGAA 308
                                                                                                                                                                                             362
                                                                                                                                                                                                                                                              429 TGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTATCGTACGTGCACG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
/do_xref="txxon:4577"
/do_xref="txxon:4577"
/clone_lib="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_stage="Z weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 15mm NaC!"
                                                                                                                              183 CACCACCACGAGGTCACCACGCGCACGCTTCGTGGTGCGCGAGCCACGGTCGAA
                                                                                                                                                                                                                  Gaps
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 648;
 Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 178; DB 14;
Pred. No. 0;
0; Mismatches 3;
                                   5
   DB 10;
Score 200; DB Pred. No. 0; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1201 W. Gregory Dr., Urbana, IL
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:21621161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.0%;
99.1%;
   Query Match 34.8%;
Best Local Similarity 99.3%;
Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.0
Best Local Similarity 99.1
Matches 328; Conservative
```

```
Search completed: June 16, 2003, 08:38:46
Job time : 1170.61 secs
                       õ
                                           g
                                                                    ò
                                                                                            d
                                                                                                                     à
                                                                                                                                           g
                                                                                                                                                                    à
                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                BQ619315 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6C06_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6C06_SK.abl similar to No homology, mRNA
423
                                                                                                                                                       483
                                                                                                                                                                                                                              532
                                                                                                              484 GCACGCACTCACCTCTCTACAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .648
/organism="zea mays"
/db_xref="taxon:4577"
/clone="RNOSEQGC06_SK.abl"
/clone="RNOSEQGC06_SK.abl"
/clone="lb="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 CCAGGGCTAACTGAGCCGCCGGCGGCGTCCACGCCCGTTCGTGCTTGCCTGCGTG
                                                                                                                                                CCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTATCGTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics of plant stress tolerance Unpublished (2002) Contact: Mark Fredricksen Department of Plant Blology University of Illinois 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 2172655473
                                                                                                                                                                                                                                              100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
31.0%; Score 178; DB
Best Local Similarity 99.1%; Pred. No. 0;
Matches 328; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bohnertlab@life.uiuc.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
                                                                                                                                                                                                                                                                                                                                                                                               GI:21621309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 c
                                                                                                                                                                                                                                                                                                                                                                       sequence.
BQ619315
BQ619315.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172
                                                                                                                                                 424
                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                         RESULT 15
BQ619315
LOCUS
                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
 à
                       g
                                               ò
                                                                     g
                                                                                                                      g
                                                                                                                                                                    a
                                                                                                à
                                                                                                                                                                                                                     g
                                                                                                                                                ð
                                                                                                                                                                                              à
                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
543
                                   483
                                                               GCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT
                            CCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTATCGTACGT
                                                                                  424
                                                        484
```

**: ****	7 8		v 8	- v Ž			* 1	
तेब् क								
***				•	•			
\$1	,			,	3.		*	
							* *	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1							* 9	.1
9.5 6. **								7 m
	. 5							
			· .					•
<b>%</b>					*			4
			•		pe.			1
		. *				• * * * * * * * * * * * * * * * * * * *		· Jan
			- TO			* -	N. 8	
	· ·		_ ^ _					
			•	\$ 00 H		Ž.	s 17	
							4.	
						- '	· · · · · · · · · · · · · · · · · · ·	
							12.	
20				*			* ***	
					****		,	•
2		- (						
			, E				**	
-			2. Sec. 1997	*		•	*	
				₹		Ţ.	*	0 t
				•				1
	25		*					
ř			•					
								×e
6							•	
	0 ,							
			* · · ·				· · · · · · · · · · · · · · · · · · ·	*
10				. 8				
44.5								
					•			1
				*				* * * * * * * * * * * * * * * * * * *
			a. m. () . m	$ ilde{\psi}$				* **
			* * * * * * * * * * * * * * * * * * *					
	7 6			•		•		•
1				,				
Y			0					,
**								
				·				
S. A. S. A.			*					
Ĺ								
					*			
							•	
7							•	
k Gra			•					,
						•		
	•							
h		-			•			
8								
								V.
					•			
								•
			•					4
			•				<del>.</del>	₽5 <sub>1</sub>
2					10		had the seguine	3.
-12				ىد.		*	The state of the s	With the Control of t

us-10-090-035-1.rge

```
June 16, 2003, 04:03:20 ; Search time 1984.2 Seconds (without alignments) 9915.101 Million cell updates/sec
                                                                                                                                               4109280
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      2054640 seqs, 14551402878 residues
                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                                                                                                                                                                                            OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                     0
                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                  Word size :
                                                                                                                                                                                                                                                     Searched:
                                                                                     Run on:
```

of Freedoms. Ersering tittse 40 summaries	ge	3: 9b_ncg:" 3: 9b_1n:*	 	 *:Td_dp :0	ö,	 12: gb_sy:* 13: qb_un:*	 	 5		 _		-	-		en htg	em_htg	-	e E	-	-	em_sy:*	9 F	em_ntgo_	<b>5</b>

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

NES Description .	ALT136 BC0034 AL6323 AL6323 AL6323 AL6323 AL6323 AL6323 BC0163 AL1336 AL1336 AL1336 AL1336 AL1336 AL3338 BC0332 AL3338 AX34659 AX34659 AX34659 AX34659 AX34659 AX34659 AX34659 AX34659	MENTS  Dp mRNA linear PRI 20-MAR-2002 667D1012 (from clone DKF2p667D1012).  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae, Homo. W., Weil, B. and Wiemann, S.  Am Klopferspitz 18a, D-82152
SUMMARIE	· womwannnnna x x x x x x x x x x x x x x x x	ALIGNMI 3454 bg DKFZp66 Cdata; C nates; C nates; C
93	• • • • • • • • • • • • • • • • • • • •	cDNA 84343 ; Chou ; Prin A., ME
Length	2454 2836 2836 2837 2837 2838 2838 2838 2838 2838 2838	mRNA GI:19 GI:19 GI:40 Aetazo Itheri to 34 EBEYER
>'q	17.00 17	HSM802993 HPOMO sapiems AL713659 AL713659.1 human. HOMO sapiems Eukaryota; h Mammalia; Eu I (bases I Koehrer,K., Direct Submi
Score	1120 121 122 123 123 123 123 123 123 123 123	
Result No.		RESULT 1 HSM802993 LOCUS DEFINITION VERSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE

Genome CA 94305

```
Mus musculus, RIKEN cDNA 2810429K11 gene, clone MGC:31645 IMAGE:4527027, mRNA, complete cds.
                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov scries: IRAL Plate: 16 Row: p Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg, R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                              WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Pravyed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
nstitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:4052341"
/tissue_type="Kidney, hypernephroma"
/clone_lib="NIH_MGC_58"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.9%; Score 121; DB 9; I
Liarity 100.0%; Pred. No. 7.3e-55;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pDNR-LIB"
82 c 107 g 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2776)
                                                                                                                                                                                                                                                                                                                                                                                           identity to protein.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC034120.1 GI:21707638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 121; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          676 A 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 A 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
BC034120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                  REMARK
                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"HigerpysclkcektforrhhlirhokthidkiskCecgknf
Ronshlashqrvhaegksckgqevgespgtrkrprappvpkchvctecgksfgrrhhl
vrhwlthigekpfocprceksfgrkhhldrhllthdggsprnswdrgtsvf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI 12-JUL-2001
      Martinsried, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. WiemanneGkfz-heidelberg-de; sequenced by BMFZ (Blomedical Research Center at the Charite, Berlin/Germany) within the CDNA sequencing consortium of the German Genome Project.
                                                                                                                             This clone (DKFZp667D1012) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                         /tissue_type="lymph node"
/clone_lib="667 (synonym: hlno2). Vector pSportl; host
DH10B; sites Not1 + Sal1"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="295.8 cR from top of Chr12 linkage group"
/clone="DKFZp667D1012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.0%; Score 122; DB 9; Length 34
100.0%; Pred. No. 2.2e-55;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unknown zinc finger protein"
/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="cap28468.1"
/db_xref="G1:19584344"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens, clone IMAGE:4052341, mRNA.
BC008387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3288. .3293
/gene="DKFZp667D1012"
3306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene-"DKFZp667D1012"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="DKFZp667D1012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DKFZp667D1012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            756 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC008387.1 GI:14249997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 596)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.09
Best Local Similarity 100.0
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3426 AA 3427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675 AA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
BC008387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

ö

Gaps ö

```
438 c
                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 17.9
Best Local Similarity 100.
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                              Ø
                                                                                                                                                                                                                                                                                                                              982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2826 A 2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676 A 676
                                                                                                                                                                                                                                                                                                    polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                   polyA_site
                                                                                                                                                                                                source
                    AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
HSM803701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                           can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2830 bp mRNA linear PRI 12-JUL-2002
AL832170
AL832170.1 GI:21732714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Scries: IRAK Plate: 44 Row: j Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                 /db.xref="taxon:10090"
/db.xref="taxon:10090"
/clone="MGC:31645 IMAGE:4527027"
/tissue_Ltype="Eyo, retina, mouse strain C57Bl\6"
/clone_ltb=host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%; Score 121; DB 10; Length 2776; 100.0%; Pred. No. 7.8e-55; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                          /note-"Vector: pCMV-SPORT6"
                                                                                                                                                                                                                          /organism-"Mus musculus"
                                                                                                                                                                                                 Location/Qualifiers
1. .2776
                                                                                                                                                                                                                                                                                                                                    /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.9
Best Local Similarity 100.
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                      analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2749 A 2749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           676 A 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                              Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSM803477
                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

```
Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERWANY Chone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2): Email s.w.temannéwkfz-heidelberg.de; Sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKF266660316) is available at the RZDD in Berlin. Please contact the RZDD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY: Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mlps.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                           3383 bp mRNA linear PRI 10-JUL-2002
ALB32393 GI:21732956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUL 2002) 1, D-85764 Neuherberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2): Email a wiemand@discheiderg.de; Sequenced by BMF2. Blomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Project.
This close (DKF2pG6XX1712) is available at the RZPD in Berlin
Please contact the RZPD: Ressourcenscentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: close@rzpd.de Further
information about the close and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.

1. 3383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
1 (bases 1 to 2830)
Wambutt,R., Heubner,D., Mewes,H.W., Well,B. and Wiemann,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 3383)
Kochrer, K., Bayer, A., Mewes, H.W., Well, B. and Wiemann, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 121; DB 9; 1
Pred. No. 7.8e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.9%,
100.0%; Pre-
0; F
```

```
BC034163.1 GI:21706753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334
                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
AK026865
LOCUS
 VERSION
KEYWORDS
SOURCE
                                                                             AUTHORS
                                                                                                   JOURNAL
                                                                                                                                              REMARK
COMMENT
                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOO bp mRNA linear ROD 07-AUG-2002 Mus musculus, Fc receptor, IgE, high affinity I, gamma polypeptide, Clone MGC:36077 IMAGE:5065647, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                           615
 /clone="DKFZp667K1712"
/tissue_type="lymph node"
/clone_lib="667 (synonym: hlno2). Vector pSportl; host
DH10B; sites NotI + SalI"
321. 3236
3250
                                                                                                                                                            /note="chemically treated genomic DNA (Homo saplens)"
176 c 1443 g 3154 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :
0
                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6486;
                                                                                                                  Length 3383;
                                                                                                                                                                                                                                                                                                                                                                                                                                Schacht, O. diseases associated with angiogenesis plagnosis of diseases associated with angiogenesis Patent: WO 0246454-A 80 13-JUN-2002; Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.9%; Score 121; DB 6; Length 64
100.0%; Pred. No. 8.1e-55;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              linear
                                                                                                               17.9%; Score 121; DB 9; I
100.0%; Pred. No. 7.9e-55;
.ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                               DNA
                                                                                  928
                                                                                                                                                                                                                                                                                                                             AX458534 6486 bp .Sequence 80 from Patent W00246454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                  663 g
                                                                                                                                                                                                                                                                                                                                                               AX458534.1 GI:21725198
                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct.
synthetic construct
artificial sequences.
                                                                                  552 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity 100.
121; Conservative
                                                                                                                   Query Match 17.9°
Best Local Similarity 100.°
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1713 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A 3363
                                                                                                                                                                                                                                                                          3371 A 3371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676 A 676
                                                                                                                                                                                                                                                    676 A 676
                                                                                   1210
                                                              polyA_signal
                                                        ya_signa
polya_site
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                     AX458534/c
LOCUS
                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
BC034163
                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                          염
                                                                                                                                                                                   쇰
                                                                                                                                                                                                          ö
                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                 δ
```

V

```
AKO26865
HOMO Sapiens CDNA: FLJ23212 fis, clone ADSU01518, highly similar to AF182844 Homo sapiens VPS28 protein mRNA.
                                                                                                                                                                                                                                                                                 Noracter MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Ascquencing by: Sequencing Group at the Stanford Human Genome

DNA Scanford on Viversity School of Medicine, Stanford CA 94305.

Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MISAVILFLLLVEQAAALGEPOLCXILDAVLFLXGIVLTLLYC
RLKIQVRAAIASREKADAVITGLNIRSQETYETLKHEKPPQ"
183 c 124 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 58 Row: o Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753829.
                          Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 800)

Strausberg, R.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor
                                                                                                                                                                            Submitted (12-JUL-2002) National Institutes of Health, Mammalian Submitted (12-JUL-2002) National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Wammary tumor metastatized to lung. Tu arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NCI_CGAP_Lu29" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Fc receptor, IgE, high affinity I, gamma polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.8%; Score 120; DB 10;
llarity 100.0%; Pred. No. 2.6e-54;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .800
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="CzECH II"
/clone="MGC:36077 IMAGE:5065647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pcMv-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAH34163.1"
/db_xref="G1:21706754"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="LocusID:14127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45. .305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 120; Conserv
house mouse.
```

```
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Similar to myoglobin"
/proteah_id="AAH14547.1"
/db_xref="G1:15778933"
/translation="MGLSDGEWOLVLNVWGKVEADIPGHGGEVLIRLFKGHPETLEKF
DKFKHJKSEDEWKASEDLKKKHGATVLTALGGILKKKGHHEAETKPLAGSHATFHKIPV
EXTERISECTION-SKHPGDFGAADAQGAMNKALELFRKDMASNYKELGFQG"
278 c 314 g 242 t
                                                                                                                                                                                                                                                                                                                                                    found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616
                                                                                                                                                                                                                                                                                                                                          Clone distribution: MCC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Serles: IRAL Plate: 19 Rover of Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885476.
                                                                                                                                                                                   cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadandsystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
          Direct Submission
Submitted (24-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:13548 IMAGE:4244838"
/tissue_type="Skeletal Muscle"
/clone_lib="NIH MGC_81"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.8%; Score 120; DB 9; I
100.0%; Pred. No. 2.6e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62, Created)
67, Last updated, Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; RNA; HUM; 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens clone FLB4701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.(
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000
09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF113689.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF113689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF113689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                         REMARK
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF113689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genter; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Parall:cdnatl:cdnatledms.u-tokyo.ac.jp, Tel:81-3-5449-5286, Par:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert construction; Research Association for Blotechnology; CDNA library Construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J191 bp mRNA linear PRI 26-SEP-2001 Homo sapiens, Similar to myoglobin, clone MGC:13548 IMAGE:4244838, BC014547
                                                                                                                                                    1 (sites)
Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A.,
Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M.,
Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T.,
Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1191)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                  Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens VPS28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                     oligo capping; fis (full insert sequence).
Homo saptens adipose tissue cDNA to mRNA, clone_lib:ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1034 /note="highly similar to AF182844 protein mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8%; Score 120; DB 9; Le
100.0%; Pred. No. 2.6e-54;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="ADSU01518"
/tissue_type="adipose tissue"
/clone_lib="ad"
/note="cloning vector pME185FL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 1. 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 g
                      GI:10439824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC014547.1 GI:15778932
                                                                                                                                                                                                                                                                                                             (bases 1 to 1034)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 120; Conservative
                                                                        clone: AbSU01518.
                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ACCESSION
                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
BC014547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

found

рę

[2] [-1298

-1298

source

Key

```
BC016332 1388 bp mRNA linear PRI 05-NOV-2001 Homo sapiens, ubiquitin-conjugating enzyme E2 variant 2, clone MGC:23763 IMAGE:4109228, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MODICCEARGTFAISLFKILGEEDNSRNVFFSPMSISSALAMVFM
GAKGSTAAQMSQALCLYKDGDIHRGFOSLLSEVNRTGTQYLLRTANRLFGEKTCDFLP
DFKEYCOKFYQAELEELSFAEDTECRKHINDWYAERTEGKISEVLDAGTVDPLTKLY
LVNAIYFKGKWNEQFDRYTRGMLFKTNEEKKTVQMMFKEAKFKMGYADEVHFGVLEL
PYVEEELSWYILLDDNYTDLAYKE"

250 c 279 g 310 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 29 Row: m Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA g1: 4505790.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg.R.
Direct Submission
Submitted (29-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                     Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Glbbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Similar to serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8" /protein_id="AAH34528.1" /db_xref="G1:21961225"
                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:24899 IMAGE:4780455"
/tissue_type="Skin, normal"
/clone_lib="Nul_CGAP_Skn3"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.8%; Score 120; DB 9; I
ilarity 100.0%; Pred. No. 2.7e-54;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="vector: pcmv-sPORT6.ccdb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC016332.1 GI:16740953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63. .791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
hes 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC016332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT · 12
BC016332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'BC034528 1319 bp mRNA linear PRI 26-JUL-2002 Homo sapiens, Similar to serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8, clone MGC:24899 IMAGE:4780455, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G., Zhou W., Bi J., Zhang Y., Liu M., He F.; Functional prediction of the coding sequences of 32 new genes deduced by analysis of cDNA clones from human fetal liver"; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 1319)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (24-JUL-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ueme collection (MGC), cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G., Zhou W. Bi J., Zhang Y., Liu M., He F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: MGC help desk main: Separation of the MGD and the MGD and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Collection (MGC), Cancer Genomics Office, National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-DEC-1998) to the EMBL/GenBank/DDBJ databases.
Department of Experimental Hematology, Institute of Radiation
Beijing Taiping Road 27, Beijing 100850, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1298 BP; 484 A; 253 C; 220 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.8%; Score 120; DB 17;
100.0%; Pred. No. 2.7e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"/clone="FLB4701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/note="HQ1219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family-"Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC034528.1 GI:21961224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete cds.
BC034528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ношо
```

Best Loca Matches

g ò g

ô

LOCUS DEFINITION

RESULT 11 BC034528

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

REMARK COMMENT

REFERENCE

ö

Gaps

ö

Indels

```
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC032462
BC032462.1 GI:21595557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 1493)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.(
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               .766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383
                                                                          π.
Ж
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human ,
                                                                                                                                                                                                                                SOUTHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
BC032462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov SALISS: IRAL Plates 32 Row: b Collumn: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="ubiquitin-conjugating enzyme E2 variant 2"
/protein_id="AAH16332.1"
/db_xxef="G1:16740954"
/tanslation="MAVSTRYVEDEDEEGGKGVGDGTVSWGLEDDEDWTLT
/translation="MAVSTRYVEGERYPERPEREEGGKGVGDGTVSWGLEDDEDWTLT
RWTGMIIGPPRTVYENIYSLKVEGERYPERPERPESPSVREVTKINMNGINNSSGMVDARS
IPVLAKWQNSYSIKVVLQELRRIMMSKENMKLPQPPEGQTYNN"
179 c 271 g 346 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC006018 11near ROD 07-AUG-2002
Mus musculus, MyoD family inhibitor, clone MGC:5939 IMAGE:3488088,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
1 (bases 1 to 1462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                     //organism="Homo sapiens"
/db_xref="LocusID:7336"
/db_xref="tocusID:7336"
/db_xref="tocusID:7336"
/clone="MGC:23763 IMAGE:4109228"
/tissue_type="Bone marrow, acute myelogenous leukemia"
/clone_lbb="MIH_MGC_55"
                                                                Mark Ketteman, Anuradha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                     and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 120; DB 9; Length 100 Pred. No. 2.7e-54;
DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact. amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Keti Madan, Stephanle Rodrigues, Amy Sanchez and Mich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8%; Sco. 100.0%; Pred. No. 4... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pDNR-LIB
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA, complete cds.
BC006018
BC006018.1 GI:13543726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Lou. Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     .484
                                                                                                                                                                                                                                                         1. .1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
BC006018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
```

g ò a

```
1. .1462, "Organism="Mus musculus" "Abd_xref="texon:10090" "Abd_xref="texon:10090" "Amap="C57BL/G1" "Amap="C57BL/G1" "Amap="C57BL/G1" "Amamary Lumor. WAP-TGF alpha model. 7 months old, gross tissue." "Alab_host="Bh10B" "Alab_host="Bh10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="Locusid:17140"
//db_xref="Locusid:17140"
//translation="MSQVSGQCPSRCDAPHGVPSAALDPAQTMSLLPGLEVARSTHPV
EASSEEGFPERAAPSHPHDSGLRAQQALNSIDLDVPTEAVTCOPQGNPQGCTPLLPNG
SSHDHLSPEGSAGHAGGSKAHRKLQTHPSLGSQAGRKSRGSARSASOVPLQAQ
EDCCVHGILSGLFCEFTLCANILDATGGSCSSEDSCLCCCCGGGECADCDLPCDL
DCGIVDACCESADCLEICMECCGLCFSS"
423 c 407 g 249 t
                                                                                                                                         found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRMX Plate: 7 Row: o Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754665. Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens, hypothetical gene supported by BC017964, clone MGC:40428 IMAGE:5197243, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="MyoD family inhibitor"
/protein_id="AAH06018.1"
/db_xref="GI:13543727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Score 120; DB 10;
100.0%; Pred. No. 2.7e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pcMV-SPORT6"
```

```
Beguin, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559
                                     9250668
                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                          PUBMED
REFERENCE
AUTHORS
                                                                                                                          JOURNAL
JOURNAL
                    MEDLINE
                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                          FEATURES
                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 64 Row: h Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MVRAAVAATKAWLSGGVLRCWEPWGGRGFGIGKSRRPRRQGPGA
GLGGRAQKRSREGRERPPLGAAGLGLVSRPQGARGHPRGKKAPLAARPVTRHARPSQGR
PLVLYLECSGDRGTVLRFQTVPTRFPQKAPPAGWGVVVEAGLSDAEQEVASRISYPFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Neb site: http://www.nisc.nih.gov/
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G., Breen,K., Brikley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brikley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brikley,C.,
Brooks,S.,
Hansen,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskerillo,C., Maskerilan,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Voqt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRT 15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beguin, P., Wang, X., Firsov, D., Puoti, A., Claeys, D.,
Horisberger, J.D. and Geering, K.
The gamma subunit is a specific component of the Na, K-AIPase and
modulates its transport function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subunit of sodium potassium ATPase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Brain, adult, 6 pooled whole brains"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical gene supported by BC017964"
/protein_id="AAH32462.1"
/db_xref="GI:21595558"
  Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XINAKATP 1500 bp mRNA 1:
X.laevis mRNA for Na,K-ATPase gamma subunit.
Y11587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.8%; Score 120; DB 9; I
100.0%; Pred. No. 2.7e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MGC:40428 IMAGE:5197243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note-"Vector: pCMV-SPORT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1493
/organism="Homo sapiens"
/db_xref="LocusID:144714"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y11587.1 GI:2052283
ATPase; gamma subunit;
NA+, K+-ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
XLNAKATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
/db_xref="swiss-prot:013001"
/tanslation="madaQDDMsQMoDKFTYDYETIRRGGLIFAAIAFVVGMLIIFSG
TRRGGRKGLRALIDDM"
1 249 c 260 g 432 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                             Direct Submission
Submitted (26-FEB-1997) P. Beguin, University of Lausanne,
Institute of Pharmacology and Toxicology, Rue du Bugnon 27, 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                 Length 1500;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                              /product="gamma subunit of Na,K-ATPase"
/protein_id="CAA72326.1"
/db_xref="G1:2052284"
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Xenopus laevis"
/db_xref="taxon:8355"
/cell_line="A6"
EMBO J. 16 (14), 4250-4260 (1997)
97392454
                                                                                                                                                                                                                /tissue_type="kidney"
63. 248
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: June 16, 2003, 07:55:55 Job time : 2000.2 secs
                                                                                                                                       Location/Qualifiers
1. .1500
                                                                                                                            Lausanne, Switzerland
                                              (bases 1 to 1500)
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 120; Conserv
```

exp

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Word size Searched:

```
Human secreted pro
Human secreted pro
DNA encoding novel
Human polynucleoti
Human secreted pro
Human secreted pro
                                                                                                                             Mouse neuronal PAS
Human CDNA clone B
Human immune syste
Chemically treated
Human jamune syste
Human gene regulat
Chemically treated
Human gene regulat
Signal transductio
Human chemically p
Human chemically p
Human immune syste
                                                                                                                                                                                                                                                                                                                                       DNA transcription
Human anglogenesis
Human nervous syst
Human ovarian and
                                DNA encoding human
                                                                                                                                                                                                                                                                                                           Chemically pretrea
Human immune syste
                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence #
Human pancreatic r
Genomic sequence #
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human reproductive
Human reproductive
Human immune/haema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 1mmune/haema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                  prostate
                                                                                                                    Human secreted
Mouse neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate expression marker cDNA 58653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                        ABL70561
ABL33356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK78761
AAK79574
AAK81312
                                                                                                                                                                                                                                                             ABK40074
ABL32837
                                                                                                                                                                                                                                                                                          ABL32911
AAS45399
                                                                                                                                                                                                                                                                                                                                                                  ABA17044
                                                                                                                                                                                                                                                                                                                                                                                                          AAD16672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-2000, 2000US-183319P.
16-MAR-2000, 2000US-189862P.
25-MAY-2000, 2000US-207454P.
09-JUN-2000, 2000US-211314P.
18-JUL-2000; 2000US-21907P.
 ABV58662 standard; cDNA; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2002 (first entry)
                          804
1097
1097
1194
1204
1457
1985
2008
2171
6577
6577
                                                                                                                                                                                                                                                                                                      15832
15832
15832
40324
177.8
177.8
177.8
177.8
177.8
177.8
177.8
177.8
177.8
177.8
177.8
177.8
177.8
177.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABV58662
                                                                                                                                                           0 0 0 0 0 0 0 0 0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human scretted pro
Human cDNA encodin
Human polynucleoti
Human anglogenesis
Human prostate exp
Human prostate exp
Human prostate exp
Human prostate exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate exp
Human secreted pro
                                                                               June 16, 2003, 03:58:29; Search time 222.269 Seconds (without alignments) 6849.143 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                     1: /SIDS2/gcgdata/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
4: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
5: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
5: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
6: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
7: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
7: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
7: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
7: /SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
7: /SIDS2/gcgdata/geneseqn-embl/NA1991.DAT:*
7: /SIDS2/gcgdata/geneseqn-embl/NA1992.DAT:*
7: /SIDS2/gcgdata/geneseqn-embl/NA1993.DAT:*
7: /SIDS2/gcgdata/geneseqn-embl/NA1993.DAT:*
7: /SIDS2/gcgdata/geneseq-geneseqn-embl/NA1993.DAT:*
                                                                                                                                          US-10-090-035-1
676
1 acccacgcgtccacgc......aaaaaaaaaaaaaaaa 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                  rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                              2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                       - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV58662
AAC60033
AAS31262
ABQ66586
ABQ67050
ABV5006
ABV58008
ABV58809
                                                                                                                                                                                                   OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2645
2645
6486
439
452
484
516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  &
Query
Match I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.9
17.9
17.9
17.9
17.9
17.8
17.8
```

Database :

MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Score

ě

Result

121 121 121 121 121 120 120

Schlegel R, Endege WO, Monahan JE;

Komatsoulis G;

```
Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS31262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS31262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antilafective; gynaecological; antibacterial; neural disorder; cancer; immune disease; reproductive disorder; proliferative disorder; gastrointestinal disease; wound healing; infectious disease;
                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                            (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                    (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                  Sequence 381 BP; 196 A; 70 C; 49 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 23;
Pred. No. 3.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                        17.9%; scot.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein gene 9 SEQ ID NO:19.
                                                                                               Claim 1; Page 11255; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC60033 standard; cDNA; 1119 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0125359.
99US-0168664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2000; 2000WO-US06824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 121; Conservative
                                                                                                                                                                           (a) assessing whether(b) monitoring the pr(c) assessing the effcancer in a patient;
       WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200056766-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                      In a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC60033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288
                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                            batient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC60033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
```

ద

ò

g ò g

ò

٨

```
The polynucleotide sequences given in AAC60025-C60071 encode the human secreted proteins represented in AAB34854-B34900. Sequences AAB34901-B34976 are fragments of proteins encoded by the genes, and also proteins with which they share sequence homology. The proteins have cartivities based on the tissues in which their encoding genes are activities based on the tissues in which their encoding genes are activities based. Examples of the proteins activities include: neuroprotective; expressed. Examples of the proteins activity; nephrotropic; vulnerary; general gastrointestinal activity; nephrotropic; antiinfective; gynaecological; and antibacterial. The human secreted proteins, polynucleotides, antagonists and antagonists of the invention can be useful in treating, preventing and/or diagnosing various discorders and conditions such as neural, immune, miscular, reproductive discorders and conditions will assume the course of the course of the sequences AAC60016-C60024 and AAB34853 are used in the course of the protein and characterisation of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted extracellular matrix protein; ss; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial, ophthalmic; cytostatic; antialzhelmers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA encoding a novel extracellular matrix protein, Seq ID No 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                        Human secreted proteins and gene sequences encoding them, useful for detection, prevention, and treatment of various disorders such as cancer and immune system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1119 BP; 448 A; 141 C; 182 G; 348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 17.9%; Score 121; DB 21; Local Similarity 100.0%; Pred. No. 2.2e-28; nes 121; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                Claim 1; Page 355; 442pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS31262 standard; cDNA; 2645 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and nucleotide sequences.
WPI; 2000-594574/56.
P-PSDB; AAB34862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1114 A 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         676 A 676
```

ö

615

```
Ruben SM;
                                                                                        20000S-0241786
20000S-0241787
20000S-0241809
20000S-0241809
20000S-0244617
20000S-0246474
20000S-0246474
20000S-0246477
20000S-0246477
20000S-0246477
20000S-0246477
20000S-0246524
20000S-0246527
20000S-0246526
20000S-0246526
                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
                                  2000US - 0179065
2000US - 0186628
2000US - 0186364
2000US - 0186350
2000US - 0198174
2000US - 0198123
2000US - 029467
2000US - 0219467
2000US - 021486
2000US - 021487
2000US - 021487
2000US - 021487
                      17-JAN-2001; 2001WO-US01348
WO200155368-A1.
                                                                                                                                                                                                                                                               -SEP-2000;
           02-AUG-2001
```

2000US-217496P

```
17-JAN-2001; 2001US-0764870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0-0CT-2000
            11-APR-2002
ovel human secreted extracellular matrix proteins (SPS). The condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPS. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression. The polynucleotides may be administered to down regulate expression. The polynucleotides may be administered to down regulate expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPS may also be used as antigens to produce antibodies and to identify modulators (agonists and antegonists) of the SPS. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPS in samples. The disorders include for example: Immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rhemmatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. malanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) ardio-(*Cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fung and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antibucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                     proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                      Nucleic acid molecules encoding human secreted extracellular matrix
                                                                                                                                                                              invention relates to isolated nucleic acid molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.9%; Score 121; DB 22;
100.0%; Pred. No. 1.7e-28;
tive 0; Mismatches 0;
                                                                                                                                             Claim 1; SEQ ID No 76; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ66586 standard; cDNA; 2645 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.9°
Best Local Similarity 100°
Matches 121; Conservative
                        WPI; 2001-465572/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002042386-A1.
                                      P-PSDB; AAU19691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2642 A 2642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    676 A 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ66586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ66586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
```

```
The invention relates to novel genes (ABO66521-ABO66785) and proteins (ABP47846-ABP48110) useful for preventing, treating or ameliorating
                                                                                                                                                                                                                                                                New nucleic acid encoding human proteins, useful for diagnosis, treatment and prevention of e.g. osteoporosis, also related polypeptides and antibodies
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 76; 235pp + Sequence Listing; English.
                                                                                                                      Barash SC
                                                                                                                      Rosen CA, Ruben SM,
                                                                                                                                                                                WPI; 2002-470713/50
P-PSDB; ABP47911.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
```

S

```
RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV50206
           *888888888888888888
                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                              615
medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, annibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastroolitestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. addison's disease, allergies, autoimmune themolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sciences, rheumatoid arthritis and ulcerative collis; (c) cardiovascular disorders such as myocardial ischemens; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; anglogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antitheumatic; antiathritic; antidiabetic; antipsoriatic; antiathritic; antidiabetic; antipsoriatic;
                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequata.uspto.gov/sequence.html?DocID=999909764870.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anglogenesis associated genes, useful for determining methylation status, e.g. in dlagnosis or treatment of cancer
                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                       Length 2645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human angiogenesis associated polynucleotide SEQ ID NO 80.
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                          Sequence 2645 BP; 827 A; 506 C; 513 G; 799 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 80; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid fragments from chemically treated
                                                                                                                                                                                                                                  Query Match 17.9%; Score 121; DB 24; Best Local Similarity 100.0%; Pred. No. 1.7e-28; Matches 121; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
ABQ67050/c
ID ABQ67050 standard; DNA; 6486 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2001; 2001WO-EP14320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2000; 2000DE-1061338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                 and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-500450/53.
                                                                                                                                                                                                                                                                                                                                                                                                       2642 A 2642
                                                                                                                                                                                                                                                                                                                                                                                676 A 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200246454-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schacht 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ67050;
     8288888888888888888888888
                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   675
The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences, are used to evaluate their methylation status and/or elated oligomers, are used to evaluate the methylation status and/or diagnosis and treatment of eye diseases, proliferative retinopathy, necowascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by necowascularisation, site as and crown's disease. Inflammatory bowel diseases, ulcers and crown's disease. The sequence data for this patent did not form part of the printed section, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; carcinogen; pharmacodyanamic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                      Length 6486;
                                                                                                                                                                                                                                                                                                                                       Sequence 6486 BP; 1713 A; 176 C; 1443 G; 3154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                    17.9%; Score 121; DB 24;
100.0%; Pred. No. 1.3e-28;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 50197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 9776; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABV50206 standard; cDNA; 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-183319P.
2000US-189862P.
2000US-207454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.9 Best Local Similarity 100. Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer;
pharmacogenomic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3363 A 3363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           676 A 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L6-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV50206;
```

us-10-090-035-1.rng

```
a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                             cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-2000;
16-MAR-2000;
                                                                                  in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                 ABV58008
                                                                                                                                                                                                                                                                                                                                                                                       ABV58008;
                                                                                                                                            patient;
                                                                                                                                                                                                                                                                                                                                            ABV58008
                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                           g
       5555555555555555<del>X</del>8
                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                              ð
     The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                      9/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; ss.
                                                                                                                   selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastassized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for detecting presence of prostate cancer, stage of prostate cancer

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                       Length 439;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                   Sequence 439 BP; 179 A; 117 C; 69 G; 69 T; 5 other;
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                      tch al Similarity 100.0%; Pred. No. 6.1e-28; 120; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 59273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 11362; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                           ABV59282 standard; cDNA; 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L7-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 ABV59282;
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                    557
                                                                                                                                                                      patient
                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                Matches
                                                                                                                        (e)
(t)
                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                   ABV5928.
                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                    g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
                                                                                                                                                                                                                                                                                                                                                                                                                             616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                     (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                   17.8%; Score 120; DB 23; Length 452;
                                                                                                                                                                                                                                                                                                                      Query Match 17.8%; Score 120; DB 23; Leuyun Best Local Similarity 100.0%; Pred. No. 6e-28; Matches 120; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             Sequence 452 BP; 199 A; 91 C; 72 G; 89 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 57999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 11145; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; cDNA; 484 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
```

```
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                             17-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
                                                                                                                                                      Best Local Simi
Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2001
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Ношо
                                                                                                                                                                                                                                                                                RESULT 1(ABV56624
       8888888888888888
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                               셤
                                                                                                                                                                                    à
                                                                                                                                                                                   ö
                                                                                                                                                                                                                                         616
                                                                                                                                                                                                              comprising
                                                                  cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
(a) assessing whether a patient is affilted with prostate cancer in a patient;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
(d) assessing the efficacy of a therapy for inhibiting prostate
                                                in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                 Gaps
                                                                                                              [1] is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule (I) comp a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
                                                                                                                                                                                  ö
                                                                                                                                                             Length 484;
                                                                                                                                                                                 0; Indels
                                                                                                                                      Sequence 484 BP; 230 A; 97 C; 82 G; 74 T; 1 other;
                                                                                                                                                          17.8%; Score 120; DB 23;
100.0%; Pred. No. 5.9e-28;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 55880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 10790; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monahan
                                                                                                                                                                                                                                                                                                                 ABV55889 standard; cDNA; 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-183319P.
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                           17-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2001.
                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                      ABV55889;
                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                             RESULT 9
ABV55889
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                   à
                                                                                                                                                                                                                                          ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                          (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tate of
useful
(c) assessing the eliteacy of a therapy for inhibiting prostate cancer (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; a composition for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer
                                                                                                                                                                                                                                                        (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                               17.8%; Score 120; DB 23; Length 516; 100.0%; Pred. No. 5.8e-28; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                       Sequence 516 BP; 239 A; 93 C; 91 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 56615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 10918; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-189862P.
2000US-207454P.
2000US-211314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABV56624 standard; cDNA; 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-183319P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200160860-A2.
```

```
selecting a composition for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001.
                                                                                                                                                                                                                                                                                            04-DEC-2001
                                          patient;
                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                8888888
                                                                                                                                                          g
                                                                                                                                                                               à
                                                                                                                                                                                                  셤
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising
                                                                                                                                                                       9/9
                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                     selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprisi a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
    assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                           Gaps
                                                                            (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                       ö
                                                                                                                    Length 544;
                                                                                                                                       0; Indels
                                                                                                Sequence 544 BP; 220 A; 141 C; 97 G; 84 T; 2 other;
                                                                                                                     Score 120; DB 23;
Pred. No. 5.7e-28;
                                                                                                             17.8%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 11260-11261; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                        Human prostate expression marker cDNA 58681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monahan JE;
                                                                                                                                                                                                                                                                            ABV58690 standard; cDNA; 579 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-183319P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-189862P.
2000US-207454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-255281P
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endege WO,
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2000;
                  in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlegel R,
                                                                                                                                                                                                                                                                                                                     13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2001
                                                                                                                                         120;
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                 ABV58690
                                                                      patient
                                                                                                                                Best Loca
                                                                                                                                                                                                                                                        RESULT 11
ABV58690
                                                                                                                                                                                                                                                                                       8888888888
                                                                                                                                                                                 g
                                                                                                                                                                                                      ò
```

```
The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used the prevention, treatment and diagnosis of diseases associated with imappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                      616
                                                                                                                                                                                                                                                                                                                                                                                                                                                              assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; arthinicrobial, ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder;
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                              1) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                              17.8%; Score 120; DB 23; Length 579; 100.0%; Pred. No. 5.6e-28; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                             Sequence 579 BP; 269 A; 106 C; 82 G; 121 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding human secreted protein, Seq ID No 107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      claim 1; SEQ ID No 107; 753pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS33148 standard; cDNA; 804 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombosis; wound healing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001WO-US01347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-2000; 2000US-0179065.
                                                                                                                                                                                                                                                                                             17.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                         Query Match 17.8 Best Local Similarity 100. Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-451931/48.
P-PSDB; AAU20439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155326-A2
```

us-10-090-035-1.rng

17-OCT-2000; 2000WO-US28664

10-MAY-2001

```
creations and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) antibodies in samples (e.g. by enzyme linked immune/autofimmune diseases (e.g. fir) the classical control of the ceangle: immune/autofimmune diseases (e.g. HIV). The chuman immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease, neurological diseases (e.g. Alzheimer's disease, cardio-' carbovascular disorders (e.g. cardiac arrest, tachycardia, cangina and thrombosis), infections caused by bacterial, viruses and fungi and ocular disorders (e.g. cardiac arrest, tachycardia, agoniats, antagonists and antibodies can also be used to promote wound of primary tissues. AAS33043-AAS33046 represent human secreted protein coding sequences, PCR Primers, and related sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein-encoding gene 11 cDNA clone HCNDV12, SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; dimune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzhehamer's disease; skinflammation; disease; cognitive disorder; schizophrenia; asthma; skinfloyder; psorlasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; mgiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; thection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.8%; Score 120; DB 22; Length 804; 100.0%; Pred. No. 5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human secreted protein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 804 BP; 286 A; 167 C; 208 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding partner identification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD08201 standard; cDNA; 1097 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193..378
/*tag- a
/product- '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD08201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
    $$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
AMON8191-AAD08213 represent CDNAS corresponding to 19 human secreted protein genes, and AAE03764-AAE03786 represent the proteins they encode. Drotein genes, and AAE03764-AAE03786 represent the proteins they encode. C AAE03787-AAE03800 represent human secreted proteins they encode. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted protein in a sample or by determining the mutations in the new genes. Specific uses are described for each of the 19 genes, based on the tissues in which they are most highly expressed, or and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental aborders, neurological disorders (e.g., Theumatoid arthritis), inflammation, altergaes, neurological disorders, diseases of the immune system, altergaes, neurological disorders, genging dusorders, and infections, psorlasis), sepals, diabetes, atherosclerosis, cardiovascular disorders, pregnancy-related disorders, and infections. The proteins can also be used to all wound the aling and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting culture of primmary tissues, to regenerate tissues, to identify their connate ingands or binding partners, and in chemotaxis, and can be used to as a food additive or preservative to modify storage properties.

C and indians specific for a protein of the invention and each of allowed and allowed a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        919
                                                                                                                                                                                       Baker K, Ebner R;
D, Young PE, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                          Novel human secreted proteins and nucleic acids for diagnosing, preventing and treating neurological, cardiovascular, infectious, autoimmune, gastrointestinal, bone disorders, cancer, particularly ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 120; DB 22; Length 1097;
Pred. No. 4.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1097 BP; 458 A; 182 C; 231 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                   ur DW, Olsen HS, Bak
Ruben SM, Duan RD,
, Soppet DR, Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted protein-encoding cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Sco...
100.0%; Pred. No....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 380-381; 421pp; English.
                                                                                                                                                                                       Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD05430 standard; cDNA; 1097 BP
                                                                                                                                                                                                    Rosen CA, Ru
e CE, N1 J,
                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                             99US-0163085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.8%
Best Local Similarity 100.0
Matches 120; Conservative
                                                                                                                                                                                                                            Moore PA, Birse CE,
                                                                                                                                                                                                                                                                WPI; 2001-328782/34.
P-PSDB; AAE03774.
                                                                                                                                                                                     Wei P,
                                                                             02-NOV-1999;
                                                                                                     17-DEC-1999;
                                                                                                                                                                                   Fiscella M,
                                                                                                                                                                                                      Komatsoul1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AAD05430
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SX S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

AAD05430;

/product = "Mature human secreted protein"

WO200132837-A1

/\*tag= b 265..375

sig\_peptide mat\_peptide ö

0; Gaps

Length 1097; Indels 9/9

```
Claim 1; Page 446; 535pp; English.
                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                             01-NOV-2000; 2000WO-US30037.
                                                                                                                    05-NOV-1999; 99US-0163577.
30-JUN-2000; 2000US-0215137.
  17-JUL-2001 (first entry)
                                                                     /*tag=
                                                                                      /*tag=
                                                                                                                                           WPI; 2001-316490/33.
                                                                                                                                               P-PSDB; AAE01587
                                                                                                WO200134623-A1
                                                        Homo sapiens
                                                                                                      17-MAY-2001
                                                                            sig_peptide
                                                                                  mat_peptide
                                                                                                                                     Ruben SM,
```

```
as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic Immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding CDNA of the invention.
cognate ligands or binding partners, and in chemotaxis, and can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemla; anglogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemla; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel central nervous system protein #76.
                                                                                                                                                                                                                     Sequence 1097 BP; 458 A; 182 C; 231 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                      17.8%; Score 120; DB 22;
100.0%; Pred. No. 4.5e-28;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK43496 standard; cDNA; 1194 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001; 2001WO-US01332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180628
2000US-0184664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0190076
2000US-0198123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0205515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0214886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0215135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0217496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0216647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0217487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                    Matches 120; Conservative
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200155318-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .9-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK43496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK43496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88888888888
                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the protein transments or variants. AAE016131-AAE01660 represent human secreted proteins transments or variants. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their aswaple or by determining the presence of amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the protein and developing products for the diagnosis or treatment of the protein proliferative disorders, diseases of the immune system, proliferative disorders, the diagnosis or treatment of allerydes, neurological disorders, diseases of the immune system, allerydes, neurological disorders, schizophrenia, asthma, allerydes, neurological disorders, schizophrenia, asthma, skin disorders (e.g., psorialsis), sepsis, diabetes, atheroscierorsis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to ald wound the health organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their
                                                                                        Human secreted protein-encoding gene 7 cDNA clone HCNDV12, SEQ ID NO:52.
                                                                                                                                                 Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; haematopoietic disorder; immune system disorder; developmental abnormality; haematopoietic disorder; inflammation; allorgy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; Alzheimer's athma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; pregnancy-related disorder; call culture; chemotaxis; food additive; gene therapy; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 29 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product= "Human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Komatsoulis GA, Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
193..378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193..264
/*tag= b
265..375
```

2000US-0224519 2000US-0225213

14-AUG-2000; 14-AUG-2000;

\*

```
0000US-0236369
                                                                                                                             000US-0237038
                                                                                                                                                                           2000US-0246523
                           22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
```

08 - NOV - 2000) 17 - NOV - 2000) 17 - NOV - 2000) 17 - NOV - 2000) 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-JAN-2001; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 06-DEC-2000; 08-DEC-2000; 17-NOV-2000; -DEC-2000; 17-NOV-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000 08-DEC-2000 11-DEC-2000 

Rosen CA, Barash SC, Ruben SM; (HUMA-) HUMAN GENOME SCI INC

WPI; 2001-581633/65. P-PSDB; AAU87166.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 1; SEQ ID No 86; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. cardiac immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. daphagia, cancer immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. disorders e.g. disorders e.g. disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial

CC infarct. CC epithell CC primary CC primary CC polypep CC increass Cuery Match Best Local Matches II Oy 555 CO Db 1077 CO DD 1133	infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,	Query Match 17.8%; Score 120; DB 23; Length 1194; Best Local Similarity 100.0%; Pred. No. 4.4e-28; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	557 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	617 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
infarctio epithelia maintain primary t polypepti increase Duery Match Best Local S Watches 120 1070 1070	n. The post cell post cell post cell post cell post cell post cell cell cell cell cell cell cell cel	imilarit ; Conse	TCAAAAAA 	AAAAAAA              AAAAAAAA
A A A A A A A A A A A A A A A A A A A	infarctio epithelia maintain primary t polypepti	ery Match st Local S tches 120	1070	617
	888888	On Bee	oy og	oy d

Search completed: June 16, 2003, 06:54:02 Job time: 230.769 secs

Sequence 24, Appl Patent No. 5168051 Sequence 5, Appl1 Sequence 23, Appl

Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 42, Sequence 19, Sequence 9, A Sequence 9, A Sequence 9, A Sequence 10, Sequence 10, Sequence 10,

us-10-090-035-1.rni

```
CURRATION G SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ACLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36.627
REFERENCE/DOCKET NUMBER: 10.50.126
TELECOMMUNICATION: (415) 343-4341
TELEFONE: (415) 343-4341
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                APPLICANT: MCKAIGHt, Steven L.
APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8%; Score 120; DB 2; 100.0%; Pred. No. 1.8e-35; ive 0; Mismatches 0;
US-09-602-877A-95
US-08-811-994-64
US-08-817-459-1
US-08-555-678-1
US-08-555-678-1
US-08-655-678-1
US-08-678-1
US-08-678-1
US-08-678-1
US-08-678-1
US-09-678-1
US-09-678-1
US-09-678-1
US-09-678-1
US-09-678-1
US-09-678-1
US-09-678-1
US-08-678-1
US-08-678-1
US-09-678-1
US-08-678-1
US-08-678-1
US-08-678-1
                                                                                                                                                                                  US-09-372-422A-23
                                                                                                                                                                        US-08-971-089-5
                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                             5168051-9
                                                                                                                                                                                                                                                                  Sequence 2, Application US/08785310A Patent No. 5840532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2082 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                          CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
2IP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 120; Conservative
                                 6671
6671
6671
98
1454
1117
2806
1582
1582
1582
2323
22671
1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linea
 TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11r
MOLECULE TYPE:
                                                                                                                                                                                                                                                         US-08-785-310A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-785-310A-2
  Query Match
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                             June 16, 2003, 06:35:31; Search time 47.0496 Seconds (Without alignments) 4406.275 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appl
Applil
Applil
Applil
Applil
Applil
Applil
Applil
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2
Sequence 6
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                 882724
                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-785-310A-2
US-09-370-838-151
US-08-702-344-26
US-08-628-417-6
US-09-245-041-10
US-09-245-041-10
US-09-014-969-14
US-09-014-969-14
US-09-014-380-14
US-09-073-569-1
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-363-708-3
US-09-463-238-3
US-09-297-535-23
US-09-297-535-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-243-560B-1
                                                                                                                                                                                  441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                                                                                                                    OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                        Issued_Patents_NA:*
                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1813
2269
2269
2246
2634
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match 1
                                                                                                                                                                                                        0
                                                                                                         Title:
Perfect score:
                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Word size :
                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                               Sedneuce:
                                                                                                                                                                                   Searched:
                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   è
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 0
```

ö

0; Gaps

Length 2082; 0; Indels

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
APPLICANT: Racle, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, VIKKI
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: BROODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                          Sequence 15.1, Application US/09370838

Sequence 15.1, Application US/09370838

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: Serist, Heather Roadoh
APPLICANT: Serist, Heather Son THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS FOR THERR USE
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475c1
CURRENT APPLICATION NUMBER: US/09/370.838
CURRENT FILING DATE: 1999-08-09
EARLIER PILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 151
LENGTH: 3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 17.6%; Score 119; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.8e-35;
Matches 119; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/702,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/08702344 Patent No. 5723315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02140
                                                                                                                   US-09-370-838-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-702-344-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                 g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.5%; Score 118; DB 1; Length 240; 100.0%; Pred. No. 1.5e-34;
                                                                                                                                                                                                                                                                   Length 144;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08628417
Patent No. 5627054
GENERAL INEORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
TUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL ADDRESSEE: DEFENSE COMMAND STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC) CITY: ABREDEN PROVING GROUND STATE: MARYLAND
                                                                                                                                                                                                                                                                       17.5%; Score 118; DB 1; 1 100.0%; Pred. No. 1.7e-34;
                                                                                                                                                                                                                                                                                     100.0%; Pred. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERNCE/DOCKET NUMBER: DAM 398-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: oligodeoxynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,72,
TELECOMMUNICATION INFORMATION
TELEPHONE: (617), 498-8224
                                                     TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   LENGTH: 144 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLLGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                           Query Match 17.5
Best Local Similarity 100.
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 21010-5423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE:
US-08-628-417-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                      US-08-702-344-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-628-417-6
                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                           δ
```

ö

```
APPLICANT: Zlanghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CLOOIISICIP CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2011-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1.
                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LaValile, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Racie, Lisa A.
APPLICANT: Arbery David
APPLICANT: Spauding, Vikxi
APPLICANT: Spauding, Vikxi
APPLICANT: Spauding, Vikxi
APPLICANT: Spauding, Vikxi
APPLICANT: Roselino, Michael J.
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%; Score 118; DB 4;
100.0%; Pred. No. 9.9e-35;
tive 0; Mismatches 0;
                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
                                                                                                                                                                                                                                                   Sequence 1, Application US/09797906
Patent No. 6329188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.(
Matches 118; Conservative
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 87 Cambraction
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
               Matches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: M
                                                                                                                                                                                                                                  US-09-797-906-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-797-906-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                   à
                                                                               g
                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY FILE REFERENCE: 7853-136 CURRENT APPLICATION NUMBER: US/09/245,041 CURRENT FILING DATE: 1999-02-05 EARLIER FILING DATE: 1999-07-21 EARLIER FILING DATE: 1998-07-21 EARLIER FILING DATE: 1998-10-20 NUMBER OF SEQ ID NOS: 131 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10 LENGTH: 1051
                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.5%; Score 118; DB 4; Length 1051; 100.0%; Pred. No. 1.1e-34; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1447;
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/09443041A
Sequence 27, Application US/09443041A
Sequence 27, Application US/09443041A
SEQUENCE 27, Application Sequence 27, APPLICANT: Rafalski, Antoni
APPLICANT: Selen, Senoi Mederi 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR APPLICATION NUMBER: 60/109,283
SOFTWARE: Microsoft Office 97
SEQ ID NO. 37
SEQ ID NO. 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 118; DB 4;
Pred. No. 1e-34;
     0; Mismatches
                                                                                                                                                                                                                                       Sequence 10, Application US/09245041 Patent No. 6274339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%; S
100.0%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus US-09-245-041-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Glycine max
.US-09-443-041A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           APPLICANT: MOORE, K. APPLICANT: Nagle, D.
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                    US-09-245-041-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-443-041A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Simi
Matches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                     ð
                                                                        g
                                                                                                                                          a
                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

ö

```
Length 117;
          APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 5356
CLASSIFICATION: 5356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.3%; Score 117; DB 1; Best Local Similarity 100.0%; Pred. No. 4.1e-34; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09073569; Patent No. 6084088; GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Grossmann, Angelika; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS; NUMBER OF SEQUENCES: 15
CORRESPONDENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: TymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                          NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-824
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGHH: 117 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
Merberg, David
                                                                                                                                                                      CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-702-344-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-073-569-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09817180
Patent No. 6340584
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01183
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                     0; Indels '0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.5%; Score 118; DB 4; Length 2674; 100.0%; Pred. No. 9.1e-35; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   Length 2447;
                                                                                                                                                                                                                                                                                                                                               Query Match
17.5%; Score 118; DB 2; I
Best Local Similarity 100.0%; Pred. No. 9.3e-35;
Matches 118; Conservative 0; Mismatches 0;
        APPLICATION NUMBER: US/09/014,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08702344; Patent No. 5723315
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
                                                          ATTORNEY AGENT INFORMATION:
NAME: Spruger, Sizanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPHONE: (617) 898-8284
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.5 Best Local Similarity 100. Matches 118; Conservative
                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-014-969-14
                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-702-344-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-817-180-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-817-180-1
```

g δ

셤 Š 0; Gaps

us-10-090-035-1.rni

```
Sequence 1, Application US/09394645
Patent No. 6380371
               REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
TELEFAX: 206-442-6678
                                                                                                                                                                                                                               ; NAME/KEY: Coding Sequence; LOCATION: 88...1362

; COTHER INFORMATION:
US-09-071-224 -3
                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1813 base pairs
                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: human
US-09-394-645-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-243-560B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-394-645-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                 <del>a</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.3%; Score 117; DB 3; I Best Local Similarity 100.0%; Pred. No. 2.3e-34; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lok, SI
APPLICANT: Lok, SI
APPLICANT: Presnell, Scott R.
APPLICANT: Jeluberg, Anna C.
APPLICANT: Gllbert, Teresa
APPLICANT: Glbert, Teresa
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Zymogenetics
1201 Eastlake Ave East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09071224 Patent No. 6271343 GENERAL INFORMATION:
                                                                    ATTORNEY AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                            HAME/KEY: Coding Sequence Coding Sequence COATION: 34...1344
US-09-073-569-1
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                         TELEFAX: 206-442-6678
     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: 1ine
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-071-224-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
Gaps
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sassetti, Christopher M.
APPLICANT: Sassetti, Christopher M.
APPLICANT: Rosen, Steven R.
TILLE OF INVENTION: Endoglycan: A NOVEL PROTEIN HAVING SELECTIN
TILLE OF INVENTION: LIGAND AND CHEMOKINE PRESENTATION ACTIVITY
FILE REFERENCE: 6510-122US1
CURRENT APPLICATION NUMBER: US/09/394,645
CURRENT FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
      Length 1813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2269;
                                            0; Indels
Query Match
17.2%; Score 116; DB 4; I
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
Matches 116; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/09243560B
; Patent No. 6195882
; GENERAL INFORMATION:
APPLICANT: Sassetti, Christopher M.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.9%; Score 114; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.9%; Score 114; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 114; Conservative 0; Mismatches
```

ö

Φ

```
g
  셤
                                           ö
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2246;
                                                                                                                                                                                                                                                                       Length 2269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.7%; Score 113; DB 4; Length 224 Best Local Similarity 100.0%; Pred. No. 6.1e-33; Matches 113; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Illinois
COUNTRY: United States of America
ZIP: 66060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,708
                                                                                                                                                                                                                                                                         Query Match 16.9%; Score 114; DB 4; Best Local Similarity 100.0%; Pred. No. 2.6e-33; Matches 114; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOVEL SHC BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34451
TELECOMMUNICATION INFORMATION:
TELEPAX: (312) 474-6300
TELEPAX: (312) 474-6300
TELEPAX: (312) 474-6448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FILE REFERENCE: UCAL097US1
CURRENT APPLICATION NUMBER: US/09/243,560B
CURRENT FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: US 60/074,389
PRIOR FILING DATE: 1998-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: CDNA; DESCRIPTION: /desc = "mouse PAL cDNA"; US-09-363-708-3
                                                                                                       NUMBER OF SEQ ID NOS: 10
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09363708 Patent No. 6399747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Schmandt, et al.
TITLE OF INVENTION: NOVEL S
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2246 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-243-560B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illino:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
```

558

δ

Search completed: June 16, 2003, 08:47:01 Job time : 54.0496 secs

```
Sequence 37, Appl Sequence 4765, Ap Sequence 465, Appl Sequence 465, Appl Sequence 212, Appl Sequence 27, Appl Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCGGAGGACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTACTGCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCGGAGGACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACCCACGCGTCCGCCCACGCGTCCGCAGCATCCACAAGCACTTCGAAGGACCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCCCGGCCCAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT SIMMONS, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REPERBENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
FIOR PAPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Score 676; DB 9; Length 676;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 676; Conservative 0; Mismatches 0; Indels
0 US-09-822-849A-37

0 US-09-878-574-4765

US-10-012-822-44

US-10-076-622-465

US-09-551-621-465

0 US-09-825-301-21

0 US-09-825-301-21

0 US-09-825-301-21

0 US-09-825-83A-465

0 US-09-978-84-85

0 US-09-967-867-465

0 US-09-967-867-467

US-09-907-812-12

US-09-907-812-12

US-09-907-841-212

US-10-175-738-27

9 US-10-175-738-27

9 US-10-175-738-27

9 US-10-176-75-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/10090035; Patent No. US20020170089A1
      ) NAME/KEY: CDS
; LOCATION: (89)...(367)
US-10-090-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-10-090-035-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 17, Appli
Sequence 76, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 106, Appl
Sequence 106, Appl
Sequence 109, Appl
Sequence 344, Appl
                                                                                                                               June 16, 2003, 07:57:31; Search time 149.802 Seconds (without alignments) 6534.570 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 US-09-960-332-1058
US-10-091-4873-709
US-10-091-483-344
US-09-764-891-7491
US-09-764-891-9815
US-09-764-81-9815
US-09-760-352-1301
US-09-960-352-6539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 US-10-090-035-1

9 US-10-090-035-3

9 US-10-090-035-5

9 US-10-090-035-9

9 US-10-090-035-17

9 US-10-090-035-17

10 US-09-048-80-76

10 US-09-948-820-38

10 US-09-948-820-38

10 US-09-950-35-1106

10 US-09-560-35-1106

10 US-09-764-891-7491

10 US-09-764-891-7491

10 US-09-764-891-9915

10 US-09-764-891-9915

10 US-09-764-891-9915

10 US-09-764-891-9915

10 US-09-960-352-1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                     1029858 seqs, 724030393 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*
                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                         OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000.0
466.3
466.3
466.3
466.3
227.8
25.0
117.9
117.6
117.6
117.6
117.6
117.6
117.6
                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vord size :
```

Database :

searched:

Run on:

ö

Gaps

9 9

ջ

449

382 389 442

```
CCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTATCTATGTCTGTGGTTGACTGG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGAGGTCCACGAGGCAGGGAGGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGAGGTCCACGAGGCGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGCCGGCTTCGGCCGCCGCCGGCGGCGTCCAGCAGCACGTCCAAGGAAGTTC
                       GAGGAGGICGACACGGICTCACGCGCCGCCGACCACCACCACCACCATGGICACCAC
                                                                          GGCGAGGTCCACGAGGGCGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGG
                                                                                        130 GGCGAGGTCCACGAGCGAGGGAGCTTCCTCGCCAGGGTAACTGAGCCGCCGGGGG
                                                                                                                            TIGIGCAGGGICATCGTACTTGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                Length 577;
                                                                                                                                                                                                                                                                                                                                                             APPLICATE: Simmons, Carl R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE OF INVENTION: Proteins and Uses Thereof CURRENT APPLICATION NUMBER: US/10/090,035 CURRENT FILING DATE: 2002-02-28 PRIOR APPLICATION NUMBER: 60/272,227 PRIOR PILING DATE: 02/28/2001 NUMBER OF SECIED NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 313; DB 9; 1
Pred. No. 9.9e-144;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10090035 Patent No. US20020170089A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.3%;
nilarity 99.4%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (99)...(377)
US-10-090-035-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 463; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 5
LENGTH: 577
                                                                                                                                                                                                                                                                                                                US-10-090-035-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                   443
    210
                            263
                                                    270
                                                                                323
                                                                                                                                 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                    g
                                                                                                                                  ö
                                                                                                                                                         Q
                                                                                                                                                                                    ŏ
                                                                                                                                                                                                          g
                                                                                                                                                                                                                                     ö
                           Q
                                                    g
                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540
                                                                                                                                                                                                                                                                                       900
                                                                                                                                                                                                                                                                                                                                        420
                                                                                                                                                                                                             480
                                                                                                                                                                                      480
      GCACCAATGGGTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 CCGGCCGGCTTCGGCCGCCGCCGCGCGCGCTCCAGCACGTCGTCAAGGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAG
                                                                                                                                                                                                                                      GCACTCAGCTCCTGTACGACAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGT
                                                                                                                                                                                                                                                               481 GCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGT
                                            241 CCACCACCACCATGTTCACACGCGCCCACGGCTTCGTGTGTGCGCGAGACCAGGTCGA
                                                                                                                                               GCCTAACTGAGCCGCCCGGCGCGCCACCACGCCCGTTCGTGCTTGCCTGCGTGCCTT
                                                                                                                                                                                      421 ATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCAC
                               CCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGA
                                                                                                                                     GGCTAACTGAGCCGCCGGCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATE: Simmons, Carl R.

APPLICATE: Simmons, Carl R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible File Reference: 35718/242990

CURRENT APPLICATION NUMBER: US/10/090,035

CURRENT FILING DATE: 2002-02-28

PRIOR PELICATION NUMBER: 60/272,227

PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 313; DB 9; Length 57
Pred. No. 9.9e-144;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10090035 Patent No. US20020170089A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAAAAAAAAAAA 676
                                                                                                                                                                                                                                                                                                                                                                                               661 AAAAAAAAAAAAA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.4%;
Matches 463; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (96)...(374)
US-10-090-035-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-10-090-035-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                       199
                                   241
                                                                                     301
                                                                                                              301
                                                                                                                                       361
                                                                                                                                                                361
                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                           481
                                                                                                                                                                                                                                                                                           541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                          g
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                          ò
                                                                                                                                                                                                               g
                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                           ò
                                                                                     ò
                                                                                                            셤
                                                                                                                               ŏ
         g
                                   ò
                                                         원
```

ö

ö 142

Gaps

ö

202

166 262

106

226 322

```
227 GGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGACATCAACACCTGCACC 286
                                                                                                                                                                                                                                                                                                                                                                               237 ACCACCACCACCACGAGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
                                                                                                                                                                                                                                                                                                                                                          83 GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                  143 CCGGCCGGCTTCGGCCGCCACGGCGCGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 CCGCCGGCTTCGGCCGCCACGCGGCGCGTCCAGCAGCACGTCAAGGAGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 GAGGAGGTCGACACGGTATCACGCGCCGCCGACCACCACCACCACCATGGTCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGGCCACGGCTTCGTGGTGCGCGAACACGGGTCGAGGAGGACATCAACACCTGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 GGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 GGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGCTAACTGAGC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/10090035
Fatent No. US/20020170089A1
GENERAL INFORMATION:
APPLICANT Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
FRIOR PILING DATE: 0.2728/2001
NUMBER OF SEQ ID NOS: 25
SCYTAREE FEASEEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH::524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 524;
                                                                                                                                                                                                                                                                                  Length 529
                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 100.0%; Score 169; DB 9; I Similarity 100.0%; Pred. No. 3.5e-73; 59; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                Score 188; DB 9;
Pred. No. 1.7e-82;
0; Mismatches 2
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - A,T,C or G
                                                                                                                                                                                                                                                                                  27.88;
99.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.39
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (57)...(338)
NAME/KEY: misc_feature
LOCATION: (1)...(524)
OTHER.INFORMATION: n = A
                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (53)...(331)
US-10-090-035-9
                                                                                                                                                                     ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simil
Matches 169; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-090-035-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                        250 ACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGGCTAACTGAGCCGCCCGGCGGCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTTATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 TCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCT 536
   443 TIGIGCAGGGTCATCGTACTIGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATT 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 ACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                       Sequence 7, Application US/10090035
Patent No. US20020170089A1
GENERAL INPORMATION:
TILL INPORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
FILE REFERENCE: 35718/244990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                          Sequence 9, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 261; DB 9; I
Pred. No. 2.9e-118;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.6%;
Best Local Similarity 99.7%;
Matches 311; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGTAATACTAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11111111111
550 TCGTAATACTAA 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (99)...(380)
US-10-090-035-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
                                                                                                                                                                                                                         US-10-090-035-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                 ò
                                                                      ద
                                                                                                            ð
                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

ö

ö

```
2642 A 2642
                                                                                 676 A 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-948-820-38
                                                                                                                                                                             US-09-832-129-21
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                     ò
                                               g
                                                                                 ò
                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGGCGCAGGGAGGCTTCCTCG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 ACCACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG 267
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                ;
0
                                                                                              357 CCAGGGCTAACTGAGCCGCCGGCGGCGGCATCCACGCCCGTTCGTGC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 2645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                  Sequence 75, Application US/10125540
Publication No. US20030059875A1
GENERAL INFORMATION:
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT214C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
PILOT APPLICATION NUMBER: 05.002-04-19
SIGHT APPLICATION NUMBER: 05.002-04-19
SOFTWARE: PATENTIN VOICE: 646
SOFTWARE: PATENTIN VOICE: 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.9%; Score 121; DB 9; 1
Best Local Similarity 100.0%; Pred. No., 9.6e-50;
Matches 121; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 121; DB 10;
Pred. No. 9.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.9%; Scor.
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 76, Application US/09764870
; Patent No. US20020042386Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-764-870-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2642 A 2642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 A 676
                                                                                                                                                                                                                                                                                                                                                                           ID NO 76
ENGTH: 2645
                                                                                                                                                                                         US-10-125-540-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-764-870-76
                                  297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
셤
                                                             셤
                                                                                            ò
                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                919
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. 3.2e-49; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Score 120; DB 9; 100.0%; Pred. No. 3.2e-49;
                                                                                                                                                                                                                            Sequence 21, Application US/09832129

Publication No. US20030027297A1

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: 19 Human secreted proteins

FILE REFERENCE: PZ045P1

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 0CT/US00/28664

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 1999-11-02

PRIOR FILING DATE: 1999-11-02

PRIOR FILING DATE: 1999-11-02

PRIOR FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PATCHIN VET. 2.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/09948820
PUblication No. US20030050460A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: P2034p1
CURRENT APPLICATION NUMBER: US/09/948,820
CURRENT FILING DATE: 2001-09-10
PRIOR PILICATION NUMBER: US/09/55,391
PRIOR PILICATION NUMBER: PCT/US99/26409
PRIOR APPLICATION NUMBER: PCT/US99/26409
PRIOR PILING DATE: 1999-11-09
PRIOR FILING DATE: 1998-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.8%; Score 120; DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-832-129-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-948-820-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
```

ö

```
Query Match
Best Local Similarity 100.(
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo saptens
US-09-764-872-709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo saptens
US-10-091-483-344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-091-483-344/c
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-764-872-709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11058, Application US/09960352
Patent No. US20020137139A1
GENERAL INCORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
                                                                                                                                                                                                            Sequence 106, Application US/10239676

Sequence 106, Application US/10239676

Publication No. US20030082609A1

GENERAL INFORMATION:

APPLICANT: OEEK, Alexander

APPLICANT: DEFENDENCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation

FILE REFERENCE: 2013.1003

CURRENT APPLICATION NUMBER: US/10/239,676

CURRENT FILING DATE: 2002-09:24

PRIOR APPLICATION NUMBER: PCT/EP01/03968

DE 10019173.8

DE 10019173.8

DE 10043826.1

PRIOR FILING DATE: 2001-04-06

2000-04-06

2000-04-06

2000-06-30
                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (2778, 2845..2846, 2865, 2916, 9325, 10589, 10612, 10809, 10817)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: unsure
; LOCATION: (10821, 10827, 10830..10831, 10839, 12552, 13433, 15042)
US-10-239-676-106
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
17.8%; Score 120; DB 9; I
Best Local Similarity 100.0%; Pred. No. 2.5e-49;
Matches 120; Conservative 0; Mismatches 0;
   Mismatches
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 106
LENGTH: 15832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-960-352-11058/c
                                                                                                                                                                                                              US-10-239-676-106/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                       ö
                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                  Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al. TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies CURRENCE: PA125
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
PLIOT APPLICATION data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE REFERENCE: PT21.2C1
CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT TILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 346
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 344
LENGTH: 165
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                Query Match
17.6%; Score 119; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 119; Conservative 0; Mismatches 0;
                                                                                                                                                                                              17.6%; Score 119; DB 10;
100.0%; Pred. No. 1.2e-48;
tive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11058
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 709, Application US/09764872
Publication No. US20030050231A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 344, Application US/10091483 Publication No. US20030049650A1 GENERAL INFORMATION:
```

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                    Sequence 7491, Application US/09764891
Sequence 7491, Application US/09764891
Sequence US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7491
LENGTH: 165
                                     ö
Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.6%; Score 119; DB 9; Length 165; Best Local Similarity 100.0%; Pred. No. 1.2e-48; Matches 119; Conservative 0; Mismatches 0; Indels
Query Match 17.6%; Score 119; DB 9; Length 16: Best Local Similarity 100.0%; Pred. No. 1.2e-48; Matches 119; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-891-7491
                                                                                                                                                                                                                                              US-09-764-891-7491
                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
                                                                                                                                            ð
                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             å
```

Search completed: June 16, 2003, 10:24:24 Job time: 155.802 secs

8 127 120 187 180 244

g à ò g a

ç

a

ò Q ò g ò g ð

å

BASE COUNT ORIGIN

```
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 21726554Dr., Urbana, IL 61801, USA
Email: bohnertlab@life.uluc.edu.
Location/Qualifiers
1. 648
/organism="zea mays"
/db_xref="taxon:4577"
/clone="Inb="Salt stressed Zea mays roots cDNA library"
/fesue_type="Roots"
/dev_atage="2 weeks old"
/note="vector: pBluescript SK+; Stressed 24 hours at 150
mm Nacl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ619318 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6D01_SK.abl Salt stressed Zea mays roots CDNA library Zea mays CDNA clone RNOSEQ6D01_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                               GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 126
                                                                                                                                                                                                                                                                                                     GACACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 119
                                                                                                                                                                                                                                                                                                                                110 GGTGAGGTCGGTCCGGCCCGGCTTCGGCCGCCACGGAGGCGGCGTCCAGCACGT 179
                                                                                                                                                                                                                                                                                                                                                                                               364 TAACTGAGCCGCCCGGCGCGCGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCCTTATG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCGGCGCCCA---ACCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACATCAACACCTGCACCGGCGAGGTCCACGAGGCAGGGAGGCTTCCTCGCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAAT
                                                                                                                                                                                                                                    DB 14; Length 648;
                                                                                                                                                                                                                                / Score 508.6; DB 14; Length
Pred. No. 1.5e-46;
0; Mismatches 14; Indels
                                                                                                                                                                                             100 t
                                                                                                                                                                                            183 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:21621312
                                                                                                                                                                                                                               tch
al Similarity 96.98.7
530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600 AAAAAA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 AAAAAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boduence.
BO619318
BO619318.1
EST.
                                                                                                                                                                                         172 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea
                                                                                                                                                                                                                             Query Match
Best Local S:
Matches 530
                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484
                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
BQ619318
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                ç
                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                   å
                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ619315 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6C06_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6C06_SK.abl similar to No homology, mRNA
                                                                                                                                                                 GGTGAGGTCGGTGGCCCGGCCGGCTTCGGCCGCCACGGCGGCGGCGTCCAGCAGCACGT 186
                                                                                                                                                                                                                   CCACCACCATGGTCACCACGGCGACGGCTTCGTGGTGCGGGAGACCAGGGTCGAGGA 303
                                                                                                                                                                                                                                                                                                                     423
                                                                                                                                                                                                                                                                                                                                                                                                                                                             543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC lade; Pantochdeae; Andropogoneae; Zea.

1 (bases 1 to 648)
Mang.H. and Bohnert, H.J.
Genfomtes of plant stress tolerance
Unpublished (2002)
                                                                                                                                                   GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA
      mays roots cDNA library'
                                                                                                                                                                                                                                                                                                                                                                                                         364 TAACTGAGCCGCCGGCGGCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCCTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                           Stressed 24 hours
                                                                                                                                   <u>ښ</u>
                                                                                                           648;
                                                                                                           Length
                                                                                                    Score 508.6; DB 14; Length
Pred. No. 1.5e-46;
0; Mismatches 14; Indels
/clone_lib="Salt stressed Zea ma
/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+;
                                                                   100
                                                                183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mark Fredricksen
Department of Plant Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:21621309
                                                                                                    75.2%;
ilarity 96.9%;
Conservative
                                                                 193 c
                                                    MM NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111111
AAAAAAA 606
                                                                                               Query Match
Best Local Similarity
Matches 530; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BO619315
BO619315.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
```

604

à

RESULT 2 BQ619315 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

484 480 544

299

363 359 543

mays

483

303

243

Gapa

ë

THIS PAGE BLANK (USPTO)

```
187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                          Best_Local
Matches 53
                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
 LOCUS
                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                  243
                                                                                                                                                                                                                                                                                                                                                                                       483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACC
clade, Panicoldeae, Andropogoneae, 2ea.
                                                                                                                                                                 /clone="RNOSEQGEOI_SK.abl"
/clone_lb="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAAT
                                                                                                                                                                                                                                                                                                  GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCA
                                                                                                                                                                                                                                                                                                                                       CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCCGGCGCCA---ACCACCA
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                         Score 508.6; DB 14; Length 648; Pred. No. 1.5e-46; 0; Mismatches 14; Indels 3;
                         Tanus, I (bases I to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
Illinois
Illinois
Tel: 2172655473
Email: bohnertlabelife.uluc.edu.
Location/Qualifiers
                                                                                                                                                                                                                             100 t
                                                                                                                                               /organism="Zea mays"
/db_xref="taxon:4577"
                                                                                                                                                                                                                             183 g
                                                                                                                                                                                                                                                         75.28;
                                                                                                                                                                                                                              193 c
                                                                                                                                                                                                                                                                    al Similarity 96.9
530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111111
AAAAAAA 606
                                                                                                                                                                                                                                                                                                                                                                                                                    244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                       127
                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                           304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900
                                                                                                                                                                                                                                                                     Local
                                                                                                                                        source
                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                     AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
BQ619337
                              REFERENCE
                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      음
                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g.,
                                                                                                                                                                                                                                                                                                                                                                          ö
```

```
BQ619337 648 bp mRNA linear EST 27-JUN-2002 RNOSEGGE12_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEGGE12_SK.abl similar to No homology, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 GACACACCAAGCGTCGGCACCAATGCCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGICIGITGACIGGITGIGCAGGGICAICGIACTIGGCIATCGIACGIGCACGCA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CICAGCICCIGIACGAAITACGACAAIAAGCICGIGACCIGAAIAAAACTICIICGIAAI 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at 150
                                                                                                                                                                                                                                                                                                 /db_xref="taxon:457"
/db_xref="taxon:457"
/clone="RNOSEQ6E12_SR.abl"
/clone=!RNOSEQ6E12_SR.abl"
/tissue_type="Roots"
/dev_stage="2 weeks old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTTATCACGCGCCGCCGCCCA---ACCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGACATCAACACCTGCACCGGCGAGGTCCACGAGGCGCAGGGAGAGCTTCCTCGCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAACTGAGCCGCCCGGCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCCTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript SR+; Stressed 24 hours mM NaCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 508.6; DB 1
Pred. No. 1.5e-46;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                          Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
1. .648
                                                                                                                                                                                                                                                                                                                                                                                                  183 9
                                                              GI:21621331
                                                                                                                                                                                                                                                                                                                                                                                                                                    75.2%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                   193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                    BQ619337
BQ619337.1
                                                                                                                                                                                                                                                                                                                                                                                                   172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244
```

THIS PAGE BLANK (USPTO)